

# Chapter 21

## Preventing Pandemics: Earth Observations for One Health



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### Personal Story

I study ecology & evolution, a field that enables me to get outside and take in the wonder of the natural world. So it wasn't exactly optimal when I, and thousands of other college students, had to start taking classes from a laptop in the living room in March of 2020. I dearly missed the walks in the woods with my classmates and professors, drawing out the delicate web of connections between trees and deer and ourselves. Inundated with pandemic news, I saw plenty of discussion of pangolins and wet markets, but little of our larger relationship with animals and nature, which I view as integral to explaining the emergence of COVID-19. In the evolutionary history of *Homo sapiens*, nature has been our adversary, something to resist and exploit for our own survival. The persistence of this deep-rooted urge has contributed to our attempted conquest of and separation from the wild world. But the pandemic has emphasized that we're just as much a part of nature as we always have been: pull on one thread in the vast tapestry of life, and you might not expect what will unravel. Humans cannot survive in a vacuum, nor would that world be nearly as vibrant as the one we have today. Understanding of and connection with the natural world is vital to not only conservation, but our own health and wellbeing. So take a walk outside; observe the life that persists everywhere you look. It's all connected—and so are we. *Maya Mishra*

### Introduction

Somewhere in a cave in southern China, a colony of bats rustles and squeaks. The stone floor is coated in guano, or bat excrement, lending a musky scent to the air. Soon the bats will take flight for the evening, soaring through the sky in search of prey. During their nightly ranging, these bats will consume many insects, keeping

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populations in check and therefore playing an important role in their ecosystems (Kunz et al., 2011). They also provide prey for avian raptors (Wu et al., 2019), and for humans, they possess commercial value for their role in traditional medicine (El-Sayed & Kamel, 2021).

Bats also have a hidden physiological talent: they can play host to a number of diseases, enabling them to spread pathogens to each other and to other creatures without becoming sick themselves (O'Shea et al., 2014). Unfortunately, this natural advantage also threatens human health: diseases can be transmitted to other animals through contact with the bats or their feces and can then make the leap to humans, sometimes to devastating worldwide effects (Wang & Eaton, 2007).

In our third year of the COVID-19 pandemic, many of us have become unexpectedly familiar with zoonotic diseases, those infections originating in animals. But we tend to lose sight of the broader context in which this pandemic emerged. The zoonotic origins of COVID-19 are not unique: about three-quarters of emerging diseases newly recognized by epidemiologists can be traced to animals (Rabozzi et al., 2012), and zoonoses make up 60% of the total number of infectious diseases affecting humans (Meurens et al., 2021).

In the pandemic age, there is no need to overstate the necessity of monitoring disease emergence and investigating the factors that affect this process. Humanity's increasing encroachment into the Earth's wild places has brought people and livestock into a higher degree of contact with wildlife (Rabozzi et al., 2012). Diseases are therefore more likely to be transmitted from wildlife to domestic animals, where they then can make the jump to humans in an event known as a "spillover" (Rabozzi et al., 2012).

However, we know much less about the specific conditions that influence disease spillovers. Studying disease emergence involves not only human factors, but also those concerning animals and the environment. These three areas are united through the framework of One Health. This term encompasses a way of approaching scientific and legislative issues with an interdisciplinary perspective that recognizes the overlapping priorities of human, animal, and environmental health. Today, this approach has been institutionalized by such organizations as the United States' Centers for Disease Control and Prevention (CDC), which has had a One Health Office since 2009 (One Health, 2021), and has been adopted as a key principle by others, including the World Organization for Animal Health ("One Health," n.d.).

The One Health framework also clarifies the role of Earth observations (EO). EO, which encompass a wide range of data types on relevant environments and habitats worldwide, can be gathered via remote sensing by spaceborne satellites. The instruments aboard these satellites can collect data within each facet of One Health: on the human and animal side, they can track animal presence, land use change, and deforestation from space, identifying the areas in which humans or livestock might encounter wild animals. In terms of environmental health, satellites can assess ecosystem health through various imaging methods as well as gathering precipitation and climate data that govern where disease-transmitting species can occur. The National Aeronautics and Space Administration (NASA)'s fleet of satellites has been collecting these and similar EO for years.

In this chapter, I discuss uses of EO in a One Health framework to prevent disease spillover and reduce disease burden worldwide. The data enable three broad approaches that align with the three One Health areas: wildlife-based approaches, which center around the wild animals that carry disease; environment-based approaches, which focus on climate and habitat variables that dictate where species may occur; and human-based approaches, which track human impacts on wild areas and assess the risk of spillover. Critically, all of these categories can be integrated with other interdisciplinary forms of data—including social, economic, and political information—to succeed in preventing disease. I conclude by discussing past examples of EO use to predict and prevent disease through a One Health framework and emphasize how preventative measures must address causes, rather than symptoms, of relevant human behaviors in order to avert disease emergence and decrease burden.

