

Wisconsin builds bioinformatics team to enhance surveillance of infectious diseases using next-generation sequencing data



CONTRIBUTOR: *Abigail Shockey, PhD, Data Scientist, Wisconsin State Laboratory of Hygiene*

CATEGORY: **Epidemiology and Laboratory Capacity (ELC)**

CATEGORY: **Public Health Data Science Workforce**

Wisconsin State Laboratory of Hygiene's bioinformatics team was able to double in size with the use of federal funding. This increased capacity allowed them to improve their computational infrastructure and to develop cloud-based infrastructure. This team supports next-generation sequencing workflows and analyzes these data to inform public health response.

Next-generation sequencing (NGS) is a powerful and rapidly advancing technology that has enhanced public health. NGS allows for the detection of outbreaks and explores how any pathogen spreads, evolves, and/or develops antimicrobial resistance by sequencing and analyzing its genome. Bioinformaticians are highly specialized personnel that have been trained to interpret NGS data and develop new computational tools to analyze it.



The "What"

Prior to the COVID-19 pandemic, the Wisconsin State Laboratory of Hygiene's (WSLH) bioinformatics team had only one full-time bioinformatician and one bioinformatics post-doctoral fellow whose primary focuses were enhancing WSLH's computing infrastructure and analyzing outbreaks of antimicrobial resistant organisms. Using Epidemiology and Laboratory Capacity for the Prevention and Control of Emerging Infectious Diseases (ELC) funding, WSLH was able to hire two full-time bioinformaticians, which allowed WSLH to perform SARS-CoV-2 surveillance and outbreak analysis using NGS data.



More stories are available at stories.cste.org

SUBMITTED JUNE 2023



The “So What”

Expanding its bioinformatics team gave WSLH the personnel capacity necessary to analyze SARS-CoV-2 NGS data. Additionally, these new bioinformaticians improved WSLH’s effort to onboard new computational workflows for analyzing NGS data from other pathogens, including *Streptococcus pneumoniae* and *Candida auris*. These workflows will serve as the foundation for monitoring more pathogens in the future. This includes but is not limited to tuberculosis, enterovirus, and respiratory syncytial virus.

Growing its bioinformatics team also improved WSLH’s computational infrastructure. With more bioinformaticians on staff, WSLH was able to evenly distribute the process of workflow development and data analysis among the bioinformatics team, which resulted in more time available for the development of cloud-based infrastructure where workflows could be executed.



The “Now What”

As described above, monitoring pathogens using NGS allows for detection of outbreaks and exploration of how pathogens spread and evolve. NGS analysis is critical to informing public health response, and its role in public health will only continue to grow as the technology advances. Public health labs need the support of bioinformaticians to interpret NGS data and develop new computational workflows for analyzing it.

In the future, WSLH aims to transition its existing workflows entirely to its cloud-based infrastructure, fully automate them, and develop new workflows to enhance the surveillance of infectious disease. Continued funding beyond COVID-19 is necessary to maintain WSLH’s bioinformatics team with institutional knowledge and accomplish these goals.

Key contributors to this project include Dr. Kelsey Florek, Wisconsin State Laboratory of Hygiene.