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Sonar: A High-Performance Multi-Pathogen Genomic Surveillance System

Inhalt

The COVID-19 pandemic highlighted the critical importance of functional genomic surveillance and rapid outbreak detection. Here, we present Sonar, an open-source, high-performance tool for multi-pathogen genomic surveillance capable of computing, storing and efficiently querying genomic mutations and metadata of millions of samples. The tool consists of the following three main components: a) an intuitive and interactive web application enabling any user to explore genomic data, track pathogen dissemination, and analyze sample characteristics; b) a robust backend architecture designed for systematic storage, annotation, and retrieval of mutations and customizable metadata, scalable to diverse pathogens; c) a versatile command line interface for genomic analysis tasks such as sequence alignment, variant calling, annotation and advanced querying, that integrates seamlessly into subsequent bioinformatics workflows. Sonar has been successfully deployed and validated at the Robert Koch Institute, Germany's public health institution, and applied to various viruses, including SARS-CoV-2, RSV, HIV, Influenza, Ebola, and Dengue. The generic design of Sonar facilitates immediate processing of emerging pathogens, significantly reducing response times. Its flexible structure supports future extension to other zoonotic and environmental pathogens, aligning with the One Health approach to enhance global pandemic preparedness and informed public health decision-making processes.

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Graduate Student

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Yes, I am a Junior Scientist.

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