Innovative combinations of EO data have the potential to decrease the burden of existing diseases as well as to assess the risk of spillover events in time and space. If we can predict where and when spillovers are likely to occur, we can take steps to prevent them. As the COVID-19 pandemic has emphasized, informed preventative measures—enabled by Earth observations—could save millions of lives from disease and death.

## Wildlife-Based Approaches

Zoonotic diseases, by definition, have animal hosts, or reservoir species, in which the pathogens circulate. Aquatic birds are the reservoir for influenza (Parrish et al., [n.d.](#)); SARS, and likely COVID-19, has their reservoir in bats (Li et al., [2005](#)). Reservoirs are part of the reason that zoonotic diseases are so difficult to eliminate: even if cases in humans can be significantly reduced—a difficult task in itself—future interactions between humans and the host species could facilitate new spillovers of the pathogen, leading to additional outbreaks.

It is therefore critical to investigate where these reservoir species are located, as well as any movements and behaviors that may bring them into close contact with humans. To this end, EO provide invaluable insight that can be paired with in situ data for more comprehensive wildlife tracking. A plethora of innovative combinations of data are available to inform future efforts to decrease potentially disease-spreading human-wildlife interactions by promoting conservation, benefiting both humans and other species.

The keystone of wildlife-based approaches to preventing disease is spatial tracking data on the reservoir species themselves. In the past, radio trackers required researchers to carry an antenna and monitor the creature of interest on foot or in a vehicle or aircraft, requiring significant time and energy investments (Robertson et al., [2012](#)). Satellites have streamlined this process, allowing scientists to collect larger quantities of accurate location data without spending long hours in the field.

GPS trackers placed on individual creatures rely on orbiting satellites to deliver location data to scientists. While one might envision the classic large collar on an elephant or lion, researchers worldwide are collaborating through the International Cooperation for Animal Research Using Space (Icarus) to tag and track smaller animals using a satellite-based system (About Icarus, [n.d.](#)). Icarus' focal species include a number of reservoir taxa, including birds and bats. Animals can be tracked in real time, with the data routed to Movebank, an open-access database (Kranstauber et al., 2011; The Internet of Animals, [n.d.](#)). Icarus and other similar initiatives can provide platforms for forecasting movement and migration patterns to reduce human-wildlife contact, therefore also lessening the risk of a spillover event.

Direct tracking data can be supplemented with other spatial data to paint a clearer picture of species presence, abundance, and behavior. Camera trapping data can be used to estimate the abundance of reservoir species individuals in a set area. The Wildlife Insights database represents one such collaboration in the field, containing over 22 million camera trap images analyzed by artificial intelligence, which can provide data on species presence and abundance around the world (Wildlife Insights, [n.d.](#)).

Citizen science data can also be used to monitor species locations and distributions, through widely accessible phone applications such as iNaturalist (iNaturalist, [n.d.](#)) and eBird (eBird Science, [n.d.](#)). Anyone may submit species sightings, which provide large and spatially far-ranging datasets to scientists. While the quality of these data can vary, citizen science can provide an important supplement to other data sources. By tracking which species have been observed by people in different locations, it can also provide insight, if not an exact measure, of the degree of human-wildlife interaction, which could inform estimates of spillover risk.

Knowing where reservoir species are located is critical information to preventing spillover events. However, as suggested by the One Health framework, species distributions must be integrated with human population characteristics in order to accurately assess and mitigate the risk of disease transmission.

## Environment-Based Approaches

All species have specific environmental requirements to persist long-term in their habitats—they can only survive in certain temperature ranges, for example, or they might require particular levels of rainfall. As climate change increases temperatures around the world, affecting seasons and weather patterns, the geographic ranges in which species can exist are also changing (Lippi et al., 2019). Mapping key environmental variables allow us to project the future range shifts of key species in order to determine populations at risk. The environmental variables observed by satellites, including temperature, rainfall, and land cover type, are critical to projecting where and when species will exist, in turn contributing to predictions of where disease may emerge. This allows preventative measures to be deployed to get ahead of outbreaks and manage risk.

Thus far, this work has largely been conducted with insect vectors of disease, such as mosquitoes (Lippi et al., 2019), ticks (Slatculescu et al., 2020), and flies (Moore & Messina, 2010). These vectors carry many known diseases, including malaria, Lyme disease, and sleeping sickness, and previously unknown illnesses are emerging at a rapid rate (Bartlow et al., 2019). The World Health Organization estimates that vector-borne diseases cause over 700,000 deaths globally each year, with cases well into the hundreds of millions (Vector-Borne Diseases, n.d.).

