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An Agenda-Setting Report: Biome Monitoring for Human Health

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Submitted in partial satisfaction of the requirements for Master of Public Health

Yale School of Public Health

Environmental Health Sciences

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Abstract

In light of the COVID-19 pandemic and the increasing frequency with which zoonotic diseases of pandemic potential have emerged in recent decades, it is vital to seek new methods of preventing disease outbreaks before they occur. Novel information age technologies have the potential to change the game for infectious disease outbreak monitoring. This paper addresses the overall opportunity that exists for biome surveillance as a means for health monitoring, particularly the way that the domains of technological and biological sciences can unite to prevent the next pandemic before it gets a chance to take hold. This report outlines the numerous methods that exist to connect biological health to human health with technology as an intermediary. There are technologies that can monitor at either the individual level or on the scale of entire habitats, either remotely or on-site, and through either invasive measurements or non-invasive sensing.

The key opportunities in this space and important next steps are as follows. First, it is vital to integrate predictive capabilities into existing disease mapping and tracking tools. Second, it is necessary to explicitly outline biological health indicators for inclusion in technological processes. Third, we must strengthen methods to quantitatively assess biodiversity loss. Fourth, we should improve indices for species occurrence, leaf area, taxonomic diversity, vegetation height, and above-ground biomass. Fifth, there is a need to refine spatially-explicit and temporally-effective ecosystem health assessments. Last, but certainly not least, it is of the utmost importance to enhance and develop more precise viral sequencing capabilities. If all of these goals are achieved, we will be in a much better position to prevent and respond to future infectious disease outbreaks and to protect the health of human populations around the world.

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Current Landscape

The objective of this paper is to outline the ways in which the technology and biology sectors can come together to monitor ecosystem health, with this assessment to be used to protect human health from novel infectious diseases. Too many people have referred to the COVID-19 disaster as a 'once-in-a-century event', which is true when you consider that the last global respiratory pandemic came nearly one hundred years ago. If we continue on with business as normal after this pandemic subsides, however, we will be faced with another existential threat much sooner than one hundred years from now.

Human activity has brought us into potential contact with thousands of unknown viruses. In mammals alone, it is estimated that there are 40,000 as-yet-unknown viruses, of which 10,000 have zoonotic potential to jump into human beings (Carlson et al., 2019). Bats, the most likely source for the SARS-CoV-2 virus, could themselves host thousands more unknown coronaviruses (Yong, 2020). Antibody testing in rural China, where SARS-CoV-2 originated, shows that a substantial number of individuals are infected with a novel virus from contact with bats every year; it just so happens that a majority of these viruses aren't further transmissible (Wang et al., 2018). As seen with SARS-CoV-2, it just takes one highly transmissible virus to lead to uncontrollable spread.

The rationale of this paper is based upon the two ways to stop a zoonotic disease outbreak. The 'easier' method is to stop transmission once a spillover event has taken place, or to stop one infection from becoming two infections, and so on. The more difficult way to go about this is to stop zero infections from becoming one infection (Yong, 2020). I believe that the only way to go about preventing one infection from ever taking place is for technology to be applied to monitor the wild habitats where these 40,000 unknown viruses are lying in wait. This paper will outline some of the areas in which stakeholders in the biological sciences and those in the technology field can come together to assess zoonotic disease threat within ecosystems. The technologies of interest will be identified, and their relevance to human health will be outlined as well. The hope is that this paper serves as a starting point for stakeholders on either side of this potential partnership to come together and set in motion a large network of technologies that monitor ecosystem health.

Ecosystem Health is Correlated with Human Health

It is well-known that human behavior is drastically altering the composition of our planet, often for the worse. Beyond the overarching aspect of climate change, recent centuries have seen a stunning loss of biodiversity and human encroachment on wild animal habitats, changing the way we interact with other species and increasing our potential for coming into contact with novel infectious diseases. In recent decades, human populations have been exposed to emerging infectious diseases in the HIV/AIDS and COVID-19 pandemics, as well as SARS, MERS, and various influenza outbreaks. What follows in this section is a discussion of how biodiversity, and by extension the health of ecosystems and biomes, can impact the health of human populations.

