New technologies in predicting, preventing and controlling emerging infectious diseases

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Abbreviations: CDC, Center for Disease Control and Prevention; ECDC, European Center for Disease Control and Prevention; EpiSPIDER, Semantic Processing and Integration of Distributed Electronic Resources for Epidemics; EWARN, Early Warning Alert and Response Network; FRED, Framework for Reconstructing Epidemic Dynamics; GIS, geographical information system; GLEAM, Global Epidemic and Mobility; GOARN, Global Outbreak Alert and Response Network; GPHIN, Global Public Health Intelligence Network; GPS, Global Positioning System; ILI, Influenza-like illness; MeRS, Middle East Respiratory Syndrome; ProMED, Program for Monitoring Emerging diseases; SARS, Severe Acute Respiratory Syndrome; WHO, World Health Organization (WHO); WNV, West Nile virus.

Surveillance of emerging infectious diseases is vital for the early identification of public health threats. Emergence of novel infections is linked to human factors such as population density, travel and trade and ecological factors like climate change and agricultural practices. A wealth of new technologies is becoming increasingly available for the rapid molecular identification of pathogens but also for the more accurate monitoring of infectious disease activity. Web-based surveillance tools and epidemic intelligence methods, used by all major public health institutions, are intended to facilitate risk assessment and timely outbreak detection. In this review, we present new methods for regional and global infectious disease surveillance and advances in epidemic modeling aimed to predict and prevent future infectious diseases threats.

Introduction

Global surveillance of emerging infectious diseases aims in rapidly detecting changes in the incidence rate of endemic diseases and in promptly recognizing and characterizing syndromes caused by previously unknown pathogens of epidemic potential. Once a novel infectious threat is identified surveillance of the disease spread is paramount in order to apply and assess preventive and control measures. Novel or re-emerging infectious diseases usually first occur in a certain population or geographic area, however they can swiftly disperse locally or globally given their mode of transmission and pandemic potential. The ongoing Ebola virus outbreak in West Africa, the emergence of Middle East respiratory syndrome corona-virus (MERS-CoV), the re-emergence of chinkugunya virus, the recent 2009 A/H1N1 influenza pandemic and 2003 SARS outbreak, all highlight the importance of large-scale infectious diseases surveillance networks. Emergence of infectious diseases is associated with human factors such as population density, travel, trade, changes in land use, environmental factors and the interaction between humans and wildlife. Technological progress has facilitated efforts of disease monitoring and it has made possible to construct mathematical models for the study of disease dynamics and epidemic prediction. A better understanding of human mobility patterns has enabled simulation of the spread of SARS and novel Influenza A/H1N1 viruses. Models have the potential to identify hotspots of emerging infectious diseases, where an emerging pathogen is more likely to occur. Changing trends in communication patterns and the expansion of social media poses new challenges but also offers new possibilities for infectious diseases prevention. The purpose of this review is to present novel methods for regional and global infectious disease surveillance and to describe advances in pathogen discovery and epidemic modeling that aim to predict and prevent future public health threats (Table 1).

Methods

We performed a literature search for articles in the English language of the electronic database PubMed, Cochrane Reviews, Google Scholar, the US Centers for Disease Control and Prevention website, WHO publication websites, using combinations of the search terms “technologies,” “new,” “emerging infectious diseases,” “zoonoses” “detection,” “prevention,” “pandemic” “event-based surveillance” and “surveillance” before December 2014. Studies cited by the articles identified in the search were also reviewed.

