REVIEW ARTICLE

AI IN MEDICINE

Jeffrey M. Drazen, M.D., *Editor*, Isaac S. Kohane, M.D., Ph.D., *Guest Editor*, and Tze-Yun Leong, Ph.D., *Guest Editor*

Advances in Artificial Intelligence for Infectious-Disease Surveillance

John S. Brownstein, Ph.D., Benjamin Rader, M.P.H., Christina M. Astley, M.D., Sc.D., and Huaiyu Tian, Ph.D.

Florence Nightingale's innovative "rose diagram" of preventable deaths revolutionized data-driven disease surveillance.[1] Raw hospital mortality data collected during the Crimean War were transformed into a compelling, visual insight — poor sanitary conditions killed more people than battle wounds did. This act of synthesizing noisy, complex data into an elegant, effective message was the foundation for a royal commission to track morbidity and mortality and thus launched a new era in which analytic methods were used to better monitor and manage infectious disease. In the more than 160 years since the first publication of Nightingale's rose diagram, tools and technology for translating high-density data and uncovering hidden patterns to provide public health solutions have continued to evolve. Manual techniques are now complemented by machine-learning algorithms. Artificial intelligence (AI) tools can now identify intricate, previously invisible data structures, providing innovative solutions to old problems. Together, these advances are propelling infectious-disease surveillance forward.

The coronavirus disease 2019 (Covid-19) pandemic has highlighted the speed with which infections can spread and devastate the world — and the extreme importance of an equally nimble, expeditious, and clever armamentarium of public health tools to counter those effects. Throughout this crisis, we have witnessed a multitude of AI solutions deployed to play this role — some much more successful than others. As new pathogens emerge or old challenges return to command our attention, the incorporation of the lessons learned into our public health playbook is a priority. In this review article, we reflect on the effects of new and long-standing AI solutions for infectious-disease surveillance. AI applications have been shown to be successful for a diverse set of functions, including early-warning systems,[2,3] hotspot detection,[4,5] epidemiologic tracking and forecasting,[6,7] and resource allocation[8] (Fig. 1). We discuss a few recent examples.[9,11,12] We begin with how AI and machine learning can power early-warning tools and help distinguish among various circulating pathogens (e.g., severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2] vs. influenza virus). We then discuss AI and machine-learning tools that can backtrack epidemics to their source and an algorithmic method that can direct an efficient response to an ongoing epidemic. Finally, we emphasize the critical limitations of AI and machine learning for public health surveillance and discuss salient considerations to improve implementation in the future.

From the Computational Epidemiology Laboratory (J.S.B., B.R., C.M.A.) and the Division of Endocrinology (C.M.A.), Boston Children's Hospital, Harvard Medical School (J.S.B., C.M.A.), and Boston University School of Public Health (B.R.), Boston, and the Broad Institute of MIT and Harvard, Cambridge (C.M.A.) — all in Massachusetts; and the State Key Laboratory of Remote Sensing Science and Center for Global Change and Public Health, Beijing Normal University, Beijing (H.T.). Dr. Brownstein can be contacted at john.brownstein@childrens.harvard.edu or at Boston Children's Hospital, 300 Longwood Ave., BCH3125 Bldg., Boston, MA 02115.

Dr. Brownstein and Mr. Rader contributed equally to this article.

N Engl J Med 2023;388:1597-607.
DOI: 10.1056/NEJMra2119215

AI APPLICATIONS IN DISEASE SURVEILLANCE

EARLY WARNING

Early-warning systems for disease surveillance have benefitted immensely from the incorporation of AI algorithms and analytics.[14-16] At any given moment, the Web is flooded with disease reports in the form of news articles, press releases,

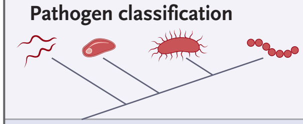
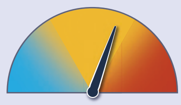
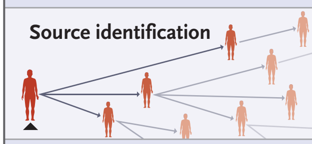
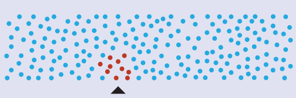
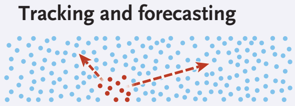
Function	Examples
Early warning 	• Natural-language processing of news sources to identify outbreaks (Freifeld et al., *JAMIA* 2008) • Unsupervised machine learning of social media data to detect unknown infections (Lim, Tucker, and Kumara, *J Biomed Inform* 2017)
Pathogen classification 	• Convolutional neural network model for reading antibiograms (Pascucci et al., *Nat Commun* 2021) • Convolutional neural network model to automate malaria microscopy and diagnosis (Liang et al., *IEEE* 2016)
Risk assessment 	• Reinforcement learning of Covid-19 positivity rates to target limited testing in Greece (Bastani et al., *Nature* 2021) • Machine-learning models including random forest and extreme gradient boosting to use syndromic surveillance for Covid-19 risk prediction (Dantas, *PLoS One* 2021)
Source identification 	• Automated data mining of electronic medical records to uncover hidden routes of infection transmission (Sundermann et al., *Clin Infect Dis* 2021) • Supervised machine learning in combination with digital signal processing for genomic tracing of Covid-19 (Randhawa et al., *PLoS One* 2020)
Hotspot detection 	• Neural computing engine to correlate sound from hospital waiting rooms with influenza spikes (Al Hossain et al., *Proc ACM Interact Mob Wearable Ubiquitous Technol* 2020) • Multilayer perceptron artificial neural network model to detect spatial clustering of tuberculosis (Mollalo et al., *Int J Environ Res Public Health* 2019)
Tracking and forecasting 	• Real-time stacking of multiple models to improve forecasts of seasonal influenza (Reich et al., *PLoS Comput Biol* 2019) • Machine learning to combine new data sources for monitoring Covid-19 (Liu et al., *J Med Internet Res* 2020)

Figure 1. Various Functions of Artificial Intelligence (AI) for Infectious-Disease Surveillance.