The unprecedented loss of biological diversity that has stemmed from anthropogenic causes has a very profound influence on human health. A major way that biodiversity loss threatens human health and safety is by increasing the risk and incidence of infectious disease outbreak, both for known vectors and for unknown vectors. In the case of known diseases, high diversity in the community of vertebrate hosts for the vectors of West Nile virus (WNV) and Lyme disease (LD) is known to reduce risk (R.S. Ostfeld, 2009). In human-dominated, low-biodiversity communities, the primary reservoirs for these diseases are species with a high prevalence, which lead to high infection prevalence in the generalist vectors that subsequently infect humans (mosquitoes for WNV and ticks for LD). Conversely, where there is a high diversity in native

species, the mosquito and tick vectors feed from a wider range of species that are not reservoirs for these diseases, and are therefore less likely to infect humans (R.S. Ostfeld, 2009). Therefore, for known infectious zoonotic pathogens, high biodiversity is crucial for protecting humans from exposure and from outbreaks.

In the field of planetary and ecological health, this phenomenon is known as the 'dilution effect'. Species living in highly diverse communities tend to dilute the effect of the reservoir species and thus reduce disease risk (Richard S Ostfeld, 2017). Most human diseases are zoonotic in origin and often predominate in low-diversity communities, making these areas potentially vulnerable to disease outbreaks (Richard S Ostfeld, 2017).

Biodiversity loss is intricately linked to habitat fragmentation, a situation which also represents a threat of novel infectious disease emergence. Habitat fragmentation is the destruction and partitioning of wild habitats into smaller areas, and often corresponds with human activities encroaching on the boundaries of these newly fragmented habitats, and it is this disruption on wild habitats that causes a reduction in biodiversity (Daszak et al., 2001). This loss of biodiversity, which has been shown to improve conditions for zoonotic infectious disease reservoirs, combined with the habitat encroachment by people into newly-fragmented, species-rich areas may increase the risk of exposure to novel infectious diseases from wildlife (Wilkinson et al., 2018).

The *One Health* framework is an emerging concept in the health sciences which connects human, animal, and environmental health into a single framework. This is based on the knowledge that roughly 70 percent of emerging diseases in humans originate from other species, and this interspecies transfer stems from stresses to environmental systems, including *habi*tat and biodiversity loss (Malloy et al., 2019). Human health and prosperity is directly connected to those

of the systems around us, and when our actions impact species around us, the *One Health* framework indicates that we will eventually feel the consequences of our behavior.

Human activity in the form of deforestation is a concrete example of how we have altered ecosystems and caused habitat fragmentation on a massive scale. There is evidence that habitat fragmentation from deforestation has led to the emergence of Ebola virus disease, has the potential to introduce numerous avian infectious diseases to humans, and has likely caused the current COVID-19 pandemic (Contini et al., 2020; Rulli et al., 2017; Sehgal, 2010). Using novel technologies to assess areas of habitat fragmentation and low biodiversity represents a massive opportunity for technology and biology to connect for the common good. These often siloed sectors have a mutual interest in addressing these issues. For the biological community, it represents untapped possibilities for rapid advancement. For the technology sector, this represents an opportunity to address an existential issue of concern that has the potential to touch all corners of the globe, as we know all too well given the trials that SARS-CoV-2 has put on societies around the world.

At some high level, there has always been a deep connection between biological health, or the health of ecosystems, and the health of human populations. The current tension in this stems from the fact that most humans have for long periods of time not realized that this relationship exists. We now are beginning to understand it, particularly in the context of COVID-19, which has touched every aspect of human civilization after a spillover event from contact with wild animal species. Because of this and of the increased frequency of emerging infectious disease events in recent decades, such as HIV/AIDS, SARS, MERS, and now COVID-19, it is vital that we monitor systems that give rise to these viruses, and we must do so in new ways. Currently, there exist methods for monitoring biomes and ecosystem health. These techniques will be outlined in the following section on *Technology for Ecosystem Monitoring*.

Technology for Ecosystem Monitoring

'Technology' is a broad term with innumerable applications. Within technology for biome monitoring, we are largely referring to techniques to measure biodiversity, such as remote satellite sensing, and techniques to assess species, such as sequencing tools for analyzing genomic sequences.

The technology industry has considered the importance of using technological innovations to promote nature conservation, but stakeholders realize that there are some steps that are necessary to take before this can become a reality. First, the conservation sector needs to build a community of practice with technological actors, rather than exclusively with governments or NGOs on which this burden often falls (Joppa, 2015). Within this conservation-technology community, it is then important for these groups to work with a wide array of stakeholders (governments, private sector, universities, conservation agencies, etc.) to create, implement, and sustain solutions (Joppa, 2015).

