

More Than Just Cases III: Using Bioacoustic Signals to Map the Animal Hosts of SARS-CoV-2¹

Even without the benefit of philosophical reflection, anyone who has spent some time in an enclosed space with an excited bat knows what it is to encounter a fundamentally alien life form.²

—Thomas Nagel, “What Is It Like To Be a Bat?”

by John Hessler

Viruses are strange creatures. They are not really alive, but are only fragments of genetic code floating about, marking time in the cells of an innocent reservoir, until they begin jumping and replicating, thereby making their presence felt in the world. All of us have become more familiar in recent months with these facts, as the SARS-CoV-2 virus, which causes COVID-19, has come into all our lives.

Over the last few decades many new and previously unknown zoonotic viruses have made the jump from animal hosts to humans. The Nipah, Hendra, Ebola, Marburg, HIV-1, HIV-2, SARS-CoV, and the more recent SARS-CoV-2 viruses are all of this kind.³

RNA (ribonucleic acid) viruses, like SARS, are small and limited in the amount of information their genomes can contain and hence have no way to check the mutations and errors that accumulate within them as they replicate. These viruses compensate for this difficulty by producing massive numbers of virions (individual virus particles) within the individuals they infect, thereby achieving efficient transmission and ensuring, at least their temporary, evolutionary survival.⁴

Many newly emerging viruses have one critically important thing in common—their reservoirs and the animals suspected of transmitting the viruses to humans, are bats.⁵ Over the decades, the zoonotic viruses that have managed to make the jump from animals to humans have a variety of origins: from rodents, to monkeys, to wild birds, to pigs. Measles probably came from domesticated sheep and goats, HIV-1 from chimpanzees. Lately, however, there have been many that seem to have originated in the order, *Chiroptera*.⁶

No one knows why the ecology and lifestyle of bats seems so conducive to them acting as hosts for viruses,

but it seems their ability to fly, a unique trait in mammals, and to move into and out of local populations and spatially distant groups, seems important. The fact that they roost close together, in tight communities packed into caves and in trees, sometimes in uncountable numbers, helps to maintain a supply of infected individuals. These same traits of mobility and the cryptic location of their roosts also make them difficult to find, to study in detail, and to map accurately.

With the emergence of SARS-CoV-2 and the outbreak of COVID-19, there has been renewed interest in mapping the location of the many species of bats that are host reservoirs for a whole series of RNA viruses. In the case of SARS-CoV-2, the principal genus of bats involved in the transmission of SARS-like viruses is *Rhinolophus*.⁷ The genus *Rhinolophus* are part of the larger family *Rhinolophidae*, and for phylogenetic reasons they are included as part of the same suborder as megabats, the *Yinpterochiroptera* (shown in yellow) [Figure 1] and not, as are most echolocating microbats, in the suborder *Yangochiroptera*.⁸

Known collectively and popularly as horseshoe bats, they have recently come into contact with humans as both a source of food and also in their role in traditional medicine. The one hundred and six species of horseshoe bats are divided into six subgenera, and little is known of the lifestyle and distribution of most species. Efforts to determine and map their biogeography have been difficult and hampered by the complex, and mostly unknown, ecology of the genus.

The two species that have been implicated and appear to be reservoirs for a virus that is genetically close to the SARS-CoV-2 found in humans are *Rhinolophus affinis* and *Rhinolophus malayanus*. Generally, they eat