Mosquitoes are colloquially known as the world's deadliest animal, causing between 700,000 and 2.5 million deaths every year (Kamerow, 2014). Different species of mosquito carry a number of zoonotic pathogens, the deadliest being malaria, which is carried by *Anopheles* mosquitoes (CDC, 2020): half the world's population lives at risk of the disease (Kamerow, 2014). Other species of mosquito harbor yellow fever, Zika, and West Nile virus, among others (Avšič-Zupanc, 2013). These diseases' high burden makes tracking mosquito abundance and distribution critical to preventing significant morbidity and mortality.

Because of the temperature and rainfall dependence of mosquitoes' life cycles, the highest burden of mosquito-borne disease cases occurs in warm, tropical areas where the insect can reproduce and cause infection year-round (Le et al., 2019). Mosquito forecasting based on temperature and precipitation variables has become an important tool, especially in areas that experience this increased burden. EO provide consistent and accurate data to drive these models (Chuang et al., 2012), with variables such as vegetation density and water content measured by the Landsat and Sentinel satellites (Tsantalidou et al., 2021). Predictions of mosquito density allow public health institutions to roll out preventative measures, including public awareness campaigns and insecticidal efforts (Giordano et al., 2018).

In a similar manner, tick abundance can also be predicted using EO. Ticks are another significant contributor to the overall vector-borne disease burden worldwide, carrying Lyme disease, tick-borne encephalitis, and other illnesses (Slatculescu et al., 2020). For ticks, evaluating a combination of climate variables as well as habitat suitability in terms of land cover and use is necessary to determining where these species may establish in our changing world (Slatculescu et al., 2020). Past studies have relied on satellites for these data, including Landsat for land cover imagery (Slatculescu et al., 2020) as well as Terra's Moderate Resolution Imaging Spectroradiometer (MODIS) for the normalized difference vegetation index (NDVI), or "greenness," of plant matter (Da Re et al., 2019). Tick species distribution models predict that warming temperatures will significantly increase the abundance of ticks in northern areas, which previously had low burdens of insect presence and consequently tick-borne illness (Sagurova et al., n.d.; Slatculescu et al., 2020). With science providing a foundation for proactive management, these areas can now prepare for heightened tick presence with campaigns to educate the public on tick-safe behavior and make healthcare providers aware of the risk.

Ticks and mosquitoes are two of the most widely studied insect vectors, but the principles of climate and habitat discussed here can also be applied to other species, including the tsetse fly, which carries sleeping sickness (Moore & Messina, 2010), and the kissing bug, which transmits Chagas disease (Klotz et al., 2014). Vector

ranges are predicted to shift and expand with our changing climate (Bartlow et al., 2019), and EO data can be employed to train models and predict these shifts under various future climate scenarios. For the communities projected to be at a heightened risk of disease burden, these studies have and will provide a critical head start on disease prevention.

While species distribution modeling for health-related purposes has historically been applied largely to insect species, it can also be used to an extent for mammalian and avian reservoir species. Variations in climate or ecosystem structure can affect habitat use, migration patterns, and other relevant animal behaviors, and these key factors can in turn affect the degree of human contact with species that could spread disease.

## Human-Based Approaches

In a final application of the One Health framework, measuring the presence and effects of humans on wildlife habitat is especially critical to determining disease risk. Human activities, including logging, agriculture, and construction, among others, have increasingly encroached on the habitats of many species. These endeavors increase the likelihood of human-animal contact that may lead to a spillover event in two main ways. First, the people conducting these activities spend a large amount of time in largely intact natural habitat, increasing the chance they may encounter wildlife. Additionally, there is evidence across multiple reservoir taxa and study systems to suggest that when habitat is fragmented or destroyed, disease transmission from wildlife increases (Goldberg et al., 2008; Plowright et al., 2011; Suzán et al., 2008). This makes it more likely that people living and working in these areas will not only encounter wildlife, but also that this wildlife will be carrying and transmitting disease.

EO have long been used to visualize habitat degradation, including tracking deforestation with Landsat imagery (Souza et al., 2013) and wildfire effects with instruments aboard the Suomi National Polar-orbiting Partnership (NPP) satellite (Ba et al., 2020). EO can also provide data on human encroachment by measuring urban expansion with MODIS (Mertes et al., 2015) as well as land use change for agricultural intensification, again with Landsat (Kontgis et al., 2015). These data can all inform integrated models of spillover risk that incorporate human, animal, and environmental factors.