Internet-based surveillance

Event-based surveillance

Traditional, passive surveillance relies on routine reporting by healthcare facilities of structured pre-defined information regarding events and diseases. This type of surveillance requires the
Table 1. Table summarizes the effective technologies and resources presented in the article which are being used a national or international level for the prediction, detection and control of emerging infectious disease threats. Examples of each resource are also given as well as their main applications

| Technologies/Resources | Example | Application |
|------------------------|---------|-------------|
| Event-Based Surveillance | GPHIN, ProMED-mail, HealthMap, EpiSPIDER, BioCaster | Outbreak and emerging public health threat detection (i.e., SARS) |
| Web-based Real-time Surveillance | Google Trends, Google Flu Trends | Real-time monitoring of disease activity (i.e. seasonal influenza activity) |
| Early Warning and Alert Response Networks | GOARN | Detection of public health threats Communication between institutions, Implementation of preventive and control measures (i.e., WHO Global Alert and Response) |
| Infectious Diseases Modeling | Agent-based models, Metapopulation models (GLEAM, FRED, gravity model) | Epidemic simulation Assessment of disease spread determinants, Design of containment interventions |
| Social Media | Foodborne Chicago, Flu NearYou | Participatory epidemiology (i.e. foodborne illnesses, seasonal influenza activity) |
| New technologies in Pathogen Discovery | Genome Wide Sequencing, Microarrays, Bioinformatics | Pathogen/Virus discovery Wildlife sampling and surveillance, Predictive modeling, Determinants of host susceptibility, Animal models |

existence of a public health network, it is often expensive and is associated with a delay of approximately 2 weeks from data acquisition to dissemination. With the advancement of computational science, event-based surveillance has emerged as a complimentary method to traditional indicator-based surveillance.

Event-based systems mainly collect and analyze unstructured information from diverse sources, including news reports, social media and internet-based searches. It is true that the majority of data regarding first reports of infectious diseases events currently derives from informal sources like media reports and the Internet. Digital surveillance systems aim in detecting events with epidemic potential earlier than official notifications. The Global Public Health Intelligence Network (GPHIN) is one of the most important event-based surveillance systems that systematically scans a multitude of such informal sources, including web sites, electronic discussion forums, news reports, online newspapers and the email listserve of the Program for Monitoring Emerging Diseases (ProMED-mail, www.promedmail.org) for unusual disease events and rumors for outbreaks. GPHIN processes approximately 3000 news items per day, however one fourth of those may represent duplicates or irrelevant data. In some but not all event-based systems, generated raw data is then being investigated, verified through official sources and assessed in terms of its epidemiologic significance by specialist teams. The significance of GPHIN was highlighted during the Severe Acute Respiratory Syndrome (SARS) outbreak when, in November 2002 and February 2003, it issued the first alert of unusual respiratory illness in Guangdong Province, China to WHO and GOARN members, triggering an international response.

Other widely used event-based systems are Argus, HealthMap (www.healthmap.org/en/), EpiSPIDER (Semantic Processing and Integration of Distributed Electronic Resources for Epidemiics [and disasters]; www.epispyder.net) and BioCaster. Sophisticated data processing or text mining techniques are used by many of these systems to filter and classify articles and hence increase information relevance. Despite some overlap, these systems are complimentary since they differ in the ways information is acquired, the sources and languages used, the degree of automation and human analysis and the type of data visualization. All of which are factors that may influence their performance. In order to compare event-based surveillance systems, metrics that quantitate the significance of various data sources, the analytical methods employed and the degree of data diversity need to be developed and assessed.

In countries with weak or nonexistent national public health surveillance systems event-based methods can provide real-time information on local disease activity. In the 2010 Haitian cholera outbreak, epidemic mapping was enabled using information from social and news media, which correlated well with official reporting, albeit it was available sooner. Syndromic surveillance, which features the acquisition and statistical analysis of pre-diagnostic data (i.e. chief complaints, groups of symptoms), can also be very useful in resource-limited settings where laboratory confirmation may be lacking to support traditional diagnosis-based surveillance. Such community health related information is collected using ambulance dispatch data, emergency room discharge diagnosis, family doctor networks, help line calls, triage records and lately voluntary self-reporting systems. Syndromic surveillance systems are most widely used for influenza and influenza-like illness (ILI) and severe acute respiratory illness (SARI) surveillance. Limitations of syndromic surveillance methods include discrepancies between chief complaint and actual diagnosis and free-text data entry that may limit the computational analytic potential. Other sentinel surveillance methods include monitoring medication usage or the demand for specific supplies such as beds and ventilators and for specialized personnel. Increase in medication or supply demand triggers early warnings of a potential outbreak of respiratory disease.