Shown is a nonexhaustive list of functions of AI-aided infectious-disease surveillance and representative examples from the published literature.[2-13] Each example includes the type of AI algorithm, a brief description of its purpose, and the associated citation. Covid-19 denotes coronavirus disease 2019.

professional discussion boards, and other curated fragments of information. These validated communications can range from documentation of cases of innocuous infections well known to the world to the first reports of emerging viruses with pandemic potential. However, the volume and distributed nature of these reports constitute much more information than can be made sense of promptly by even highly trained persons, making early warning of emerging viruses nearly impossible. Enter AI-trained algorithms that can parse, filter, classify, and aggregate text for signals of infectious-disease events with high accuracy at unprecedented speeds. HealthMap, just one example of these types of systems, has done so successfully for more than a decade.[2,17] This Internet-based infectious-disease surveillance system provided early evidence of the emergence of influenza A (H1N1) in Mexico[18] and was used to track the 2019 outbreak of vaping-induced pulmonary disease in the United States.[19]

HealthMap uses natural-language processing to search through text posted across the Web for signals of infectious-disease events in real time by comparing the text with a dictionary of known pathogens and geographic areas. Algorithms are trained to ignore noise and parse relevant reports by identifying disease-related text such as the name of a pathogen and incidence numbers (Fig. 2). HealthMap then separates outbreak-related noise from other disease reports (e.g., scientific manuscripts and vaccination campaigns), using a Bayesian machine-learning classification scheme that was originally trained with data that were manually tagged

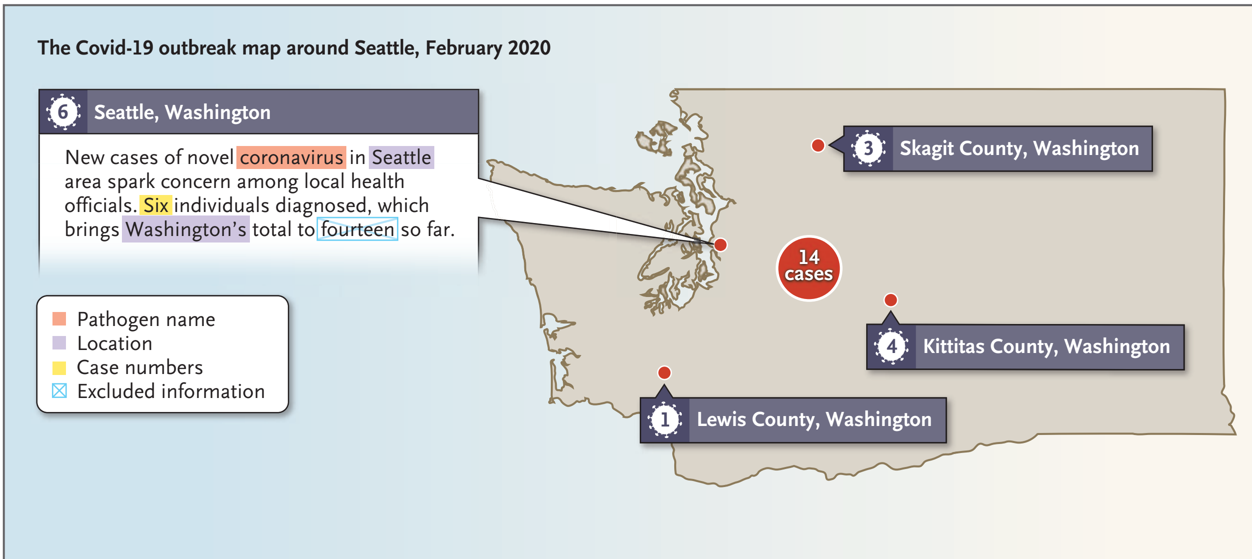


Figure 2. Example of How HealthMap Uses Natural-Language Processing to Classify Infectious-Disease Case Reports.
The natural-language processing engine of HealthMap parses text reports and can extract information such as pathogen name, location, and case numbers. It can also use contextual information to identify data that may not be relevant to this individual report. The engine can then combine multiple reports in a geographic region (Washington State, in this hypothetical example) that can be used to track disease incidence over time and identify surges before traditional surveillance methods can do so.

as being relevant. HealthMap also automatically extracts geographic information that can be used to tie multiple reports together and identify disease clusters that cross-jurisdictional public health authorities may have missed. HealthMap uses a continuously expanding dictionary with text in more than nine languages. This highlights a key advantage of AI for disease surveillance over labor-intensive, continuous manual classification — the ability to simultaneously provide worldwide coverage and hyperlocal situational awareness. This dynamic architecture enabled the December 30, 2019, HealthMap warning of a "cluster of pneumonia cases of unknown etiology," just days after the first case of Covid-19 was identified.[14,20]

PATHOGEN CLASSIFICATION

After a potential outbreak has been identified, an effective public health response requires knowledge of the underlying cause. Similar symptom patterns can be manifested by various pathogens or even by other, noninfectious causes.[21] AI has led to advances in diagnostic classification in a variety of fields,[22] including neuroimaging (e.g., improving diagnostic tests for Alzheimer's disease[23]) and oncology (e.g., detecting breast cancer[24]). Current methods of infectious-disease surveillance have similarly drawn on AI to differentiate among various pathogens or identify variants that have worrisome characteristics. By defining the pathologic characteristics of an outbreak, public health authorities are able to respond accordingly (e.g., by ensuring an adequate supply of oseltamivir when influenza cases are increasing in a region). Conversely, reliance on simple syndromic definitions can result in misidentification of an outbreak, particularly when pathogens share symptoms and routes of transmission. For example, a "Covid-like illness" syndrome suggested a false wave of Covid-19 in Canada, whereas pathogen data instead pointed to circulating seasonal viruses such as enterovirus or rhinovirus.[21]

A recent example of AI applied to determine antibiotic resistance highlights the power of an AI-driven image classification tool to aid in surveillance. The Kirby–Bauer disk-diffusion test is a simple, low-cost technique for determining bacterial susceptibility to drugs from the diameter of the area in which growth of the bacteria is inhibited around an antibiotic-treated disk in a petri dish.[9] However, measurement quality is user-dependent and can result in misclassification of bacteria as susceptible or resistant, errors that affect treatment choices for individual patients and epidemiologic surveillance capabilities. State-of-the-art laboratories use automated readers to solve the problem, but this solution is costly and not available to laboratories operating on a small budget.