A concrete example of the potential for data integration and intervention across the fields of One Health to prevent disease involves logging. Logging activity, aside from destroying habitat, involves many individuals spending a large amount of time in forests, and many loggers hunt bushmeat for supplemental income and food (Poulsen et al., 2009). This latter activity unsustainably decreases wildlife populations (Poulsen et al., 2009) and poses a high risk of spillover (Schilling et al., 2020), as hunters come into close contact with the animal's bodily fluids, facilitating disease transmission. Maps of logging activity combined with species distributions can

therefore be used to evaluate the risk of encountering reservoir species and advise loggers accordingly. EO can contribute to both of these parts: as previously discussed, wildlife can be directly tracked or modeled using climate and habitat data, and logging roads and forest degradation can be mapped using LiDAR data (Affek et al., 2017), which can be obtained from the Global Ecosystem Dynamics Investigation (GEDI) instrument orbiting aboard the International Space Station (Rangel Pinagé et al., 2019).

Besides affecting habitat, the indirect effects of humans on wildlife could alter the risk of disease spillover. For instance, artificial nightlight from human electricity use has been shown to alter the activity patterns and behaviors of birds and bats (Sanders et al., 2021), which could change the degree of potential human exposure and contact with these reservoirs. Nightlight can be measured with Suomi NPP's Visible Infrared Imaging Radiometer Suite (VIIRS) and can be integrated with animal tracking data (Ditmer et al., 2021) for a comprehensive look at behavior change and possible risks. The same principles can be applied to other indirect human effects, such as noise pollution.

The human side of the One Health trio is the one over which we have the most control: through innovative scientific investigation, we can track how our behaviors and policies with regards to nature affect our own health. Integrating human data from varied and diverse sources with those on animals and the environment is critical to creating policies and campaigns to prevent disease emergence and spread.

## Discussion

Even in the most densely populated cities, humans are deeply intertwined with the natural world in a rich and beautiful web. When we tug on one strand, the reverberations echo in directions we might not expect. Cutting down trees for timber might fulfill an economic need, but will also destroy habitat, driving reservoir species closer to humans and livestock and increasing the risk of disease transmission. The decisions we make in our stewardship of the natural world are critical to not only animal and environmental health, but also human health.

Earth observations can play a key role in this mission—from tracking individuals within reservoir species, to contributing climate data to species distribution models, to measuring human presence and expansion, satellites have become a critical source of information. EO data can be combined across these different fields to better estimate the disease burden and risk of spillover. This will allow us to employ preventative measures and hopefully avoid the next global pandemic.

While the number of these interdisciplinary projects is still small, there are several past examples of disease prevention projects that combine data across the areas of One Health. EO played a crucial role in an avian influenza early warning system, which was developed as a collaborative project between scientists at NASA, the US Department of Agriculture, and the Department of Defense (*Avian Influenza Early Warning System: Using NASA Data to Predict Pandemics*, 2010). Avian influenza

has unique spillover potential, as it is spread by highly mobile waterbirds, which can transmit the virus to flocks of domestic fowl (Avian Influenza Early Warning System, 2010). It can then more easily make the jump to human farmers, where it can cause severe illness: death rates between strains range from 2.5% to 50% (Skeik & Jabr, 2008).

The NASA models projected influenza outbreaks in time and space, relying on a comprehensive combination of data (Avian Influenza Early Warning System, 2010). Climate variables, including temperature, rainfall, radiance, and NDVI, were obtained from NASA satellites and integrated with maps of migratory flyways, species prevalence data, and local socioeconomic conditions to create a weekly forecast of illness (Avian Influenza Early Warning System, 2010). This type of interdisciplinary scientific work, which touches on each of the three One Health fields, will be critical in the future to avert possible pandemics. The framework of this system can hopefully be expanded to other zoonotic diseases in the future, such as those carried by bats, another highly mobile species.

Attempts to elucidate the social and environmental conditions surrounding spillover events are similarly critical to preventing future disease outbreaks. This work has been conducted with *Ebolaviruses*, which are thought to have their reservoirs in bats; confirmed spillovers were found to be associated with locations around forest edges and contact with bushmeat, with different strains exhibiting different characteristics (Judson et al., 2016). EO have also been employed in this space, with Landsat imagery supporting an association of Ebola outbreaks with human-intruded tropical forest areas (Tucker et al., 2002). Spillovers of Hendra virus (McFarlane et al., 2011), Nipah virus (McKee et al., 2021), and human monkeypox (Fuller et al., 2011) have also been associated through EO and other data with various environmental, human, and wildlife variables. This type of analysis, if applied more widely to known zoonoses, can be used to create spillover forecasts, warning people of the risk and therefore decreasing the likelihood of disease occurrence.

