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HUNTING PATHOGENS WITH SOFTWARE

My role on the Bioinformatics team can be very different from project to project, which makes things challenging and interesting. My focus area tends to be microbial pathogen detection, although I have branched out into human health. In the past four years at LLNL, I have helped develop databases with web applications used for sample and results tracking, developed tools in Python and R for various biological applications, searched for antimicrobial resistance and virulence genes in DNA sequence data, and performed modeling to understand the biological factors impacting wound healing. I've been able to work on software engineering, data analysis, and statistical modeling for various bioinformatics projects.

Bioinformatics at Lawrence Livermore is rapidly evolving, as technology like next-generation sequencing brings down the cost of genome sequencing. These advances lead to huge amounts of data while new algorithms in machine learning allow researchers to make sense of large datasets. Advances in high-performance computing make it possible to scale up to the new requirements in memory and speed and undertake critical data analysis.

LLNL is home to cutting-edge projects that span the spectrum of different areas in bioinformatics, including drug discovery, microbial outbreak mutation tracking, pathogen detection, and antimicrobial drug resistance. These projects have real-world impact in the areas of biodefense, environmental sampling, animal health, and human health–including the coronavirus pandemic.