The World Health Organization (WHO), the European Center for Disease Control and Prevention (ECDC) and the US Center for Disease Control and Prevention (CDC) all use both traditional surveillance methods and informal
event-based data for biosurveillance. An extensive review of the infectious diseases surveillance and environmental monitoring systems in place in the EU is presented elsewhere. However, national surveillance programs have been reluctant in incorporating event-based systems and their application during real-time health events has been limited. This may be due to weaknesses in the amount, relevance, accuracy and prompt dissemination of data generated and lack of user confidence. In Sweden, a public web tool (http://www.smittskyddsinstitutet.se) is available where timely county and national surveillance data for more than 50 communicable diseases can be openly accessed in the form of interactive maps, tables and trend curves. Also, a centralized and dedicated electronic surveillance system was developed recently by the Ministry of Health of Saudi Arabia in order to monitor disease activity during the Hajj. The Healthcare Electronic Surveillance Network (HESN) allows for rapid outbreak detection, communication between the command center and the hospitals and response to a potential public health threat. This monitoring process was particularly useful in view of the possibility of MERS-CoV spread in this area during the pilgrimage.

A main objective of public health surveillance systems is to provide early warnings regarding emerging threats to human health. The Global Outbreak Alert and Response Network (GOARN, www.who.int/csr/outbreaknetwork/en/), which was established in 2000 by WHO, uses data from GPHIN and units a large number of existing networks of laboratories and institutions to gather infectious disease intelligence in order to promptly detect and verify outbreaks, issue real time alerts and rapidly respond to global or national public health threats. During the H1N1 influenza pandemic, GOARN was activated at the WHO organizational level in order to monitor disease activity, offer technical guidance and to implement screening strategies and containment measures in order to halt the pandemic. Early warning alert and response networks (EWARN) combine indicator- and event-based methods in order to detect changes in event trends or alerts that could represent potential threats to public health. WHO offers guidance on the implementation of such EWARN systems during emergencies. Information collected through EWARN systems is disseminated to national and international public health officials allowing them to monitor disease spread and rapidly implement appropriate preventive and control measures. During the recent cholera outbreak in Haiti, an Alert and Response System was developed by the Pan American Health Organization, Regional Office of WHO to complement the national surveillance system. The system involved a network of institutions and individuals that could detect, verify, assess and timely respond to cholera cases across the country. The Alert and Response system was able to detect a rise in cholera cases in hard-to-reach communities with poor access to health centers, few weeks before the national surveillance system, which relied on data only from healthcare facilities.

**Web-based tools for real-time surveillance**

Web queries are increasingly being used as a source for syndromic surveillance. Analysis of health-related search engine queries can assist in tracking regional infectious disease activity. Google Flu Trends (www.google.org/flutrends/) was one of the first web-based tools developed for near real-time monitoring of influenza activity. It is based on the fact that the number of people searching the web using influenza related keywords is correlated with the number of people actually having influenza symptoms, hence an increase in the first may signal a rise in disease activity. Indeed, it was shown that Google Flu Trends could predict regional influenza activity 1–2 weeks earlier than reported from the Center for Disease Control and Prevention. Health related queries submitted to other search engines have also been studied in regards to their ability to estimate influenza intensity and peak incidence. Google Trends (http://www.google.com/trends/) has been used to track other communicable diseases like West Nile Virus (WNV) and dengue and has been applied in mathematical models for the prediction of peak influenza activity. However because a large volume of search queries is needed for web search-based surveillance tools, these may be more effective when applied to diseases with moderate to high prevalence and when used in developed countries with high numbers of web users.