As the One Health space continues to grow and evolve, new combinations of data will lend us yet more insight on how we can predict and prevent disease. However, the results then need to be applied through policy and public education in order to be effective. To date, studies have emphasized that human-driven climate change and habitat destruction are not only devastating ecosystems, but also putting our own health at risk by increasing the burden of disease and the probability of spillover. Worldwide, we must reframe how we look at the natural world, transitioning from a lens of exploitation to one of conservation and value. This should be reflected in legislation and funding on local, national, and international scales.

The COVID-19 pandemic has also underscored just how interconnected humans are as well. Disease proliferation anywhere is a threat to people everywhere on Earth and, therefore, the ethos of collaboration across borders and disciplines that has arisen during the pandemic should continue to be supported after we emerge. This is facilitated by databases like Movebank and Wildlife Insights, which make data widely available to scientists around the world. Investigations that focus on human-animal interaction will also need to incorporate social, political, and



economic data to a higher degree in order to more fully depict the complexities of human society—and this will necessitate changes beyond the scientific.

For instance, simply legislating against hunting bushmeat is not a feasible mechanism to reduce the risk of spillover that accompanies it. Not only have attempts to eliminate the practice without significant control measures been ineffective in the past (Schilling et al., 2020) but this approach harms communities that rely on bushmeat for subsistence (Brashares et al., 2011), rather than targeting the trade driven by higher-wealth areas that accounts for more of the overhunting and thus the spillover risk. Researchers must investigate what drives hunters to ply their trade, and legislators must pick up the mantle of addressing the roots of the issue (which are generally economic) rather than the symptoms. These principles apply to many of the human-animal interactions that may facilitate spillover events, including logging, agriculture, and construction in wild areas.

No one area of science is sufficient to predict and prevent zoonotic disease emergence and burden worldwide, just as no single government or organization can completely eliminate risk through legislation. In order to prevent the next pandemic, we must look beyond the boundaries of disciplines and nations, combining data and collaborating to protect the health of people, animals, and the environment worldwide.

## References

- About Icarus. (n.d.). Retrieved December 6, 2021, from <https://www.icarus.mpg.de/28056/about-icarus>
- Affek, A. N., Zachwatowicz, M., Sosnowska, A., Gerlée, A., & Kiszka, K. (2017). Impacts of modern mechanised skidding on the natural and cultural heritage of the Polish Carpathian Mountains. *Forest Ecology and Management*, 405, 391–403. <https://doi.org/10.1016/j.foreco.2017.09.047>
- Avian Influenza Early Warning System: Using NASA Data to Predict Pandemics. (2010). NASA Langley Research Center.
- Avšič-Zupanc, T. (2013). Mosquito-borne diseases—A new threat to Europe? *Clinical Microbiology and Infection*, 19(8), 683–684. <https://doi.org/10.1111/1469-0691.12215>
- Ba, R., Song, W., Lovallo, M., Lo, S., & Telesca, L. (2020). Analysis of multifractal and organization/order structure in Suomi-NPP VIIRS normalized difference vegetation index series of wildfire affected and unaffected sites by using the multifractal detrended fluctuation analysis and the Fisher–Shannon analysis. *Entropy*, 22(4), 415. <https://doi.org/10.3390/e22040415>
- Bartlow, A. W., Manore, C., Xu, C., Kaufeld, K. A., Valle, S. D., Ziemann, A., Fairchild, G., & Link to external site, this link will open in a new window, Fair, J. M., & Link to external site, this link will open in a new window. (2019). Forecasting zoonotic infectious disease response to climate change: Mosquito vectors and a changing environment. *Veterinary Sciences*, 6(2), 40. <http://dx.doi.org.ezproxy.princeton.edu/10.3390/vetsci6020040>
- Brashares, J. S., Golden, C. D., Weinbaum, K. Z., Barrett, C. B., & Okello, G. V. (2011). Economic and geographic drivers of wildlife consumption in rural Africa. *Proceedings of the National Academy of Sciences*, 108(34), 13931–13936. <https://doi.org/10.1073/pnas.1011526108>
- Chuang, T.-W., Henebry, G. M., Kimball, J. S., VanRoekel-Patton, D. L., Hildreth, M. B., & Wimberly, M. C. (2012). Satellite microwave remote sensing for environmental modeling of mosquito population dynamics. *Remote Sensing of Environment*, 125, 147–156. <https://doi.org/10.1016/j.rse.2012.07.018>