A group of researchers supported by Médecins sans Frontières sought to leverage AI in order to solve this problem (Fig. 3). They created a mobile application that uses a telephone camera and machine-learning algorithms to ascertain the antibiotic susceptibility of bacteria with a highly scalable approach.[9] First, the application uses a series of image-processing algorithms to focus on the disks, determine antibiotic type, and measure the growth inhibition zone by quantifying pixel intensity around each disk. Second, in order to translate the measured growth patterns into decisions about the overall resistance of the bacteria to each antibiotic disk, the application uses an AI-driven "expert system," a type of algorithm that is based on an expert-informed knowledge base, heuristics, and a programmed set of rules to emulate human decision making. The classification is obtained in conjunction with a user-validation procedure, and the results can be automatically forwarded to international institutions such as the Global Antimicrobial Resistance Surveillance System of the World Health Organization (WHO). Thus, the use of AI to expand an individual practitioner's toolbox for assessing bacteria has the far-reaching consequences of enhancing our ability to track antibiotic resistance globally.

SOURCE IDENTIFICATION

When an outbreak has been identified, the next step is to stop the outbreak by first tracing and then cutting off routes of transmission. For hospital-based outbreak detection, tracking of infections with the use of spatiotemporal clustering and contact tracing can be performed by hand to identify targets for intervention.[25] Although often effective, this method is extremely labor-intensive and can involve large-scale chart reviews, random environmental sampling, and in-depth interviews. Genetic similarities of whole-genome surveillance sequences can also be used to tie clinical cases together. However, this method cannot be used to identify sources of infection, and even when used in conjunction with traditional hospital-based outbreak detection, it may fail to identify complex transmission patterns, knowledge of which is required to direct interventions.

In the past few years, a group of researchers at the University of Pittsburgh have introduced a machine-learning layer into whole-genome surveillance to create an outbreak source identification system — the Enhanced Detection System for Healthcare-Associated Transmission (EDS-HAT).[12] EDS-HAT works by combining whole-genome surveillance sequencing and machine learning to automatically mine patients' electronic medical records (EMRs) for data related to an outbreak. The algorithm was trained by means of a case–control method that parsed the EMR data from patients known to have infections from the same outbreak (cases) and EMR data from other patients in the hospital (controls used to establish baseline levels of exposure relatedness). This form of learning guided the algorithm to identify EMR similarities (e.g., procedures, clinicians, and rooms) of cases with linked infections. Analysis of EDS-HAT determined that real-time machine learning based on EMRs in combination with whole-genome sequencing could prevent up to 40% of hospital-borne infections in the nine locations studied and potentially save money.[25]

In practice, the EDS-HAT algorithm has identified multiple, otherwise-undetected outbreaks, using as clues similarities hidden in the EMR data. Notably, it detected outbreaks with hidden transmission patterns such as methicillin-resistant *Staphylococcus aureus* infections in two patients who were in two different hospital units, both of whom underwent bedside electroencephalographic monitoring. The connection was difficult to detect by traditional methods of review because the infection culture dates were 8 days apart, but it was identified by the EDS-HAT because the procedures were performed on the same day by the same technician. In another instance, the source of a *Pseudomonas aeruginosa* outbreak among six patients in multiple units of a hospital over a period of 7 months was missed because of the wide separation of time and space. Genome surveillance suggested that the cases were all connected, and the machine-learning algorithm identified a contaminated