**Infectious diseases modeling**

With the advancement of computational science, it has been made possible to develop methodologies for epidemic simulation. These are broadly divided in 2 categories, agent-based modeling and spatially structured metapopulation models. Agent-based models require detailed data entry for each individual in the population of interest resulting in a comprehensive description of the epidemic. Structured metapopulation models take into account geographic area census data and inter-population mobility patterns, namely air travel and commuting network information in order to study disease dynamics and predict epidemic spread. There is evidence that compared to coarse-grained input data, when higher resolution contact pattern data is integrated in a computational model, the size of the epidemic is more accurately reproduced and at risk groups are more appropriately identified. Agent-based models provide a more detailed simulation however because of the amount of input data that is needed its use on a global scale is limited. On the other hand, structural metapopulation models allow for a wider range of large-scale stochastic realizations at the expense of detail. Ajelli et al., compared the results of the 2 methods of epidemic modeling in the progression of a baseline pandemic event in Italy. The obtained results for the 2 approaches showed good agreement with some differences in the epidemic size and timing of peak activity.

One of the most widely used metapopulation models is the Global Epidemic and Mobility (GLEAM) model (www.gleamviz.org). This is a stochastic model, which integrates global demographic data, air travel and short-range mobility data for the simulation of worldwide spread of influenza-like illnesses. In the GLEaM model, the world is divided in approximately 3300
subpopulations (according to geographical census areas) forming a network, which consists of more than 16,800 mobility fluxes, representing daily mobility patterns among the subpopulations. Disease dynamics are then integrated into the subpopulation and mobility network, building a framework where large numbers of in-silico epidemic scenarios can be generated in order to account for initially unknown epidemic parameters and simulate the possible spread of a novel infectious agent.33,44

Computational modeling assists in understanding the role of mobility patterns in the progression of epidemics and is an important tool in the assessment of both past and real-time epidemics and in the design of future targeted containment interventions. The hierarchy and timing of epidemic progression depends both on long and short-range mobility networks. Long-range air travel determines epidemic spread on a global level, whereas short-range commuting drives the epidemic “synchronization” of neighboring subpopulations and the epidemic “diffusion” from regions with airports to the adjacent areas.45 The complexity of air-transportation network is a major determinant of the global spread of infectious diseases and when taken into account in large-scale mathematical models, it is possible to predict epidemic patterns and to test containment scenarios.46

When data from 26 consecutive seasonal influenza epidemics and detailed commuting frequencies between regions in France were analyzed, it was demonstrated that heavy commuting correlated with an increase in the incidence of Influenza-like illness (ILI). Moreover, when epidemic simulation was applied, preferential paths of the initial epidemic propagation could be identified and it was shown that the starting site of the epidemic was of minor importance in regards to its peak timing and incidence at a national level. Taking into account the transmission dynamics of different age groups, changes in age specific commuting patterns can affect the epidemic spread.45 The progression of an infectious disease epidemic also depends on intra-city mobility patterns, which often differ between regions and cities of variable size, underlying the importance of contact heterogeneity on disease transmission dynamics. Dissecting the role of city-level and intra-city mobility patterns on epidemic spread can assist in developing more effective and timely containment strategies in the event of a real epidemic.47

Mobility networks have also been described using proxy data, like mobile phone data. However, according to the human mobility source data used, their predictive accuracy in regards to epidemic invasion timing and propagation pattern differed.48 In a resource-poor environment mobility patterns can be different than the ones observed in resource-rich countries. This was recently shown in a study that used Global Positioning System (GPS) data to track the detailed mobility patterns of 582 individuals in Iquitos, Peru, whose social interactions were found to be spatially and temporally unstructured. Moreover compared to temporally structured daily contacts, temporally unstructured daily routines resulted in a substantial increase of the epidemic size and effective reproductive number in an ILL simulation model.49 Therefore when planning control measures, it is crucial to know the specific mobility parameters that drive disease transmission within a population. Limiting or controlling human mobility is one of the first measures applied by national and international public health institutions in order to prevent the spread of infectious diseases, especially in the case of a pandemic or of an outbreak caused by a novel infectious agent. Models have been used to study the role and effectiveness of travel restrictions in delaying or halting a pandemic. Bajardi et al., used the GLeAM model calibrated on the H1N1 pandemic data to test the impact of several mobility restriction measures which differed in terms of their magnitude, topology and chronology in the pandemic timeline. It was shown that human mobility patterns vary greatly and international travel restrictions may be less effective than previously considered in containing a pandemic.50 More recently, Bogoch et al., combined international flight data and Ebola virus surveillance data in a model in order to assess the effect of air travel restrictions and exit or entry airport-based traveler screening on the potential for Ebola virus exportation. The investigators found that screening of departing travelers at airports of affected countries would likely be the most efficient measure to promptly identify individuals with symptoms consistent with Ebola virus disease.51