There are, however, actionable ways in which these ideas can become a reality. Many of the foundational structures which can act as a springboard for progress are being built that allows for information exchange between those with knowledge of nature conservation problems with those who have the technical expertise to engineer technological solutions (Joppa, 2015). It is certainly possible that novel computational technologies might completely revolutionize the practice of conservation by providing the tools and infrastructure to assess and safeguard biodiversity in entirely new ways. Its success, however, will come down to whether stakeholders can come together to define the key technological challenges and work with a wide array of potential partners to create, implement, and sustain solutions (Joppa, 2015).

There are a number of methods in which emerging technologies have the capability to conserve biodiversity. There are technologies that can identify individual animals, follow their movements, identify and locate animal and plant species, and assess the status of their habitats remotely (Pimm et al., 2015). As threats to the survival of species are increasing, these technologies have become better, faster, and cheaper. However, simply improving technologies does not address the root cause of a loss of biodiversity. For example, although we can track species and their habitats, we cannot prevent human encroachment on these habitats and any poaching that occurs in these locations or any habitat loss that occurs. What is needed in this sphere is to provide the right tools to people who can make a difference (in the case of preventing poaching) or to link the existing remote species sensing technologies to predict where as-yet-unknown populations remain (Pimm et al., 2015). In addition, the range of ecosystems that are protected is unevenly distributed. This also needs to be addressed within the relevant spheres.

The pace and scope of these technological developments are wide. What follows are examples for further discussion.

One major application for technological developments is in species tracking. From 2006-2016, there was an unprecedented expansion in technologies providing data on individual locations and individual movements. These are now smaller, satellite-based technologies as well as non-invasive methods of tracking movement. There are even technologies that can examine an individual's tissue, examining isotopes, genetic material, and perhaps even disease (Pimm et al., 2015). In the future, there are opportunities to potentially do this work through remote sensing.

There have been vast improvements in obtaining species location data. Methods include satellite-borne cameras, airplane surveillance, drones, and databases on species occurrence (these have expanded particularly rapidly). There are also DNA libraries, image-recognition algorithms,

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and automated identification of bird or bat calls that have been actively researched for a decade or more. The biggest advance thus far has been in using "citizen scientists" with smartphones, which allows individuals to deposit pictures of species, which then allows for the mapping and tracking of the distribution of animal species (Pimm et al., 2015).

High-resolution imagery, from satellites and increasingly-sophisticated drones, is freely and widely available and vast amounts of data (Pimm et al., 2015). These high-resolution images have the potential to draw attention to habitats that are threatened and encroached upon by human activity. The hope here is that these images would then direct conservation efforts and disease monitoring efforts to higher-risk locations.

There are three examples of places where improved technologies might make the most difference for biome conservation. The first is genetic barcoding, which can identify a species for only 1 USD from a small, unique, DNA sequence. There are a great majority of unknown species in groups with few taxonomic specialists, so this will soon become the most common method for discovering new species and for surveying communities in locations where not much is known (Pimm et al., 2015). The second example is of detecting species remotely from satellites, where small improvements in image resolution might offer the possibility of conducting species surveys in locations where it might otherwise be difficult or treacherous to reach (Pimm et al., 2015; Sehgal, 2010). A potential difficulty to address is processing speeds to analyze the vast amounts of data. The last example is of drones with multiple sensors, both visible and infrared, with cameras, software, and internet connectivity, which would offer better information at a cheaper cost than what you would get from either airplanes or satellites. Drones are already used in monitoring forest fires, identifying biodiversity of understory vegetation, identifying dead trees

and mortality within the canopy layer, monitoring invasive species, pests, weeds, and diseases, and monitoring animal species aerially (Pimm et al., 2015).

Feasible examples of non-invasive conservation include the footprint identification technique, scent-detection dogs, analyzing individual skin patterns, using infrared sensors to analyze canopy composition, using acoustic techniques to assess species noise and volume, and non-invasive genetic sampling (Pimm et al., 2015). Individual identification from DNA in hair, feces, and saliva can serve as an invaluable monitoring tool as the number of gene loci for individual ID increases, and genotyping errors are reduced as the technologies improve. These genetic monitoring techniques are also potentially valuable for assessing viral genome sequences; this will be touched upon in later sections of this paper.

Despite all of these technological innovations, it is important to know that no single tool will allow for the monitoring of multiple species across many diverse landscapes. It is also important to realize that the same challenges that currently exist in 'Big Data' will be relevant here, namely that of interoperability and standardization of data from different sources including government agencies, citizen scientists, and the private sector. This can present significant challenges regarding data quantity, quality, integration, as well as the cost, scope and ease of technology use.