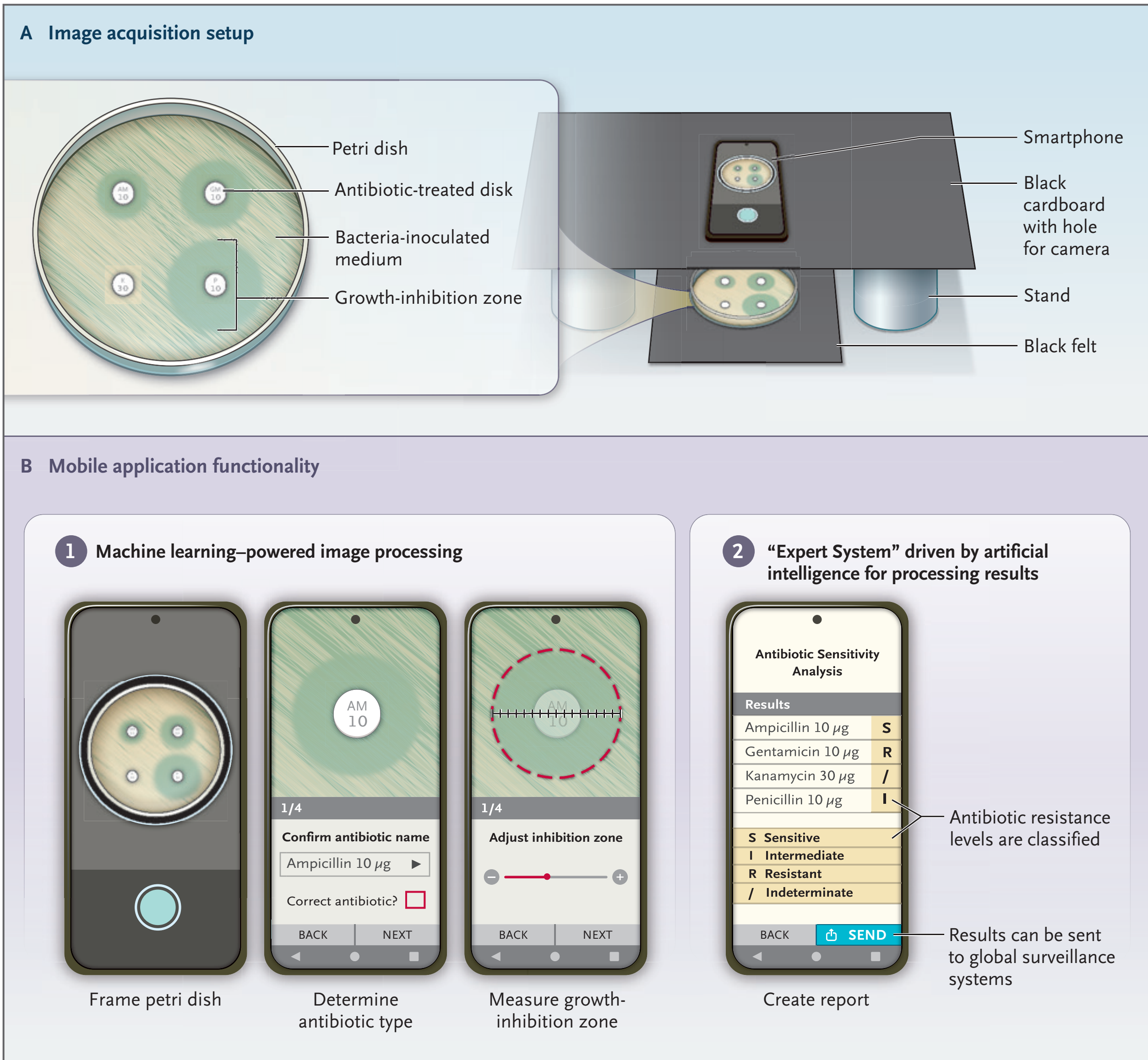


Figure 3. Example of Mobile Application to Measure Antibiotic Susceptibility with AI.

A mobile phone application developed by Pascucci and colleagues[9] uses machine learning and AI to classify bacterial susceptibility to various antibiotics. Panel A shows the image acquisition setup, and Panel B shows the mobile phone application. The application is designed to read a Kirby–Bauer disk-diffusion test, first by using machine-learning and image-processing techniques and then by organizing the results with the use of an AI-driven "expert system." The mobile application supports the ability to make high-quality reads in resource-limited settings and to forward the results to global antimicrobial resistance surveillance systems.

gastroscope as the likely source of the outbreak — an easy target for intervention. In this scenario, running a real-time AI algorithm to detect what was being missed by traditional methods resulted in early disease recognition, infection prevention, a substantial decrease in potential illness, and cost savings.

RISK ASSESSMENT

For widespread infections such as those that occur in pandemics, complete elimination of infection at a single source is unlikely. In these scenarios, vaccination,[26] contact tracing,[27] and nonpharmaceutical interventions such as movement restrictions[28] and mask wearing[29] can be

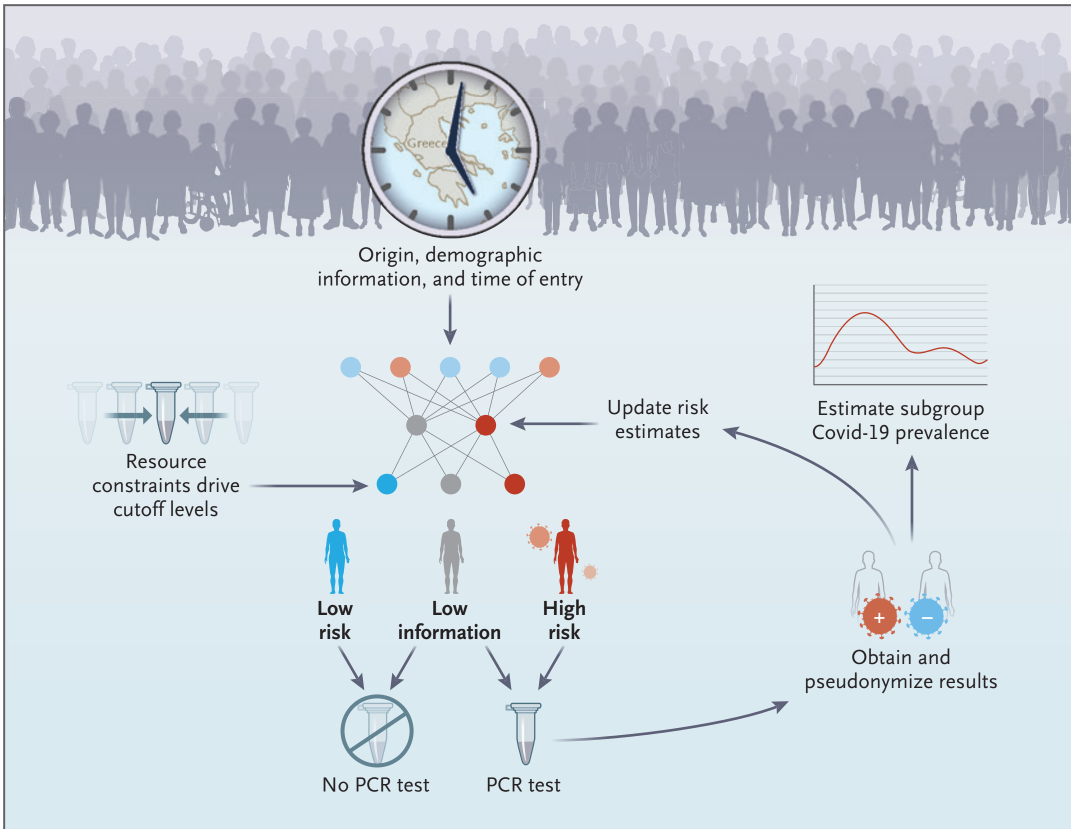


Figure 4. Example of Reinforcement Learning for Covid-19 Border Surveillance.

