

INNOVATING CROSS-DOMAIN SOLUTIONS TO DETECT EMERGING BIOLOGICAL THREATS

Characterizing The Bioaerosol Composition Using Metagenomic Sequencing For Environmental Biodetection

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Near real-time hazardous aerosols detector and identifier systems based on genomic signatures may enable early-warning to the presence of a biothreat agent in the environment, potentially reducing the consequences of a biological incident. To date, there have been several studies to characterize the air microbiome in urban environments; however, most of these have been fairly limited in scope whether bound by the number of days sampled or type of sequencing performed. The U.S. Department of Homeland Security (DHS) is currently invested in developing both detectors and identifier systems for aerosolized biothreats. For these systems to perform in both outdoor and indoor operationally relevant environments, they must be able to discriminate between the existing background aerosols and those that represent a hazardous anomaly due to a biological incident. The development of systems capable of discriminating between background aerosols and hazardous aerosols has been a substantial challenge for deployment of detector and identifier systems for DHS applications.

The Hazard Awareness & Characterization Technology Center (HAC-TC) within the DHS Science and Technology Directorate, is working with performers (University of Texas Medical Branch) to characterize the background bioaerosol content of over 800 high volume air filters from over 200 locations through the continental U.S., for application of next-generation sequencing (NGS). The ultimate goal is to understand microbiome trends and differences and enable methodologies for identification of unknown pathogens.

Starting in January 2024, air filters from environmental aerosol sample collectors located in major metropolitan areas, and at select special events, throughout the U.S. were gathered during each of the four seasons and processed for metagenomic sequencing. The resulting raw sequencing data, basecalls, sample metadata, and bioinformatic pipelines for environmental aerosol collectors located throughout the Homeland, will be shared to a public repository. Ongoing artificial intelligence/machine learning (AI/ML) activities by HAC-TC will leverage raw sequence signals to develop models and tools that enable agent-agnostic biothreat detection.

A first of its kind environmental widespread, seasonal metagenomic database will be accessible to the community to inform naturally occurring microbial background markers against which potential anomalies or novel outbreaks can be defined/detected. The ultimate goal is to achieve threat agnostic sentinel surveillance enabled by genus and species identification paired with geolocation.

The publicly available database will provide spatially and temporally comprehensive NGS information that may elucidate technologies capable of identifying anomalies and/or specific characteristics that point to the release of an unknown threat agent.

This activity impacts the defense community by providing the first comprehensive baseline environmental microbial NGS database generated from aerosol sample collectors located throughout the U.S. The publicly available database may be leveraged to inform test and evaluation of informatic pipelines or ML algorithms; and enable the maturation of technology that can detect unknown pathogens, particularly for AI/ML advancements being applied to biodetection in complex backgrounds, prediction of communicable disease spread, or to inform strategic approaches.

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