Computational approaches also help determine the characteristics and magnitude of data needed to be collected and integrated into the mathematical frameworks in order to increase the reliability and accuracy of large-scale infectious diseases modeling. The freely available open-source epidemic modeling software FRED (Framework for Reconstructing Epidemic Dynamics, http://fred.publichealth.pitt.edu/) is a flexible modeling platform that uses census-based synthetic populations and can be used by public health officials to evaluate potential intervention policies during epidemic scenarios affecting a specific population. Parameters such as transmission characteristics and natural history of the disease, vaccine and treatment access and availability, the immunological profile of the population, health-related behaviors and responses can be applied and modified by the user, in order to assess the effectiveness of different control measures.52 Using epidemic modeling, Hosseini et al., underscored the importance of national healthcare resources (apart from the contribution of air travel and trade), in pandemic spread, as resource limited countries exhibited a delay in disease reporting at the initial phase of the 2009 A/H1N1 influenza pandemic.53 As evidenced by the current Ebola virus outbreak in West Africa, socioeconomic factors and especially weaknesses of the national public health infrastructure systems can affect the local and possibly the international spread of a disease. When socioeconomic variables related but not limited to poverty, health infrastructure, child measles immunization rate, communication and urbanization and a dataset of recent infectious diseases outbreaks were incorporated in a model, high-priority regions for infectious diseases surveillance were identified.54 Hence, information on the local social and ecological context, human behavioral patterns, social inequalities, as well as the political and cultural dimensions of a community are essential for investigating risk for disease emergence and transmission. Using modeling techniques, it has been shown how social network interactions can affect disease spread but also transmit information regarding disease prevention.55

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Epidemic models have also been used for non-ILIs, like cholera or vector-borne diseases. With a gravity model constructed during the cholera epidemic in Haiti in the setting of limited surveillance data, the investigators were able to reproduce the epidemic contour and to assess the potential effects of control strategies like the distribution of vaccines and delivery of clean drinking water. A gravity model examines the interactions between spatial entities (i.e., human settlements and vector habitats) in a certain ecosystem. Changes in climate or landscape ecology may alter the spatial spread of a disease present at an ecosystem and such a modeling framework may help determine relevant risk factors or evaluate preventive and control measures.

On the basis that human and animal health are essentially interconnected and the majority of emerging infectious diseases are zoonoses, an initiative, named the One Health Initiative (www.onehealthinitiative.com), was launched in 2009, in order to bring together medical, veterinary, public health and other scientific-health and environmentally related professionals. The main aim of the initiative is to foster shared educational and research efforts toward the development of integrated surveillance systems, diagnostic tools and preventive interventions. Until now the One Health concept, has been endorsed by many national and international professional societies and organizations as well as research and academic institutions. In this regard, modeling methods are very important in identifying areas of human-animal interface where an emerging pathogen is more likely to occur. The PREDICT (www.vetmed.ucdavis.edu/ohi/predict/index.cfm) program, which is part of the Emerging Pandemic Treats Program developed by the US Agency for International Development consists of a multi-disciplinary team of experts and promotes a One Health paradigm. More specifically, it employs internet-based surveillance and active sampling from wildlife hosts together with predictive modeling, in order to identify pathogens with a potential for cross-species transmission before they infect human populations. Valliakos et al., used wild bird serological surveillance and human case data together with environmental factors like temperature, elevation, vegetation and land use, precipitation levels and population density in order to determine risk factors for West Nile Virus (WNV) spread in Greece. Results showed that disease in both humans and wild birds appeared more frequently in areas with low altitude and close proximity to water. Furthermore, when these risk factors were used in geographical information system (GIS) analysis, high-risk areas for future WNV outbreaks were identified. Study results were compared to the actual WNV incidence rate in humans in 2012 validating the model’s predictive accuracy. This risk-based approach could improve surveillance efficiency, signal early warnings for areas at increased risk for disease transmission and thus trigger prompt initiation of preventive efforts.