Eva is a reinforcement learning system used in Greece to allocate a limited supply of Covid-19 tests at the border of the country.[11] The algorithm uses information about the travelers in order to assign them to risk categories, with polymerase-chain-reaction (PCR) tests allocated accordingly. The risk estimate for each category is regularly updated to incorporate new information from the most recent batch of test results. Eva also sets testing cutoff levels, based on both risk and the available supply of tests, and makes Covid-19 prevalence estimates for each risk category. Pseudonymization refers to a deidentification procedure in which personally identifiable information is replaced by other identifiers.

used to reduce transmission. AI and machine-learning techniques have been introduced broadly for these applications, especially during the Covid-19 pandemic. For example, in China, health quick-response (QR) codes embedded in widely used mobile applications (Alipay and WeChat) have allowed for real-time assessment of transmission risk in public locations and connection to AI-driven medical chatbots that can answer health-related questions.[30] In Greece, the government introduced Eva, an AI algorithm to screen travelers for Covid-19 at the border of the country. This algorithm identified 1.25 to 1.45 times as many asymptomatic infected travelers as those identified with testing based on epidemiologic metrics (i.e., testing of persons arriving from countries with a high number of cases or deaths per capita or a high reported positivity rate).[11]

Eva uses reinforcement learning (Fig. 4) to target travelers for polymerase-chain-reaction (PCR) Covid-19 testing.[11] Rather than relying on population-based epidemiologic metrics, the algorithm sorts travelers into "types" according to their origin country, age, sex, and time of entry. Recent testing results from Eva are fed back into the system, and travelers are assigned to Covid-19 testing on the basis of recent prevalence estimates for their type. The system continues to learn by receiving updated test results from high-risk travelers (anonymously) and exploratory results from types for which it does not have recent prevalence estimates. With continuous learning, the algorithm can optimize allocation of the limited testing resources in Greece while identifying substantially more cases than those identified with the use of alternative strategies. Eva features a crucial advantage of AI over even the best-performing traditional surveillance models — the ability to continuously adapt and improve without deliberate intervention.

EXTENDED APPLICATIONS

We have highlighted just a few examples of how AI has advanced infectious-disease surveillance. Representative examples of the diverse functions and applications in this discipline are outlined in Figure 1, but since this is an evolving field, we do not provide a comprehensive listing of all extant projects. Figure 5 shows how a sample of existing and emerging AI and machine learning–aided tools might be deployed during a hypothetical respiratory outbreak to improve surveillance at multiple time points, at each step generating meaningful insights from otherwise difficult-to-interpret, multidimensional data. There are some advantages and disadvantages of using these AI–machine-learning methods (here classified as either supervised classification methods or artificial neural networks) as compared with two human-curated surveillance systems: traditional public health surveillance and nontraditional participatory surveillance.

As an outbreak starts, early signals can be detected by wearable devices such as smartwatches and smart rings, which may pick up on infections from subclinical changes (e.g., increases in the resting heart rate) before noticeable symptoms appear (Fig. 5).[31] The population aggregate of this signal can warn public health officials of an impending outbreak. Similarly, as disease courses progress, AI methods can help pinpoint outbreak hotspots from the locations where many persons have symptoms[4] or are seeking care.[32] These methods can also be used to mine social media for cases of illness based on information reported from individual persons who are posting online; these case counts have been shown to track with government case counts.[33] Public health officials can leverage AI for passive surveillance of adherence to nonpharmaceutical interventions. For example, closed-circuit television and image-recognition algorithms can be used to monitor mask wearing,[34] and privacy-preserving measures of the movements of individual persons can be used to quantify population mobility and social distancing.[35] These AI-driven approaches complement the human-curated ones, including traditional public health surveillance, which is highly accurate but has a longer latency, and participatory surveillance, which can produce insights in real time but lacks the confirmatory nature of traditional reporting.[36]

SURVEILLANCE ROADBLOCKS AND FUTURE DIRECTIONS

DATA VOLUME AND QUALITY

The availability of large quantities of low-latency data has played a large part in improving infectious-disease surveillance, but gaps remain, and vulnerabilities continue to go unnoticed. "Big data hubris" reminds us that even the most accurate AI-trained infectious-disease surveillance systems can lead to overfitting (i.e., predictions that are not generalizable because they are too tailored to specific data) and should complement rather than replace high-quality traditional surveillance.[37] Disease-tracking systems that are not supplemented by molecular testing may not be able to disentangle cocirculating infections that have similar clinical manifestations,[21] although machine classification systems may be able to improve on human intuition. In addition, the AI algorithms designed for surveillance of diseases such as Covid-19 will require frequent recalibration as new pathogen variants emerge and exogenous variables (e.g., vaccination) modify symptom presentations and affected demographic characteristics.[38,39] These systems may produce false alarms or fail to capture important signals in the presence of noise. Furthermore, machine-learning algorithms trained on low-quality data will not add value, and in some circumstances they may even be harmful.