- Da Re, D., De Clercq, E. M., Tordoni, E., Madder, M., Rousseau, R., & Vanwambeke, S. O. (2019). Looking for ticks from space: Using remotely sensed spectral diversity to assess *Amblyomma* and *Hyalomma* tick abundance. *Remote Sensing*, *11*(7), 770. <https://doi.org/10.3390/rs11070770>
- Ditmer, M. A., Stoner, D. C., Francis, C. D., Barber, J. R., Forester, J. D., Choate, D. M., Ironside, K. E., Longshore, K. M., Hersey, K. R., Larsen, R. T., McMillan, B. R., Olson, D. D., Andreasen, A. M., Beckmann, J. P., Holton, P. B., Messmer, T. A., & Carter, N. H. (2021). Artificial nightlight alters the predator–prey dynamics of an apex carnivore. *Ecography*, *44*(2), 149–161. <https://doi.org/10.1111/ecog.05251>
- eBird Science—EBird*. (n.d.). Retrieved December 8, 2021, from <https://ebird.org/ebird/science>
- El-Sayed, A., & Kamel, M. (2021). Coronaviruses in humans and animals: The role of bats in viral evolution. *Environmental Science and Pollution Research*, *28*(16), 19589–19600. <https://doi.org/10.1007/s11356-021-12553-1>
- Fuller, T., Thomassen, H. A., Mulembakani, P. M., Johnston, S. C., Lloyd-Smith, J. O., Kisalu, N. K., Lutete, T. K., Blumberg, S., Fair, J. N., Wolfe, N. D., Shongo, R. L., Formenty, P., Meyer, H., Wright, L. L., Muyembe, J.-J., Buermann, W., Saatchi, S. S., Okitolonda, E., Hensley, L., et al. (2011). Using remote sensing to map the risk of human monkeypox virus in the Congo Basin. *EcoHealth*, *8*(1), 14–25. <https://doi.org/10.1007/s10393-010-0355-5>
- Giordano, B. V., Turner, K. W., & Hunter, F. F. (2018). Geospatial analysis and seasonal distribution of West Nile virus vectors (Diptera: Culicidae) in Southern Ontario, Canada. *International Journal of Environmental Research and Public Health*, *15*(4), 614. <https://doi.org/10.3390/ijerph15040614>
- Goldberg, T. L., Gillespie, T. R., Rwego, I. B., Estoff, E. L., & Chapman, C. A. (2008). Forest fragmentation as cause of bacterial transmission among nonhuman primates, humans, and livestock, Uganda. *Emerging Infectious Diseases*, *14*(9), 1375–1382. <https://doi.org/10.3201/eid1409.071196>
- Home | Wildlife Insights*. (n.d.). Retrieved December 7, 2021, from <https://www.wildlifeinsights.org/>
- INaturalist*. (n.d.). INaturalist. Retrieved December 8, 2021, from <https://www.inaturalist.org/>
- Judson, S. D., Fischer, R., Judson, A., & Munster, V. J. (2016). Ecological contexts of index cases and spillover events of different ebolaviruses. *PLoS Pathogens*, *12*(8), e1005780. <https://doi.org/10.1371/journal.ppat.1005780>
- Kamerow, D. (2014). The world's deadliest animal. *BMJ: British Medical Journal*, 348. <http://www.jstor.org/stable/26514797>
- Klotz, S. A., Dorn, P. L., Mosbacher, M., & Schmidt, J. O. (2014). Kissing bugs in the United States: Risk for vector-borne disease in humans. *Environmental Health Insights*, *8*s2, EHI.S16003. <https://doi.org/10.4137/EHI.S16003>
- Kontgis, C., Schneider, A., & Ozdogan, M. (2015). Mapping rice paddy extent and intensification in the Vietnamese Mekong River Delta with dense time stacks of Landsat data. *Remote Sensing of Environment*, *169*, 255–269. <https://doi.org/10.1016/j.rse.2015.08.004>
- Kranstauber, B., Cameron, A., Weinzerl, R., Fountain, T., Tilak, S., Wikelski, M., & Kays, R. (2011). The Movebank data model for animal tracking. *Environmental Modelling & Software*, *26*(6), 834–835. <https://doi.org/10.1016/j.envsoft.2010.12.005>
- Kunz, T. H., Braun de Torrez, E., Bauer, D., Lobova, T., & Fleming, T. H. (2011). Ecosystem services provided by bats. *Annals of the New York Academy of Sciences*, *1223*(1), 1–38. <https://doi.org/10.1111/j.1749-6632.2011.06004.x>
- Le, P. V. V., Kumar, P., Ruiz, M. O., Mbogo, C., & Muturi, E. J. (2019). Predicting the direct and indirect impacts of climate change on malaria in coastal Kenya. *PLoS One*, *14*(2), e0211258. <https://doi.org/10.1371/journal.pone.0211258>
- Li, W., Shi, Z., Yu, M., Ren, W., Smith, C., Epstein, J. H., Wang, H., Crameri, G., Hu, Z., Zhang, H., Zhang, J., McEachern, J., Field, H., Daszak, P., Eaton, B. T., Zhang, S., & Wang, L.-F. (2005). Bats are natural reservoirs of SARS-like coronaviruses. *Science*, *310*(5748), 676–679.

