

Who belongs in the Noble lab?

A lab like ours, which does interdisciplinary research, can be daunting because prospective lab members may be unsure how much specific background in genomics and proteomics on the one hand or computer science and statistics on the other hand is required to be successful here. In practice, our lab has included trainees with diverse backgrounds. Here are some vignettes to give an idea of this breadth.

Graduate students

Robin Aguilar, Genome Sciences — I started my undergraduate degree majoring in Spanish but ended up completing my studies with a major in biochemistry with dual minors in computer science and Spanish. I became interested in computational biology much later during undergrad, and completed internships at Stanford, University of Geneva, and the Genome Sciences Summer Research Program. My previous internships have drawn from a number of interdisciplinary areas including molecular biology and genomics.

Gesine Cauer, Genome Sciences — I went to a small liberal arts college, where I majored in biology with a concentration in scientific computing and minor in psychology. While in college, and for two years afterwards, I primarily did benchwork, and my projects ranged from protein biochemistry to cancer cell signaling. However, because I like developing algorithms and dislike pipetting, I switched to computational biology. I spent another year working on a computational cancer genomics project before starting in GS. There was and still is a learning curve associated with making such a switch, but I'm fortunate to be surrounded by helpful and patient people and it has been well worth the effort.

Kianna Hales, Genome Sciences — I did my undergrad in molecular, cellular and developmental biology and informatics. I have previously worked as a therapy assistant for kids with autism spectrum disorder, as a junior computational biology intern at the Center for Infectious Disease Research, and as an undergraduate computational biology intern at Microsoft Research.

Andy Lin, Genome Sciences — My background is in molecular biology and computational biology and my interests lie in the development of statistically rigorous protocols for use in forensics. My undergraduate degree was in Cell Molecular Biology and Life Sciences Informatics. Following my undergrad degree I went to work at Pacific Northwest National Laboratory for two years prior to joining the GS department. Outside the lab I enjoy volunteering at the zoo and various outdoor activities.

Alan Min, Statistics — I did my undergraduate degree in statistics, where I did some research analyzing images of fluorescent probes for detection of epigenetic markers. I'm currently

working with Bill on research in applying Bayesian topic modeling algorithms to single cell sequencing data, where I'm drawing on a wide range of different experiences!

Jacob Schreiber, Computer Science and Engineering — I started my undergraduate program as a psychology major and ended up getting a degree in biomolecular engineering. Likewise, I started my graduate studies in the computer science department and the eScience institute but, by the end, my research was almost entirely on genomics. Despite my best efforts, I keep being drawn back to computational research in biology, potentially because it allows me to tackle important problems without the challenges of having to talk to other people.

Mu Yang, Biomedical Informatics and Medical Education — My undergraduate major was in public health, and specifically was in the environmental health track. Up until the end of my undergraduate years, my lab experiences were limited to experimental labs, mostly related to the microbiology field. I started joining a computational biology lab in my graduate program, and went on to have a masters degree in bioinformatics.

Postdocs

Giancarlo Bonora — With degrees in computer science and electrical engineering, I initially worked in the exhilarating world of financial information systems, but found myself increasingly drawn to the field of biology. I entered the newly established UCLA Bioinformatics Ph.D. program hoping to combine my computational background with my more recently acquired interest in molecular biology. I was particularly excited about the possibility of applying computational approaches to gain a better understanding of the factors that regulate genes and in turn govern cell identity.

Will Fondrie — I started undergrad as a political science major, but fortunately I ended up studying chemistry instead. As an undergraduate, I performed research in a physical chemistry lab. Although it was a great experience, I wanted to shift to a field related to biology and medicine for graduate school. I did my Ph.D. in molecular medicine, where I trained in mass spectrometry and proteomics. During my Ph.D., I also developed an interest in machine learning. It was the opportunity to combine these interests—machine learning, mass spectrometry, and proteomics—that led me to the Noble lab for my postdoc. I now work on developing machine learning methods to analyze proteomics data and I love it.

Borislav (Bobby) Hristov — I started my undergrad firmly expecting to pursue a pure math major all the way to and through graduate school but I ended up getting a degree in computer science as I liked developing algorithms and building software. My fascination with biological problems and the immense joy I experience of applying the abstract math/machine learning/comp sci techniques to try to solve these problems further bent my academic trajectory towards computational biology. I did my Ph.D in computer science at Princeton working mostly on cancer genomics algorithms and now, at the Noble lab, my research is focused on studying the Plasmodium parasite genome.

Dejun Lin — I worked on protein crystallography as undergrad and I got my bachelor's degree in biological sciences. I did computational chemistry and biophysic research on protein membrane interaction and antimicrobial lipopeptides for my PhD work. I also developed algorithms for high performance computing in chemical physics. I am currently working on applying biophysical principles and computation to genome architecture modeling.

Yang Lu — My background has been quite mixed. My undergraduate degree was software engineering and I received training targeted towards a full-stack software engineer, from low-level embedded system to high-level UI development. My master degree was computer science and I specialized in network sciences. My Ph.D. degree was computational biology and bioinformatics, and I worked on the combination of machine learning and metagenomics. During my Ph.D. training, I have taken very diverse graduate-level courses ranging from computer science, statistics, as well as industrial and systems engineering, so that I have solid knowledge in mathematical modeling and optimization. In addition, I also have rich industrial experiences, as I interned at Microsoft Research, Microsoft Bing, Tencent Research, Ericsson, etc. At Noble lab, I am working partially on computational mass spectrometry, and partially on machine learning interpretation techniques which are applicable to biomedical analysis but designed for general purpose.

Gurkan Yardimci — Despite my early ambitions to study genetics, I majored in Computer Science for my undergraduate studies as my second choice. After graduation, I pursued a master's degree in bioengineering, studying both molecular biology and machine learning for a computational biology specialization. Having combined my “computer skills” with my love of biology, I continued my graduate studies to obtain a PhD degree in computational genomics and gene regulation. For my postdoctoral studies in Noble lab, I built on top of my PhD studies by further focusing on the 3D chromatin organization and its impact on cell biology.

Ran Zhang — I majored in biological sciences in undergrad, where I did wet lab research in a cell biology lab studying autophagy. I entered graduate school with no coding experience, but I found my interest in computational biology during the first year rotation. My Ph.D. work focused on context-specific disease gene prediction, and I'm currently working on single cell data integration in the Noble lab.