Limitations in the predictive value of large-scale infectious diseases modeling include a) our incomplete understanding of human mobility patterns and their multi-scale interactions and b) the delay in understanding the virulence and epidemic parameters of an emerging pathogen at the beginning of the outbreak c) not accounting for population and contact heterogeneities that may be critical for the disease transmission dynamics, d) the fact that accuracy may decrease with small size populations.

Models should take into account that disease dynamics may change during the epidemic spread. Kamp et al., have studied the interplay between the variability of transmission networks and epidemic spread by using a flexible mathematical framework. When this framework was applied to HIV epidemics in model populations, the investigators were able to show that primary infections drive the epidemic in the setting of increased risk behavior whereas latently infected individuals play a bigger role in epidemic spread during the saturation phase of an epidemic. Such models that take into account that the dynamics of a transmission network can change during the course of an epidemic, can help public health policy makers in order to develop targeted intervention strategies.

Advances in pathogen discovery and diagnostics

The rapid development and declining cost of new molecular techniques has provided the means for enhanced pathogen discovery. A shift has been taking place in microbiological surveillance, from diagnostic pathogen identification in humans and animals to wide screening for pathogens in samples collected at hotspots for emerging infectious diseases. The advancement of high throughput sequencing methods has made it possible to rapidly acquire detailed sequence data necessary for pathogen identification and analysis in large databases for the characterization of a new agent. As the volume of available sequence data is rapidly augmenting, the need for sophisticated bioinformatics tools is paramount in order for these methods to be increasingly applied in emerging infectious disease surveillance and diagnostics. Genome wide sequencing, multiplex PCR and microarray technology are all being used for syndromic surveillance, microbial discovery and the study of population host factors that determine disease susceptibility. Molecular methods are also used to create evolutionary models for the study of viral host-switching and microbial host adaptation. The epidemic potential of newly discovered pathogens could be explored with meta-genomic methods by comparing virulence traits to available genomic databases. However, predicting transmissibility and severity of pathogenicity of a previously unknown pathogen will certainly be challenging. Also, the discovery of novel pathogenic viruses in animals species in the absence of confirmed human cases needs careful consideration before excluding the potential for human disease since clinical syndrome presenting as mild illness may remain undiagnosed.

Novel methods are employed to enhance older techniques as in this recent study by Reed et al., where the investigators developed a novel non-invasive immunologic assay to perform a sero-prevalence study of Ebola virus exposure in wild apes. Using fecal samples to test for the presence of antibodies against Ebola virus, a prevalence rate of 10% was found in the gorilla population tested revealing importantly that infection is not entirely lethal in this species. Such non-invasive approaches could prove useful in detecting an increase in disease incidence rate in animal populations at regions of human-animal interface.
Remote sensing technology
Using remote sensing technology to monitor environmental changes can be useful in disease prediction. Using satellite imaging to collect information on sea temperature and surface height and chlorophyll A levels, researchers were able to construct an environmental model that could accurately predict the actual incidence rate of a cholera outbreak in Bangladesh. Apart from water-borne diseases, satellite imaging has also been used to trace vector activity, like the distribution of the Anopheles species that drive malaria transmission in Africa and to model hantavirus pulmonary syndrome outbreaks. However, vector-borne disease outbreaks are more challenging to predict due to the dynamics of vector ecology and human behavior and the variability in host immunity between different populations. Closely monitoring climatologic parameters (i.e. rise in sea surface temperature and protracted rainfall) and vegetation and soil indices is critical in order to evaluate changes that could contribute to infectious disease outbreaks. Using such data in predictive mathematical modeling could generate early warnings to inform public health interventions that would aim in epidemic mitigation.

