

Qualification summary

U.S. Citizen

- Large-scale biological data processing, analysis (genome sequence, population variation, epigenetic/TF ChIP-chip/seq, ATACseq, gene expression RNA-seq/microarrays, microbiome 16S/metagenomics)
- Machine learning, statistics, computational modeling, high-throughput computing, experiment design
- C/C++, Java, R, MATLAB, Python, HTML, Bash, BigQuery, Terraform

Education

- **Massachusetts Institute of Technology** at Cambridge, MA August 2005–February 2012
Ph.D. in Computer Science GPA 5.00 (A = 5.00)
Advisor: Manolis Kellis
Thesis title: Computational Regulatory Genomics: Motifs, Networks, and Dynamics
National Science Foundation Graduate Research Fellow (2005-2008)
- **University of Illinois at Urbana-Champaign** August 2001–May 2005
B.S., M.S. in Computer Science GPA 4.00 (A = 4.00)
Advisors: ChengXiang Zhai, Gene Robinson, Charles Whitfield
Thesis title: Computational Methods for Modeling Eukaryotic Gene Regulation

Research

- **Verily Life Sciences**—Staff Data Scientist October 2021–Present
Verily Life Sciences—Staff Scientist March 2020–October 2021
Verily Life Sciences—Senior Scientist April 2017–March 2020
Verily Life Sciences—Scientist November 2015–April 2017
Google[x]—Quantitative Analyst July 2015–November 2015
Computational Biology Tech Lead. Research, analysis, infrastructure for Immune Profiler, Wastewater projects
- **MIT CSAIL**—Postdoctoral Associate February 2012–July 2015
Designed, analyzed high-throughput enhancer experiments; characterized RNA edited sites across hundreds of individuals, dozens of tissues; predicted links between enhancers and genes; developed model to distinguish individuals from NGS data
- **MIT CSAIL**—Graduate Research Assistant August 2005–February 2012
Developed, applied algorithms to understand regulatory dynamics of regulatory motifs, epigenetic data
NIH consortia member: 12 Drosophila, 29 Mammals, ENCODE, modENCODE, Epigenomics Roadmap, GTEx
- **UIUC Entomology**—Research Assistant February 2003–August 2005
Applied computational methods for microarray and sequence analysis of honey bee and related organisms
- **Argonne National Laboratory**—Research Intern Summer 2003
Designed genetic and statistical algorithms for identifying functional sites in BRCA1 proteins

Teaching

- **Linguam Connect LLC**—Instructor Summer 2014
CCP11/CCP13: Designed and taught online course on JavaScript programming
- **MIT Electrical Engineering and Computer Science**—Graduate Teaching Assistant Fall 2005, Fall 2008
6.095/6.047: Undergraduate/graduate computational biology course; wrote and graded homework and exam problems; led recitation sessions; delivered five guest lectures between 2008-2012
- **UIUC Computer Science**—Graduate Teaching Assistant Spring 2004, Fall 2004, Spring 2005
CS101: Undergraduate introductory computer science course in MATLAB and C; taught two laboratory sections weekly and helped write and grade exam and laboratory problems
Awarded Excellent Teaching Assistant in 2004, Outstanding Teaching Assistant in 2005