DATA SOURCE REPRESENTATION

Despite tremendous technological strides in improving the precision and accuracy of surveillance systems, they are often built on databases with structural underrepresentation of selected populations.[40] Although ensemble models can mitigate the methodologic distortions of indi-

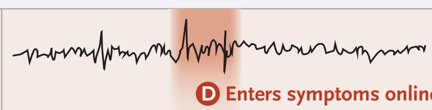
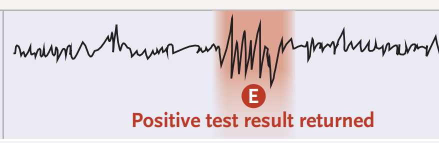
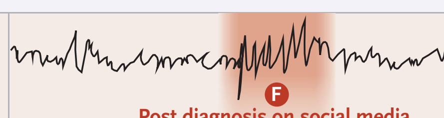
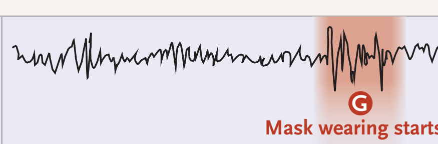
Individual event	Example of signal-generating method	Algorithm category	Signal of possible infectious disease in a population	Surveillance output
Biosignals passively measured by smartwatch	Gradient-boosting decision tree	Supervised classification		Early indication of possible outbreak
Method advantages • Early warning can direct treatment and prevent spread • Continuously measured without requiring intervention			**Method disadvantages** • Disease signal is nonspecific • Requires deployment of device before outbreak	
Cough detected by smart listening device	Regional proposal network	Artificial neural network		Spike in persons whose symptoms are detected early
Method advantages • Passively monitor with already adopted devices • Can be used in homes or larger settings (e.g., waiting rooms)			**Method disadvantages** • Requires advanced privacy protection schemes • Symptomatic person (i.e., who coughed) may be unknown	
Internet search query for viral testing site	Support vector regression	Supervised classification		Hotspot of care-seeking behavior
Method advantages • Can be inexpensive and centrally monitored • Captures behavior without requiring explicit participation			**Method disadvantages** • Testing possibly unrelated to symptom status (e.g., for travel) • Searches may not lead to testing (e.g., resource constraints)	
Symptoms entered into website	Participatory surveillance	Human curated		Real-time prevalence of possible cases
Method advantages • Information can be disseminated without bureaucratic delay • Captures mild cases that may not formally test across settings			**Method disadvantages** • Participants skew toward persons with high health literacy • Relies on syndromic definitions that may describe many causes	
Test result positive for virus	Traditional public health surveillance	Human curated		Official case counts
Method advantages • Standard diagnostic accuracy • Mandatory reporting can capture rare and dangerous pathogens			**Method disadvantages** • Verification can be slow and expensive • Requires resources that may not be available in certain settings	
Post on social media about diagnosis	Natural-language processing	Supervised classification		Real-time prevalence of confirmed cases
Method advantages • Rapid collection and dissemination of results • Wide array of users who may be missed by most other systems			**Method disadvantages** • Computationally expensive and difficult to parse signal from noise • Symptoms nonverified and can be vulnerable to Internet trolls	
Mask wearing captured by CCTV	Convolutional neural network	Artificial neural network		Nonpharmaceutical intervention levels
Method advantages • Not vulnerable to desirability bias (i.e., captures true behavior) • High level of geographic specificity			**Method disadvantages** • Highly invasive and susceptible to privacy abuse • Resource intensive, especially outside urban locales	

Figure 5 (facing page). AI and Machine-Learning Transformations of Individual Behavior into Population Health Information.

A diverse and nonexhaustive set of AI and machine-learning algorithms (here categorized as either a supervised classification algorithm or an artificial neural network) and human-curated methods can be applied throughout a hypothetical respiratory virus outbreak. Individual events, when aggregated, create a signal of possible infectious disease within a population. Detected signals are used to determine actionable surveillance measures. Each approach has distinct advantages and disadvantages, and in combination, the algorithms constitute a system for detecting and responding to an outbreak. CCTV denotes closed-circuit television.

vidual surveillance streams, they cannot adjust for systematic selection bias of an undefined proportion. A recent analysis of U.S. Covid-19 mortality data suggested that the lack of properly encoded racial information in surveillance databases was causing disparities in deaths among Black and Hispanic persons to be underreported by up to 60%.[41] This is both a moral and a methodologic issue. The resulting distortion in signal means that AI algorithms trained from these incomplete data sets or those that fail to incorporate race as reported by patients will recapitulate inequities and underestimate the resources necessary to mitigate disparate outcomes.[42]

In another instance, researchers used a database of chest radiographs in children as a control group when training image-classification algorithms to diagnose Covid-19 in broad populations.[43] Although the algorithms performed well, they were simply separating adults from children rather than identifying those with Covid-19. Researchers at the University of Padua revealed the scope of this error when they reported that one can entirely remove the lung area from an image and still predict from which database the data were derived.[44] The error in this case and the underreported Black and Hispanic mortality data noted above exemplify how public health surveillance that replaces inclusion, representation, and critical evaluation of sample selection with AI and machine learning may produce deceivingly precise but incorrect conclusions.[45]

PRIVACY

As surveillance models incorporate data streams from sources such as "digital exhaust" (i.e., extraneous data generated by persons interacting with the digital world), connected health devices, and wearable technology, issues of individual privacy will continue to grow in importance.[46,47] Considerable care must be given to balancing the requirements of high-quality open data to push research boundaries,[48] the invasiveness of AI tools, and personal privacy needs.

