

SUMMARY

14 years of experience creating software.

- Backend: Managing and auditing a SQL database with 200 million row tables, tracking 50 petabytes of files.
- Web: Used Vue, GraphQL, and Markdown to create a [website](#) with 2,000 pages and 4,000 visitors per week.
- Biological data science: Created 4 software tools published in peer-reviewed journals.
- Personal projects: Genome visualization, web applications, web analytics, network monitoring, system monitoring, web gaming, web API clients, wifi portal interaction, usage data collection, and more.

TECHNOLOGIES

Linux	Python	Bash	JavaScript	CSS	HTML	Django	Vue	SQL Server	Docker	Node
AWK	Nginx	Jupyter	PostgreSQL	Git	CI/CD	GraphQL	C	Markdown	Java	TLS

EDUCATION

Pennsylvania State University	<i>Ph.D. in Bioinformatics and Genomics</i>	2012– 2020
Georgetown University	<i>B.S. in Biology</i>	2004– 2008

EXPERIENCE | PROFESSIONAL

National Center for Biotechnology Information	<i>Software Engineer</i>	2022 – now
• Led development of a Python system for auditing a SQL Server database tracking 200 million files used by global researchers. Developed a data streaming model which reduced memory usage by 20x. Created a maintainable codebase and an automated testing system to quickly verify correctness. • Solved problems in a Python/Bash/SQL Server system managing 50 petabytes of cloud storage.		

Pennsylvania State University	<i>Computational Scientist 3</i>	2020– 2022
• Used a static site generator based on Vue, GraphQL, and Markdown to write a fast, author-friendly system powering a feature-rich community website with 2,000 pages and 4,000 weekly visitors.		

	<i>Graduate Research Assistant</i>	2012– 2020
• Built a Python pipeline to measure DNA sequencing accuracy in 1.8 terabytes of data (published). • Created a tool for processing high-accuracy sequencing data with Python, C, Bash, AWK (published twice). • Developed a pipeline in Python, Bash, and AWK for detection of length mutations in mitochondria (published). • Created a Python tool for calling DNA mutations (published twice).		

National Institute of Neurological Disorders and Stroke	<i>Summer Internship Program Student</i>	2012, 2013
• Developed a Java web application for DNA analysis and upgraded a Perl tool for finding genetic elements.		

National Institute of Allergy and Infectious Diseases	<i>Postbaccalaureate IRTA Researcher</i>	2008– 2009
• Developed a genetic test for an immune system gene (MHC) in macaque monkeys.		

EXPERIENCE | INDEPENDENT

Developing and maintaining software to solve problems, to learn, and to experiment.

• Wordle solver : Automating a well-defined problem	Django	2022
• Worktime : Personal productivity web app	JavaScript, Django, PostgreSQL	2018 – 2020
• Wikihistory : Web app for visualizing Wikipedia editing activity	Django	2017
• Assemblo : Educational web game about genome assembly	JavaScript, HTML5, CSS	2014 – 2017
• Upmonitor : System for monitoring network connectivity	Python, TLS/HTTP/TCP/ICMP	2013 – 2019
• Wifi-login : Tool for automatically logging in to wifi hotspots	Python, HTTP, Linux	2013 – 2017
• Genome Graphic Generator : Tool for creating art from your genome	Python, Pillow	2013 – 2014
• Traffic Monitor : Web analytics system written from scratch	Django, HTML5, MySQL	2011 – 2022
• Notepad : Web tool for quick, organized note-taking	Django, HTML/CSS, MySQL, Nginx	2011 – 2024