Predicting Disease Threat From Changing Land-Use Patterns

Improved remote sensing offers an avenue to analyze habitat loss, which is a massive threat to biome health (Malloy et al., 2019; Pimm et al., 2015). About two-thirds of all terrestrial species live in tropical moist forests, with the biodiversity hotspots within these biomes therefore containing a wide array of threatened species. These areas are also known to be global hotspots for emerging infectious diseases, representing a massive risk for outbreaks (Allen et al., 2017).

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There are studies that show where threatened forest remains outside of protected areas and where within these protected areas it has been lost. Species locality data leads to information on species ranges, but for continuous monitoring, it needs to be remotely sensed somehow, which would continuously provide a way to assess species health and alert stakeholders to areas where habitat changes are having a major impact on species survival (Pimm et al., 2015). In the case of human encroachment on wild habitats, this could also provide information on where humans are at a risk of coming into contact with species that are likely to be reservoirs for novel diseases. Beyond this, there are additional challenges, such as assessing the spread of disease that causes population loss in animals (Pimm et al., 2015). These diseases also have the potential to jump to humans, making it urgent to determine how to monitor that as well.

To measure biodiversity change and ways to conduct surveillance on emerging diseases, satellite remote sensing presents opportunities and challenges to assess markers of biodiversity loss as it is occurring. Eventually, the goal of using this satellite sensing technology would be as a predictor for emerging infectious diseases. Due to the geospatial nature of disease outbreak, there are certain emerging diseases that can be detected from space (Malloy et al., 2019). The World Health Organization (WHO) and United States Centers for Disease Control (CDC) already use geographic information system (GIS) technology in monitoring outbreaks, although these methods at this moment fail to include real-time environmental information, which is currently difficult to integrate into existing systems (Malloy et al., 2019). Therefore, as these methods currently are limited in their disease predictability and can only map what is already known, there is an opportunity here to integrate predictive capabilities into existing disease mapping and tracking tools. There is also an opportunity to strengthen methods to quantitatively assess biodiversity loss.

Until biodiversity loss is standardized, stakeholders will have difficulty planning interventions to address its root causes and target solutions.

Once environmental measurements are standardized, however, applications for satellitebased remote sensing in predictive health surveillance are numerous and wide-ranging. These technologies can survey a wide array of environmental conditions at a low cost and, importantly, a consistent time scale, which adds significant value to computer models that assess risk and prevalence of global disease burden that is attributable to environmental factors (some estimate this to be about 25% of global disease burden) (Malloy et al., 2019). An obstacle to measuring biodiversity from satellite remote sensing is that you cannot directly measure biodiversity from space. Rather, it must be estimated after measuring key variables that can lead to calculations of biodiversity. Biodiversity is clearly a difficult attribute to measure, so a combination of satellite remote sensing, real-time in-situ measurements, air measurements, and computer modeling are all likely to be necessary parts of a monitoring program (Pettorelli et al., 2016).

An organization known as *The Group on Earth Observations - Biodiversity Observation Network (GEO BON)* has put forth variables that can lead to biodiversity estimates (Pettorelli et al., 2016). The indicators that can be remotely sensed through current satellite technology include fractional cover, forest cover, land cover, fraction of absorbed photosynthetically active radiation, leaf area index, phytoplankton, phenology, soil moisture, fire disturbance, and inundation. In areas that are of particular interest (those that should have high biodiversity), the variables that are especially relevant are the fraction of absorbed photosynthetically active radiation, phenology, and inundation (Pettorelli et al., 2016). In the future, when technology improves and more accurate measurements can be made, indices for species occurrence, specific leaf area, taxonomic diversity, vegetation height, and above-ground biomass will also be important indicators (Pettorelli et al., 2016).

Ecologists have asserted that there is a strong need for spatially explicit and temporally effective ecosystem health assessments that are based on remote sensing data (Li et al., 2014). At present, remote ecosystem health sensing is based on one ecosystem attribute: vigor, organization, or resilience, which no longer suffices. Rather, these authors argue that effective assessments should consist of all three of the above attributes (Li et al., 2014). The main challenges that hinder efforts at comprehensive remote sensing include: scale, transportability, data availability, and uncertainties in health indicators that stem from remote sensing data. It is, however, possible that upcoming optical sensor technologies on satellites and improved data acquisition and processing tools might partly address these challenges (Li et al., 2014). In light of this, a potential way that technology and biology can come together is to more certainly outline biological health indicators and work with the technology sphere to solidify what health indicators look like.