- Lippi, C. A., Stewart-Ibarra, A. M., Loor, M. E. F. B., Zambrano, J. E. D., Lopez, N. A. E., Blackburn, J. K., & Ryan, S. J. (2019). Geographic shifts in *Aedes aegypti* habitat suitability in Ecuador using larval surveillance data and ecological niche modeling: Implications of climate change for public health vector control. *PLoS Neglected Tropical Diseases*, *13*(4), e0007322. <https://doi.org/10.1371/journal.pntd.0007322>
- McFarlane, R., Becker, N., & Field, H. (2011). Investigation of the climatic and environmental context of Hendra virus spillover events 1994–2010. *PLoS One*, *6*(12), e28374. <https://doi.org/10.1371/journal.pone.0028374>
- McKee, C. D., Islam, A., Luby, S. P., Salje, H., Hudson, P. J., Plowright, R. K., & Gurley, E. S. (2021). The ecology of Nipah virus in Bangladesh: A nexus of land-use change and opportunistic feeding behavior in bats. *Viruses*, *13*(2), 169. <https://doi.org/10.3390/v13020169>
- Mertes, C. M., Schneider, A., Sulla-Menashe, D., Tatem, A. J., & Tan, B. (2015). Detecting change in urban areas at continental scales with MODIS data. *Remote Sensing of Environment*, *158*, 331–347. <https://doi.org/10.1016/j.rse.2014.09.023>
- Meurens, F., Dunoyer, C., Fourichon, C., Gerdt, V., Haddad, N., Kortekaas, J., Lewandowska, M., Monchatre-Leroy, E., Summerfield, A., Wichgers Schreur, P. J., van der Poel, W. H. M., & Zhu, J. (2021). Animal board invited review: Risks of zoonotic disease emergence at the interface of wildlife and livestock systems. *Animal*, *15*(6), 100241. <https://doi.org/10.1016/j.animal.2021.100241>
- Moore, N., & Messina, J. (2010). A landscape and climate data logistic model of tsetse distribution in Kenya. *PLoS One*, *5*(7), e11809. <https://doi.org/10.1371/journal.pone.0011809>
- O’Shea, T. J., Cryan, P. M., Cunningham, A. A., Fooks, A. R., Hayman, D. T. S., Luis, A. D., Peel, A. J., Plowright, R. K., & Wood, J. L. N. (2014). Bat flight and zoonotic viruses. *Emerging Infectious Diseases*, *20*(5), 741–745. <https://doi.org/10.3201/eid2005.130539>
- One Health. (n.d.). *OIE - World Organisation for animal health*. Retrieved December 8, 2021, from <https://www.oie.int/en/what-we-do/global-initiatives/one-health/>
- One Health | CDC. (2021, November 17). <https://www.cdc.gov/onehealth/index.html>
- Parrish, C. R., Murcia, P. R., & Holmes, E. C. (n.d.). Influenza virus reservoirs and intermediate hosts: Dogs, horses, and new possibilities for influenza virus exposure of humans. *Journal of Virology*, *89*(6), 2990–2994. <https://doi.org/10.1128/JVI.03146-14>
- Plowright, R. K., Foley, P., Field, H. E., Dobson, A. P., Foley, J. E., Eby, P., & Daszak, P. (2011). Urban habituation, ecological connectivity and epidemic dampening: The emergence of Hendra virus from flying foxes (*Pteropus* spp.). *Proceedings of the Royal Society B: Biological Sciences*, *278*(1725), 3703–3712. <https://doi.org/10.1098/rspb.2011.0522>
- Poulsen, J. R., Clark, C. J., Mavah, G., & Elkan, P. W. (2009). Bushmeat supply and consumption in a tropical logging concession in Northern Congo. *Conservation Biology*, *23*(6), 1597–1608. <https://doi.org/10.1111/j.1523-1739.2009.01251.x>
- Prevention, C.-C. for D. C. and. (2020, July 16). *CDC - Malaria—About Malaria—Biology*. <https://www.cdc.gov/malaria/about/biology/index.html>
- Rabozzi, G., Bonizzi, L., Crespi, E., Somaruga, C., Sokooti, M., Tabibi, R., Vellere, F., Brambilla, G., & Colosio, C. (2012). Emerging zoonoses: The “One Health approach.”. *Safety and Health at Work*, *3*(1), 77–83. <https://doi.org/10.5491/SHAW.2012.3.1.77>
- Rangel Pinagé, E., Keller, M., Duffy, P., Longo, M., dos-Santos, M. N., & Morton, D. C. (2019). Long-term impacts of selective logging on Amazon forest dynamics from multi-temporal airborne LiDAR. *Remote Sensing*, *11*(6), 709. <https://doi.org/10.3390/rs11060709>
- Robertson, B., Holland, J., & Minot, E. (2012). Wildlife tracking technology options and cost considerations. *Wildlife Research*, *38*, 653–663. <https://doi.org/10.1071/WR10211>
- Sagurova, I., Ludwig, A., Ogden, N. H., Pelcat, Y., Dueymes, G., & Gachon, P. (n.d.). Predicted northward expansion of the geographic range of the tick vector *Amblyomma americanum* in North America under future climate conditions. *Environmental Health Perspectives*, *127*(10), 107014. <https://doi.org/10.1289/EHP5668>

