RIGEL: A Genomic-Based Biosurveillance Approach

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Known and unknown infectious diseases affecting humans, animals, and plants continue to emerge, re-emerge, and persist in different locations worldwide. The risk of these pathogenic agents to global security is exacerbated by the genomic diversity and lethality of manmade hybrid biothreats that represent unknown unknowns, such as threats we are not even aware that we are unaware of. Trade and travel are vulnerable and potential entry pathways to natural, accidental, or intentional introduction of known and unknown biological threats. Here we introduce a data mining and artificial intelligence approach for genomic-based biosurveillance that estimates the risks of specific commodities regarding specific pathogens. RIGEL follows implementation standards for interoperability, integration, and scalability. RIGEL ingest, stores, tracks hourly worldwide information from 102,635 biological facilities working with 9.5 million organisms from a diversity of biological sources, including but not limited to: human, animal, and plant samples; infected or suspect clinical diagnostic material; environmental samples; synthetic constructs, and genetically modified organisms. RIGEL links genomic information from 342 million nucleotide entries, more than 40 million scientific literature articles, and 761,037 patents. This information is aggregated to build worldwide institutional capability annotated in temporal and spatial scales for strategic and tactical analytics. RIGEL captures more than 194,000 officially reported disease outbreaks of agricultural relevance and ingests in near-real-time newsfeeds from 7,000 newspapers from 120 countries. Integration of data streams generated from multiple sources, including genomic and metagenomic sequencing, epidemiological surveys, news, and trade information, can be coupled with artificial intelligence and advanced visualization techniques to generate a more accurate overview of the pandemic potential of pathogens.