All of the above technologies consist of remote sensing tools, which are certainly vital in monitoring biodiversity and ecosystem health. There are, however, additional novel technical tools that can be used directly within areas of interest to assess biodiversity and any possible emerging threats to human health. At the interface of technology and the biological sciences, there are technologies that allow for rapid, large-scale species identification in hyperdiverse, highly biodiverse taxa, as well as in sequencing viral samples to assess their phylogenies, where they came from, what countries they are prevalent in, and their future potential. Below are some examples and case studies of where these technologies can be used.

Technology and biology can further come together to sequence samples of viruses that present a threat to human health and well-being. Often, viral sequence data is limited, as is the case

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in Dengue virus sequencing in Indonesia (Stubbs et al., 2020). The barriers to sequencing viruses stem from the need to ship samples from outbreaks long distances to laboratories with the correct sequencing equipment, which is time-consuming and expensive (Stubbs et al., 2020). This method also often results in a failed assessment because of low viral load in the samples or in the degradation of the viral genome during the shipping process. Novel methods of virus sequencing can address these challenges. A new multiplex PCR and Nanopore-based system for assessing viral sequences, which is a cheap, rapid, portable method for analyzing samples, can be done in the field and give immediate results, which in the case of disease outbreaks, is critical when time is of the essence to contain the spread and to develop treatments (Stubbs et al., 2020). This novel multiplex approach is promising in its capacity to recreate viral sequences, producing near complete coding-region coverage from all samples tested, compared with the current PCR technology, particularly when there were low concentrations of the virus in the samples (Stubbs et al., 2020). Although this method is promising, it is not as accurate as it could be, so there remains an opportunity moving forward to develop even more precise sequencing techniques in the coming years.

In addition to the progress mentioned above in analyzing samples of known viruses, improvements in sequencing technologies can rapidly discover new species and, potentially, asyet-unknown infectious diseases. Currently, more than 80% of all animal species remain unknown to humans, and countless viruses that only exist in animal reservoirs remain undiscovered to us as well (Srivathsan et al., 2019). In taxa that are highly diverse, there is a method known as 1D MinION sequencing that has the potential to increase the rate of species discovery using genomic sequencing to sort specimens to species, which would then use Artificial Intelligence (AI) techniques, based on a small subset of specimens, to verify the results (Srivathsan et al., 2019). These methods are low-cost and are appropriate for areas that need rapid and large-scale species discovery. Because of its work in sampling animal species, MinION sequencing has the potential to reveal unknown diversity in viruses and is especially suitable for regions with high biodiversity and limited access to appropriate laboratory facilities (Srivathsan et al., 2019).

These sequencing technologies represent a form of AI. AI presents a wide range of possibilities for data analysis in the fraction of the time that it would take human scientists to conduct on their own. Currently, there are startups and browser-based tools that can analyze large volumes of data from complex projects using neural networks and computer-sensing algorithms. These methods require sample data to train an AI algorithm to recognize sounds and images of interest, but once trained, they represent a massive increase in productivity and output over any other method that is currently available (Kwok, 2019). Moreover, while AI techniques may seem out of reach for the average user, it has become more accessible than ever. Data can either be outsourced to startups who specialize in AI for conservation, or biologists who want to learn AI, there are online classes and large user communities with many examples of sample code (Kwok, 2019). Eventually, with large amounts of data, it will hopefully be easier to identify anything out of the ordinary that represents a potential threat to biodiversity and to human health.

In light of changing ecosystem and infectious disease dynamics, it is clear that there is a critical need for technology and biology to come together. Thankfully, in recent years, there have been many advances in integrating technology for the greater good of conserving biodiversity and protecting human health. There is still a long way to go and many different actors to integrate, but the opportunities in this field are wide-ranging as we begin to imagine a post-pandemic world in which future catastrophic outbreaks can be prevented.

Opportunities Moving Forward

To begin to improve the connection between the technology and biology sectors for the purpose of reducing threats to human health, a vital first step is ensuring that there is interoperability between all of the monitoring systems in use. This means that it is necessary for communication to be consistent and for data measurement, storage, and analysis to be standardized across all systems to avoid miscommunications and potentially costly delays in information exchange. Although no single tool will be able to accomplish this massive task, making interoperability between existing systems will allow for easier analysis of vital data. Moreover, because there currently are systems that map disease spread, but lack predictive functionalities, there is an opportunity for technology and biology to come together to incorporate the predictive biological indicators of health into these models to assess possible future infectious disease outbreaks.