- Sanders, D., Frago, E., Kehoe, R., Patterson, C., & Gaston, K. J. (2021). A meta-analysis of biological impacts of artificial light at night. *Nature Ecology & Evolution*, 5(1), 74–81. <https://doi.org/10.1038/s41559-020-01322-x>
- Schilling, M. A., Estes, A. B., Eblate, E., Martin, A., Rentsch, D., Katani, R., Joseph, A., Kindoro, F., Lyimo, B., Radzio-Basu, J., Cattadori, I. M., Hudson, P. J., Kapur, V., Buza, J. J., & Gwakisa, P. S. (2020). Molecular species identification of bushmeat recovered from the Serengeti ecosystem in Tanzania. *PLoS One*, 15(9), e0237590. <https://doi.org/10.1371/journal.pone.0237590>
- Skeik, N., & Jabr, F. I. (2008). Influenza viruses and the evolution of avian influenza virus H5N1. *International Journal of Infectious Diseases*, 12(3), 233–238. <https://doi.org/10.1016/j.ijid.2007.07.002>
- Slatculescu, A. M., Clow, K. M., McKay, R., Talbot, B., Logan, J. J., Thickstun, C. R., Jardine, C. M., Ogden, N. H., Knudby, A. J., & Kulkarni, M. A. (2020). Species distribution models for the eastern blacklegged tick, *Ixodes scapularis*, and the Lyme disease pathogen, *Borrelia burgdorferi*, in Ontario, Canada. *PLoS One*, 15(9), e0238126. <https://doi.org/10.1371/journal.pone.0238126>
- Souza, J., Siqueira, J. V., Sales, M. H., Fonseca, A. V., Ribeiro, J. G., Numata, I., Cochrane, M. A., Barber, C. P., Roberts, D. A., & Barlow, J. (2013). Ten-year landsat classification of deforestation and forest degradation in the Brazilian Amazon. *Remote Sensing*, 5(11), 5493–5513. <https://doi.org/10.3390/rs5115493>
- Suzán, G., Marcé, E., Giermakowski, J. T., Armién, B., Pascale, J., Mills, J., Ceballos, G., Gómez, A., Aguirre, A. A., Salazar-Bravo, J., Armién, A., Parmenter, R., & Yates, T. (2008). The effect of habitat fragmentation and species diversity loss on hantavirus prevalence in Panama. *Annals of the New York Academy of Sciences*, 1149(1), 80–83. <https://doi.org/10.1196/annals.1428.063>
- The Internet of Animals*. (n.d.). Retrieved December 6, 2021, from <https://www.icarus.mpg.de/28546/icarus-internet-of-animals>
- Tsantalidou, A., Parselia, E., Arvanitakis, G., Kyratzi, K., Gewehr, S., Vakali, A., & Kontoes, C. (2021). MAMOTH: An earth observational data-driven model for mosquitoes abundance prediction. *Remote Sensing*, 13(13), 2557. <https://doi.org/10.3390/rs13132557>
- Tucker, C., Wilson, J., Mahoney, R., Anyamba, A., Linthicum, K., & Myers, M. (2002). Climatic and ecological context of the 1994–1996 Ebola outbreaks. *Photogrammetric Engineering and Remote Sensing*, 68.
- Vector-borne diseases*. (n.d.). Retrieved December 7, 2021, from <https://www.who.int/news-room/fact-sheets/detail/vector-borne-diseases>
- Wang, L.-F., & Eaton, B. T. (2007). Bats, civets and the emergence of SARS. *Wildlife and Emerging Zoonotic Diseases: The Biology, Circumstances and Consequences of Cross-Species Transmission*, 315, 325–344. [https://doi.org/10.1007/978-3-540-70962-6\\_13](https://doi.org/10.1007/978-3-540-70962-6_13)
- Wu, X., Pang, Y., Luo, B., Wang, M., & Feng, J. (2019). Function of distress calls in least horseshoe bats: A field study using playback experiments. *Acta Chiropterologica*, 20(2), 455–464. <https://doi.org/10.3161/15081109ACC2018.20.2.015>