Although approaches to weighing public health concerns against personal data rights will reflect community needs and surveillance objectives, the use of AI-powered, privacy-preserving forms of technology must be considered. One such type of technology is federated learning, which has recently been used for an infectious-disease surveillance study performed with the use of smartphones.[49] Federated learning brings distributed models to each participant's personal data and devices, where calculations are performed locally, and then uses those models to iteratively update a centralized model. Thus, participants' data never leave their own devices, so participants can contribute to surveillance projects without the privacy risks associated with centrally stored data.[47]

THE LIMITS OF AI

The spread of infectious diseases is an issue of hyperlocal and international concern. The Covid-19 pandemic has shown that pathogens do not recognize national borders and that seemingly inconsequential events can have far-reaching consequences (e.g., the Biogen conference held in Boston in February 2020, which was the source of hundreds of thousands of infections[50]). Although technological achievements will continue to improve our surveillance infrastructure, future outbreaks are still likely to occur. AI cannot replace the cross-jurisdictional and cross-functional coordination that is truly essential for the collective intelligence required to fight novel and emerging diseases. Collaborative surveillance networks such as the WHO Hub for Pandemic and Epidemic Intelligence in Berlin, the Center for Forecasting and Outbreak Analytics (recently launched by the Centers for Disease Control and Prevention), the Pandemic Prevention Institute of the Rockefeller Foundation, the African continent–wide Regional Integrated Surveillance and Laboratory Network, and many others are needed for ongoing endemic surveillance if we are to be prepared for the next pandemic. These groups will use AI to enhance their models but will achieve little without international cooperation to deploy them.

The future of infectious-disease surveillance will feature emerging forms of technology, including but not limited to biosensors, quantum computing, and augmented intelligence. Recent advances in large language models (e.g., Generative Pre-trained Transformer 4 [GPT-4]) hold great promise for the future of infectious-disease surveillance because these models can process and analyze vast amounts of unstructured text and may enhance our ability to streamline labor-intensive processes and spot hidden trends. Other types of technology, not yet invented, will surely make a difference. However, over the course of the Covid-19 pandemic, our current methods have been put to the test, and their performance has been highly variable. The success of the next generation of AI-driven surveillance tools will depend heavily on our ability to unravel the shortcomings of our algorithms, recognize which of our achievements are generalizable, and incorporate the many lessons learned into our future behavior.

Disclosure forms provided by the authors are available with the full text of this article at NEJM.org.

We thank Kimon Drakopoulos, Lee Harrison, and Amin Madoui for their aid in interpreting their respective projects.

REFERENCES

1. Brasseur L. Florence Nightingale's visual rhetoric in the rose diagrams. Tech Commun Q 2005;14:161-82.
2. Freifeld CC, Mandl KD, Reis BY, Brownstein JS. HealthMap: global infectious disease monitoring through automated classification and visualization of Internet media reports. J Am Med Inform Assoc 2008;15:150-7.
3. Lim S, Tucker CS, Kumara S. An unsupervised machine learning model for discovering latent infectious diseases using social media data. J Biomed Inform 2017;66:82-94.
4. Al Hossain F, Lover AA, Corey GA, Reich NG, Rahman T. FluSense: a contactless syndromic surveillance platform for influenza-like illness in hospital waiting areas. Proc ACM Interact Mob Wearable Ubiquitous Technol 2020;4:1-28.
5. Mollalo A, Mao L, Rashidi P, Glass GE. A GIS-based artificial neural network model for spatial distribution of tuberculosis across the continental United States. Int J Environ Res Public Health 2019;16:157.
6. Reich NG, McGowan CJ, Yamana TK, et al. Accuracy of real-time multi-model ensemble forecasts for seasonal influenza in the U.S. PLoS Comput Biol 2019;15(11):e1007486.
7. Liu D, Clemente L, Poirier C, et al. Real-time forecasting of the COVID-19 outbreak in chinese provinces: machine learning approach using novel digital data and estimates from mechanistic models. J Med Internet Res 2020;22(8):e20285.
8. Dantas LF, Peres IT, Bastos LSL, et al. App-based symptom tracking to optimize SARS-CoV-2 testing strategy using machine learning. PLoS One 2021;16(3):e0248920.
9. Pascucci M, Royer G, Adamek J, et al. AI-based mobile application to fight antibiotic resistance. Nat Commun 2021;12:1173.
10. Liang Z, Powell A, Ersoy I, et al. CNN-based image analysis for malaria diagnosis. In: Proceedings and Abstracts of the 2016 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), December 15–18, 2016. Shenzhen, China: Institute of Electrical and Electronics Engineers, 2016.
11. Bastani H, Drakopoulos K, Gupta V, et al. Efficient and targeted COVID-19 border testing via reinforcement learning. Nature 2021;599:108-13.
12. Sundermann AJ, Chen J, Kumar P, et al. Whole genome sequencing surveillance and machine learning of the electronic health record for enhanced healthcare outbreak detection. Clin Infect Dis 2021 November 17 (Epub ahead of print).
13. Randhawa GS, Soltysiak MPM, El Roz H, de Souza CPE, Hill KA, Kari L. Machine learning using intrinsic genomic signatures for rapid classification of novel pathogens: COVID-19 case study. PLoS One 2020;15(4):e0232391.
14. Cho A. AI systems aim to sniff out coronavirus outbreaks. Science 2020;368:810-1.
15. Alavi A, Bogu GK, Wang M, et al. Real-time alerting system for COVID-19 and other stress events using wearable data. Nat Med 2022;28:175-84.
16. Brownstein JS, Freifeld CC, Reis BY, Mandl KD. Surveillance Sans Frontières: internet-based emerging infectious disease intelligence and the HealthMap project. PLoS Med 2008;5(7):e151.
17. Brownstein JS, Freifeld CC, Madoff LC. Digital disease detection — harnessing the Web for public health surveillance. N Engl J Med 2009;360:2153-5.
18. Brownstein JS, Freifeld CC, Madoff LC. Influenza A (H1N1) virus, 2009 — online monitoring. N Engl J Med 2009;360:2156.
19. Hswen Y, Brownstein JS. Real-time digital surveillance of vaping-induced pulmonary disease. N Engl J Med 2019;381:1778-80.
20. Bhatia S, Lassmann B, Cohn E, et al. Using digital surveillance tools for near real-time mapping of the risk of infectious disease spread. NPJ Digit Med 2021;4:73.
21. Maharaj AS, Parker J, Hopkins JP, et al. The effect of seasonal respiratory virus transmission on syndromic surveillance for COVID-19 in Ontario, Canada. Lancet Infect Dis 2021;21:593-4.
22. Yu K-H, Beam AL, Kohane IS. Artificial intelligence in healthcare. Nat Biomed Eng 2018;2:719-31.
23. Punjabi A, Martersteck A, Wang Y, Parrish TB, Katsaggelos AK; Alzheimer's Disease Neuroimaging Initiative. Neuroimaging modality fusion in Alzheimer's classification using convolutional neural networks. PLoS One 2019;14(12):e0225759.
24. Kim H-E, Kim HH, Han B-K, et al. Changes in cancer detection and false-positive recall in mammography using artificial intelligence: a retrospective, multireader study. Lancet Digit Health 2020;2(3):e138-e148.
25. Sundermann AJ, Miller JK, Marsh JW, et al. Automated data mining of the electronic health record for investigation of healthcare-associated outbreaks. Infect Control Hosp Epidemiol 2019;40:314-9.
26. Greenwood B. The contribution of vaccination to global health: past, present and future. Philos Trans R Soc Lond B Biol Sci 2014;369:20130433.
27. Cui X, Zhao L, Zhou Y, et al. Transmission dynamics and the effects of non-pharmaceutical interventions in the COVID-19 outbreak resurged in Beijing, China: a descriptive and modelling study. BMJ Open 2021;11(9):e047227.
28. Tian H, Liu Y, Li Y, et al. An investigation of transmission control measures during the first 50 days of the COVID-19 epidemic in China. Science 2020;368:638-42.
29. Rader B, White LF, Burns MR, et al. Mask-wearing and control of SARS-CoV-2 transmission in the USA: a cross-sectional