Second, it is important for all organizations involved in this endeavor to agree to fully and openly share data and to cooperate with each other. This is particularly important for private sector organizations that might otherwise be competitors, and it is similarly important for governments to be transparent with what the status of the health indicators of interest are in their respective nations. As we have seen in the last couple of years, emerging infectious diseases represent an issue of international security, and must require global cooperation to solve. If these two matters in question are addressed, then it is possible that the future opportunities outlined in the rest of this section will be realized, for the benefit of the global community.

Beyond monitoring the spread of infectious diseases from animals to humans, a future challenge which represents a massive opportunity in this sphere is tracking disease spread that causes population loss within animal species. In some bat caves, 1 in 20 individuals are infected with one of thousands of as-yet-unknown coronaviruses (Yong, 2020). Human beings come into

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contact with these creatures on a daily basis, some of whom even venture into these caves (Yong, 2020). If technologies were developed to analyze viral samples and viral circulation within these bat species, it could give us a better understanding of what exists out in the world. This potentially could allow us to pre-emptively develop vaccines and treatments if there is a lot of virus circulating in these communities, which would therefore be associated with increased potential for a spillover event.

On the whole, there are innumerable opportunities for technology and biology to come together to conserve at-risk ecosystems as well as protect human health. Opportunities range from individual citizen scientists using their smartphones to monitor environmental conditions to large corporations directing time and resources towards these efforts. Microsoft's AI for Earth initiative is one such example. This program allows Microsoft to put their cloud and AI tools in the hands of those in the biological sphere that are working to solve environmental challenges (Herweijer et al., n.d.). In this endeavor, however, Microsoft is aware that conserving biodiversity and at-risk habitats cannot rely on one technology or one actor alone. If anything, this should be the biggest takeaway from this review. There are massive opportunities for many different stakeholders to work together to protect environmental and human health, but it requires ideas from many groups and cooperation on a massive scale. As with all global issues, no one perspective or one entity will be able to solve it alone.

It will take the work of multiple organizations to implement any of these new systems. The *One Health* framework discussed earlier, connects human, animal, and environmental health into a single framework. In its current state, this framework is deficient and should be updated to include technological capabilities in our rapidly changing world. All of the technological capabilities that have been developed in recent years and discussed in this report would make this

framework more comprehensive and allow organizations to actually monitor metrics in each of the three domains as they connect to each other. It would be incredibly beneficial for national Centers for Disease Control, such as the CDC we have in the United States, to integrate this novel framework into its mission and to formulate units to manage these endeavors. It would require collaboration between organizations in the public and private sectors, but as with all global problems, input is required from as many perspectives as possible to come to a solution.

Appendices

Technological methods	Individual vs. species-level	Remote vs. on-site sensing	Invasive vs. non- invasive sensing
Satellite-borne cameras	Both, depending on image resolution	Remote	Non-invasive
Airplane surveillance	Both, depending on image resolution	Remote	Non-invasive
Drones with multiple sensors	Both, depending on image resolution	Remote	Non-invasive
Databases on species occurrence	Both	Remote	Non-invasive
DNA libraries	Both	Remote	Non-invasive
Image-recognition algorithms	Individual	Remote	Non-invasive
AI algorithms	Both	Remote	Non-invasive
Citizen scientists	Both	On-site	Non-invasive
Genetic barcoding	Individual	On-site	Invasive
Footprint identification	Both	On-site	Non-invasive
Scent-detection dogs	Both	On-site	Non-invasive
Acoustic monitoring	Species-level	On-site	Non-invasive
Multiplex PCR and Nanopore viral sequencing	Both	On-site	Invasive
1D MinION sequencing	Species-level, from individual samples	On-site	Invasive

Table 1: Technological methods outlined throughout this paper with some key characteristics.

Table 2: Key opportunities for technology and biology cooperate and protect human health

Key Opportunities

Integrate predictive capabilities into existing disease mapping and tracking tools

Explicitly outline biological health indicators for inclusion in technological processes

Strengthen methods to quantitatively assess biodiversity loss

Improve indices for species occurrence, leaf area, taxonomic diversity, vegetation height, above-ground biomass

Refine spatially explicit and temporally effective ecosystem health assessments

Enhance and develop more precise viral sequencing capabilities

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