

INNOVATIONS IN NEXT GENERATION CB THREAT CHARACTERIZATION AND ASSESSMENT FOR DECISION SUPPORT

Fast-na Scanner: High-speed, Low-swap Computational Assessment Of Biological Threats

Jacob Beal Raytheon BBN **Dan Wyschogrod** Raytheon BBN **Adam Clore** Integrated DNA Technologies **Jeff Manthey**
Integrated DNA Technologies **Tom Mitchell** Raytheon BBN **Steven Murphey** Raytheon BBN

FAST-NA is an adaptation of methods from cybersecurity to biological sequence analysis. These methods efficiently compare k-mers from target and contrast sequences (e.g., a target viral biothreat versus contrast from closely related non-threat taxa) to identify short signatures indicative of the presence of the target.

When applied to pathogen detection in DNA synthesis order screening, FAST-NA produces significant improvements in performance, more than halving false positive rates while maintaining negligible false negative rates, operating three orders of magnitude faster than BLAST-based screening, and requiring only laptop-scale hardware.

This combination of extremely high-speed and low resource requirements opens up novel possibilities for both fieldable detection capabilities and the assessment of novel threats. Preliminary results applying FAST-NA to sequencing data indicate that this capability should be able to be adapted to provide real-time high-fidelity interpretation of field sequencing of complex samples.

The signatures produced by FAST-NA cover conserved functional properties of the threat that also apply to previously unseen related threats, such as new variants, emergent pathogens, and engineered organisms. For example, FAST-NA was able to identify SARS-CoV-2 using signatures for SARS and MERS. FAST-NA can also be deployed in an alternate discovery-focused configuration to assess the unique content of a threat rather than its shared content. In this discovery configuration, FAST-NA was able to identify three critical regions of the SARS-CoV-2 sequence in January 2020, one of which was later determined to be the critical functional region of the spike protein.

FAST-NA thus offers a unique combination of speed, accuracy, and low resource requirements that have the potential to provide a suite of real-time, low-SWaP computational assessment capabilities to complement fieldable next-generation sequencing capabilities for threat assessment.

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