study. Lancet Digit Health 2021;3(3):e148-e157.
30. Wu J, Xie X, Yang L, et al. Mobile health technology combats COVID-19 in China. J Infect 2021;82:159-98.
31. Gadaleta M, Radin JM, Baca-Motes K, et al. Passive detection of COVID-19 with wearable sensors and explainable machine learning algorithms. NPJ Digit Med 2021;4:166.
32. Guo P, Zhang J, Wang L, et al. Monitoring seasonal influenza epidemics by using internet search data with an ensemble penalized regression model. Sci Rep 2017;7:46469.
33. Gomide J, Veloso A, Meira W, et al. Dengue surveillance based on a computational model of spatio-temporal locality of Twitter. In: Proceedings and Abstracts of the 3rd International Web Science Conference, June 15–17, 2011. Koblenz, Germany: Association for Computing Machinery, 2011.
34. Loey M, Manogaran G, Taha MHN, Khalifa NEM. A hybrid deep transfer learning model with machine learning methods for face mask detection in the era of the COVID-19 pandemic. Measurement (Lond) 2021;167:108288.
35. Aktay A, Bavadekar S, Cossoul G, et al. Google COVID-19 community mobility reports: anonymization process description (version 1.0). April 8, 2020 (https://arxiv.org/abs/2004.04145v1). preprint.
36. Chan AT, Brownstein JS. Putting the public back in public health — surveying symptoms of Covid-19. N Engl J Med 2020; 383(7):e45.
37. Lazer D, Kennedy R, King G, Vespignani A. Big data. The parable of Google flu: traps in big data analysis. Science 2014;343:1203-5.
38. Antonelli M, Penfold RS, Merino J, et al. Risk factors and disease profile of post-vaccination SARS-CoV-2 infection in UK users of the COVID Symptom Study app: a prospective, community-based, nested, case-control study. Lancet Infect Dis 2022;22:43-55.
39. Wang Z, Wu P, Wang J, et al. Assessing the asymptomatic proportion of SARS-CoV-2 infection with age in China before mass vaccination. J R Soc Interface 2022;19:20220498 (https://doi.org/10.1098/rsif.2022.0498).
40. Developing infectious disease surveillance systems. Nat Commun 2020;11: 4962.
41. Labgold K, Hamid S, Shah S, et al. Estimating the unknown: greater racial and ethnic disparities in COVID-19 burden after accounting for missing race and ethnicity data. Epidemiology 2021;32:157-61.
42. Vyas DA, Eisenstein LG, Jones DS. Hidden in plain sight — reconsidering the use of race correction in clinical algorithms. N Engl J Med 2020;383:874-82.
43. Roberts M, Driggs D, Thorpe M, et al. Common pitfalls and recommendations for using machine learning to detect and prognosticate for COVID-19 using chest radiographs and CT scans. Nat Mach Intell 2021;3:199-217.
44. Maguolo G, Nanni L. A critic evaluation of methods for COVID-19 automatic detection from X-ray images. Inf Fusion 2021;76:1-7.
45. Bradley VC, Kuriwaki S, Isakov M, Sejdinovic D, Meng X-L, Flaxman S. Unrepresentative big surveys significantly overestimate US vaccine uptake. June 10, 2021 (https://arxiv.org/abs/2106.05818). preprint.
46. Rivers C, Lewis B, Young S. Detecting the determinants of health in social media. Online J Public Health Inform 2013; 5(1):e161.
47. Sadilek A, Liu L, Nguyen D, et al. Privacy-first health research with federated learning. NPJ Digit Med 2021;4:132.
48. Peiffer-Smadja N, Maatoug R, Lescure F-X, D'Ortenzio E, Pineau J, King J-R. Machine learning for COVID-19 needs global collaboration and data-sharing. Nat Mach Intell 2020;2:293-4.
49. Google Health. Participate in research with Google Health studies (https://health.google/for-everyone/health-studies).
50. Rimmer A. Covid-19: medical conferences around the world are cancelled after US cases are linked to Massachusetts meeting. BMJ 2020;368:m1054.