

# NEWS

## Biosurveillance in the Time of COVID-19

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The cracks in our current Western healthcare systems split and collapsed under the pressure of the COVID-19 pandemic. New variants of SARS-CoV-2 eluded much of modern science and medicine. With doctors and scientists scrambling for solutions, the general public was forced into controlled confinement for longer than any of us ever imagined. Most importantly, the COVID-19 pandemic has unearthed a startling revelation in our healthcare system: how can we prepare and quickly adapt to an ever-changing ecosystem?

Since the acceleration of climate change, events like pandemics may increase in likelihood and occurrence<sup>1</sup>. Archaic forms of viral and bacterial strains once encased in glaciers may be re-introduced into our current ecosystem<sup>2</sup>. Some of these ancient pathogens are unknown to modern science and medicine<sup>2</sup>, thus we are not fully equipped to handle unknown viral outbreaks on such a large scale. This situation, coupled with the massive loss of biodiversity, places humans in a difficult coming reality. Many diseases can be transmitted between species through the consumption of infected animals, contaminated water, and being bitten. A process termed zoonosis, in which a communicable disease jumps from non-human animals to humans, is estimated to account for approxi-



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**Development of biosurveillance methods increased to address to the challenges of the COVID-19 pandemic**

mately 75% of infectious diseases<sup>3</sup>. Some even theorize COVID-19 originates from a pathogen jumping from bats to humans<sup>3</sup>. In an effort to address these coming challenges, the development and use of biosurveillance methods has increased. Biosurveillance is the systematic way in which disease outbreaks are detected, monitored, and analyzed<sup>4</sup>. Biosurveillance adds more layers of depth in disease detection and analysis proving it effective for long-term technical use. Imagine a network where each node consists of a various entity (sector, persons, or system). These nodes comprise a large interconnected system whom's role is to examine potential or imminent biological threats. The more nodes within the network, the better the system at detecting and

tracking. Most importantly, biosurveillance is a continuous process since disease outbreak is largely covert in nature, and the people responsible for measuring changes in the environment must be ready to plan a course action when needed<sup>4</sup>.

The most important of these methodologies involves the use of artificial intelligence and machine learning. Artificial intelligence and machine learning have pioneered the ways in which epidemiologists and scientists' study communicable disease pathology. Machine learning can identify specific treatment regimens for various disease models, and these systems can also extrapolate and compare prior techniques in the process of intervention for a disease outbreak. Moreover, we

can model ways in which a communicable disease will behave over time. Effective modelling is an invaluable technique in tracking communicable diseases and requires many variables to realistically simulate the efficacy of disease outbreaks in a community<sup>5</sup>; indeed, these models are highly complex. The common sources of information that power these models are national databases such as EpiSpider, BioCaster, and HealthMap<sup>6</sup>. If you wonder how these large databases collect data, look no farther than your smartphone. Many utilize popular media sites to extract common elements or keywords from users worldwide<sup>6</sup>. Not surprisingly, prominent organizations, like the National Institute of Health (NIH), are making significant progress in developing mathematical models by creating large interconnected research communities<sup>7</sup>. Within the NIH, the Fogarty International Centre's Division of International Epidemiology and Population Studies (DIEPS) created the Research and Policy in Infectious Disease Dynamics (RAPIDD) program<sup>7</sup>. RAPIDD consists of a collaborative research network and focuses on infectious disease modelling. This program made significant strides researching transmission routes and risk factors of the Ebola and Zika epidemics; in addition, they are identifying emerging disease threats from zoonotic and non-zoonotic pathogens<sup>7</sup>. By solving leading research questions such as human behaviour and mobility during disease outbreaks, they are also able to create innovative methodological approaches to advise policy makers<sup>7</sup>. Disease-outbreak predictions do not simply serve as likelihood es-

timators, but as the degree of detriment or degree to which a population will be infected<sup>5</sup>. Some diseases raise more concern than others since some diseases may only be life-threatening to a subset of the population. With the rise of particularly concerning variants of COVID-19, some of which are much more contagious<sup>8</sup>, experts are utilizing artificial intelligence within genomic studies. Investigating the viral or bacterial genome involves genome sequencing to specify each genetic code. Mutations in genetic code happen acutely, especially for viruses<sup>9</sup>. At particular points in time, a viral vector can be at its highest potency for infection and replication<sup>9</sup>. Some even hypothesize that an algorithm which predicts genotype-based antibiotics can provide specific clinical diagnoses<sup>10</sup>. Every bacterial or viral organism has its own genetic fingerprint which makes genotype-sequencing a daunting yet crucial task. Creating a genomic intelligence system will arm officials with specific spatiotemporal information in preparation for a potential disease outbreak. Databases such as the Global Initiative for Sharing All Influenza Data (GISAID) are uncovering the sequence code for different strains of COVID-19<sup>11</sup>. This database in particular, pools many clinical, epidemiological, and gene sequencing data to create an overarching picture of current or potential viral outbreaks<sup>11</sup>. As many strains of COVID-19 as possible are sequenced to uncover the genetic code for each, thus allowing us to synthesize target therapies and procedures for combating this disease<sup>12</sup>.

Just last year, researchers dis-

covered a particular mutation which increased the infectivity of COVID-19; this mutation happens to be responsible for the spike protein of SARS-CoV2 found in Europe and the United States<sup>8</sup>. Machine learning coupled with genome sequencing will continue to uncover more about the coming COVID-19 strains. In fact, there is great possibility that the burgeoning strains will bypass some antibodies provided in current vaccines. Initial small-scale studies have suggested that Moderna and Pfizer vaccine efficacy is greatly reduced for some new SARS-CoV-2 variants<sup>13</sup>. Despite this, the building of large data-sharing networks have immense potential to accelerate the discovery and development of novel therapeutics and clinical treatment protocols before the onset of communicable disease global outbreaks. In the future, as the landscape of infectious disease begins to change and the emergence of novel disease outbreaks become more commonplace, there remains immense potential for the capacity of machine learning to improve the landscape of communicable disease research and biosurveillance. In preparing ourselves for all possibilities, we are also learning to save lives.

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