

INNOVATING CROSS-DOMAIN SOLUTIONS TO DETECT EMERGING BIOLOGICAL THREATS

Secure Bloom-filter Analysis Of Sequenced Threats In Real-time (SB-FASTR) For Wastewater

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Secure Bloom-Filter Analysis of Sequenced Threats in Real-time (SB-FASTR) enables in-field integrated early warning of emerging biological threats from wastewater sequencing across the Indo-Pacific region and reduces existing biosecurity vulnerabilities due to the lack of biosurveillance software capability in the field. SB-FASTR enables rapid detection of a much broader range of biological threats than current targeted approaches using lightweight compute resources. In addition, SB-FASTR enables operators to detect the presence of known features of genetic engineering and novel sequence anomalies that are natural or engineered in origin. This capability better equips the Joint Force and mitigates harm from emerging biothreats by significantly lowering the time to detect so that rapid provisioning of countermeasures against known biological threats. Additionally, SB-FASTR enables more rapid decision support for SMEs when faced with a novel threat by providing anomaly detection that is potentially related to engineered threats. Combined with TAK and communications support, SB-FASTR is able to process Terabytes of data down to ~1Kb Cursor-on-Target messages to provide rapid communication of biothreats via a simple GUI and TAK Plug-in as well as support reporting to CSC2 and other IEW capabilities.

SB-FASTR accomplishes these objectives by adapting and integrating two key pieces of software developed under BBN's previous biosecurity efforts:

Secure Bloom-Filter Analysis and Compression (SB-FAC), a software architecture for secure analysis (including threat detection) and compression of sequencing data for transmission from the field.

BBN Genetic Anomaly Filter (BGAF), a software pipeline for detection of anomalous and/or engineering-related sequences that was developed by BBN as part of the IARPA Finding Engineering Linked Indicators (FELIX) program.

Both SB-FAC and BGAF are built upon technology from FAST-NA, a tool developed by BBN as part of the IARPA FunGCAT program and later hardened into Commercial-Off-The-Shelf (COTS) software that is now used by major DNA synthesis providers to scan customer sequence orders for pathogens and biological toxins. Compared to current bioinformatics software solutions, FAST-NA has the necessary speed and low resource requirements to enable offline analysis of sequencing data in the field using only laptop-scale computation (with the potential to run on mobile devices). By contrast, other methods for threat analysis of sequences are less accurate (e.g., Centrifuge) and/or require larger amounts of resources and time (e.g., BLAST, SeqScreen, ThreatSeq), making them less suited to application to raw sequencing data.