Communications
Social media
Analysis of data collected through social media applications presents new opportunities as well as challenges in emerging infectious diseases surveillance. Foodborne Chicago (www.foodbornechicago.org) is a social media-censoring program launched by the Chicago Department of Public Health to monitor food-borne illnesses. It uses an algorithm to identify and respond to entries in Twitter, relevant to food poisoning. Another novel method of event-based surveillance is “participatory epidemiology,” with an example introduced by HealthMap. The application, which is called Flu NearYou (https://flunearyou.org/), allows any individual above the age of 13 living in the US or Canada to compete and submit surveys regarding influenza-like illness activity in their proximity. Apart from being a source of information, social media can also contribute in data analysis. HealthMap features user rating of posted articles based on their significance, a process that may enhance quality of disseminated data.

Mobile phones
Mobile phone data is increasingly being used to track human movements in an attempt to study the transmission dynamics and routes of importation of an infectious disease from region to region. Moreover, given the wide distribution of cellphone users and the increase in network coverage even in resource-limited countries, mobile phone technology is being used for infectious diseases surveillance purposes. Researchers in Sri Lanka developed a mobile phone-based surveillance system to monitor animal health. Also, after the 2008 earthquake in Sichuan province, China, mobile-phones with integrated software designed for infectious diseases case reporting were distributed to local healthcare agencies, providing an alternative for timely and accurate disease surveillance. Mobile phones allow for a 2-way sharing of information and can be used for data-collection to serve surveillance purposes and for disseminating important public health information to the public.

Challenges and future directions
Although internet-based surveillance systems are using increasingly more resources and sophisticated software for data acquisition and analysis, there still remains a geographical surveillance gap due to limitations in communications infrastructure, lack of equipment and diagnostic capability, shortage of trained personnel and decreased awareness in these areas leading to disease underreporting. Moreover the under-reporting of zoonoses and the separation between human and animal health even at the institutional level, hampers emerging infectious diseases surveillance efforts.

The availability of real-time surveillance data on the internet for health care policy makers to access is essential for an early and efficient response to an epidemic. Enforcing public health capacity in regions at high risk for infectious disease emergence should be an international priority. Moreover, focusing on endemic zoonoses surveillance simultaneously in both animal and human populations in emerging infectious diseases “hot-spots” using all available technology will also address some of the barriers for early outbreak detection. This is most important in those diseases where animal cases precede human ones. As it is true that most of the emerging infectious diseases are zoonoses, integrating the one-health paradigm offers a platform for building core capacities for animal and human disease surveillance.

Political interest and national trade priorities may obstruct international collaboration in the fight against infectious disease threats. Ensuring global public health should be a priority for each nation since it has been shown repeatedly how quickly an infectious disease can spread today in a highly interconnected world. Rigorous international collaboration is essential for the detection, prevention and control of an emerging infectious disease outbreak with potential for global spread. The development and application of point-of-care rapid diagnostic assays will enable faster diagnosis of infectious disease outbreaks and more efficient epidemic surveillance. However, early detection needs to be coupled with a rapid public health response and research should also focus on ways to lift barriers that may hinder such a global response.

Our understanding of the drivers and dynamics of emerging infectious diseases will continue to advance. Also, technologies evolve rapidly as new tools become available, search engine algorithms improve and computational speed increases allowing for the development of more sophisticated surveillance methods and more accurate predictive models. However, collaboration between institutions, organizations, scientists and public health networks involved in infectious diseases surveillance is vital in order to timely detect and respond to novel threats and most importantly, prevent new pandemics.

Disclosure of Potential Conflicts of Interest
No potential conflict of interest was disclosed.
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