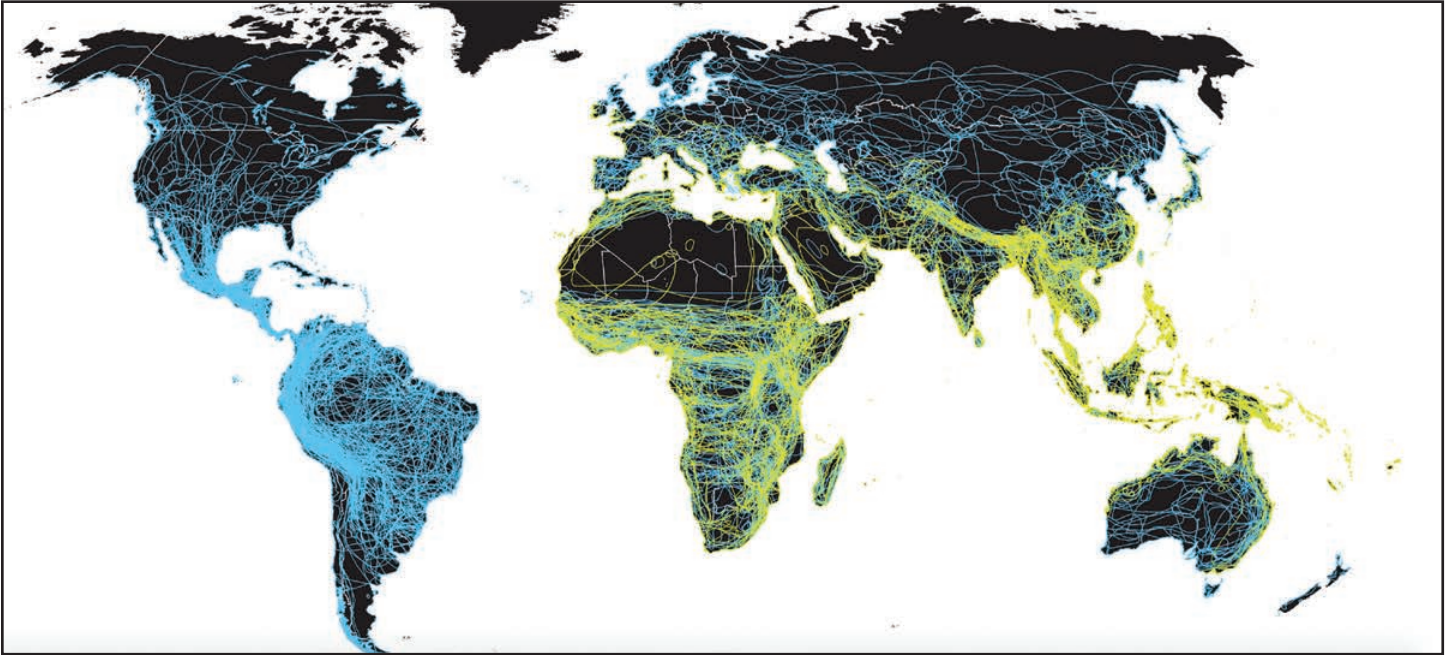


Figure 1. Distribution of the suborders of bats: *Yangochiroptera* (blue) and *Yinpterochiroptera* (yellow). *Yangochiroptera* contains most families of microbats, excluding *Rhinolophidae* and a few other families that are included for phylogenetic reasons with the Old World Megabats, the *Yinpterochiroptera*. Image courtesy of Kevin J. Olival, et al., “Possibility for Reverse Zoonotic Transmission of SARS-CoV-2 to Free-Ranging Wildlife: A Case Study of Bats,” *PLoS Pathogens* 16, no. 9 (2020).⁹

and hunt insects, by using echolocation—constant frequency calls to detect prey and find their way in the world. *Rhinolophus* bats, because they use echolocation, have evolved complex Doppler-shift compensation behavior, in order to account for flight-speed changes in the frequency of the echoes, from both prey and obstacles in their environment. Ever present as they are, efforts to map them have proven to be, over the years, extremely difficult.

One avenue of cartographic and geospatial research, which has held promise recently, is the bioacoustic mapping of the ambient sound high-frequency spectrum around locations and in habitats known to harbor insectivorous bats. Using continuous-wavelet transforms and other signal-processing techniques, the complicated high-frequency echolocation sounds, made by various species of bats living in a given location, can sometimes be resolved into their various components and identified, allowing cartographers to get a more detailed and clearer picture of their distribution, movement, and habits [Figure 3].

Signal-processing techniques allow us to calculate a time-frequency spectrum of the echolocation pulses produced by bats, which is a hallmark of the presence of a particular species at or near a sampling location. In many cases the complexity of the ambient acoustic samplings is too intertwined to be resolved with sufficient accuracy to make identifications, but because bats use both



Figure 2. Author making bioacoustic recordings in the caves of Maryland. Photograph courtesy of the author.

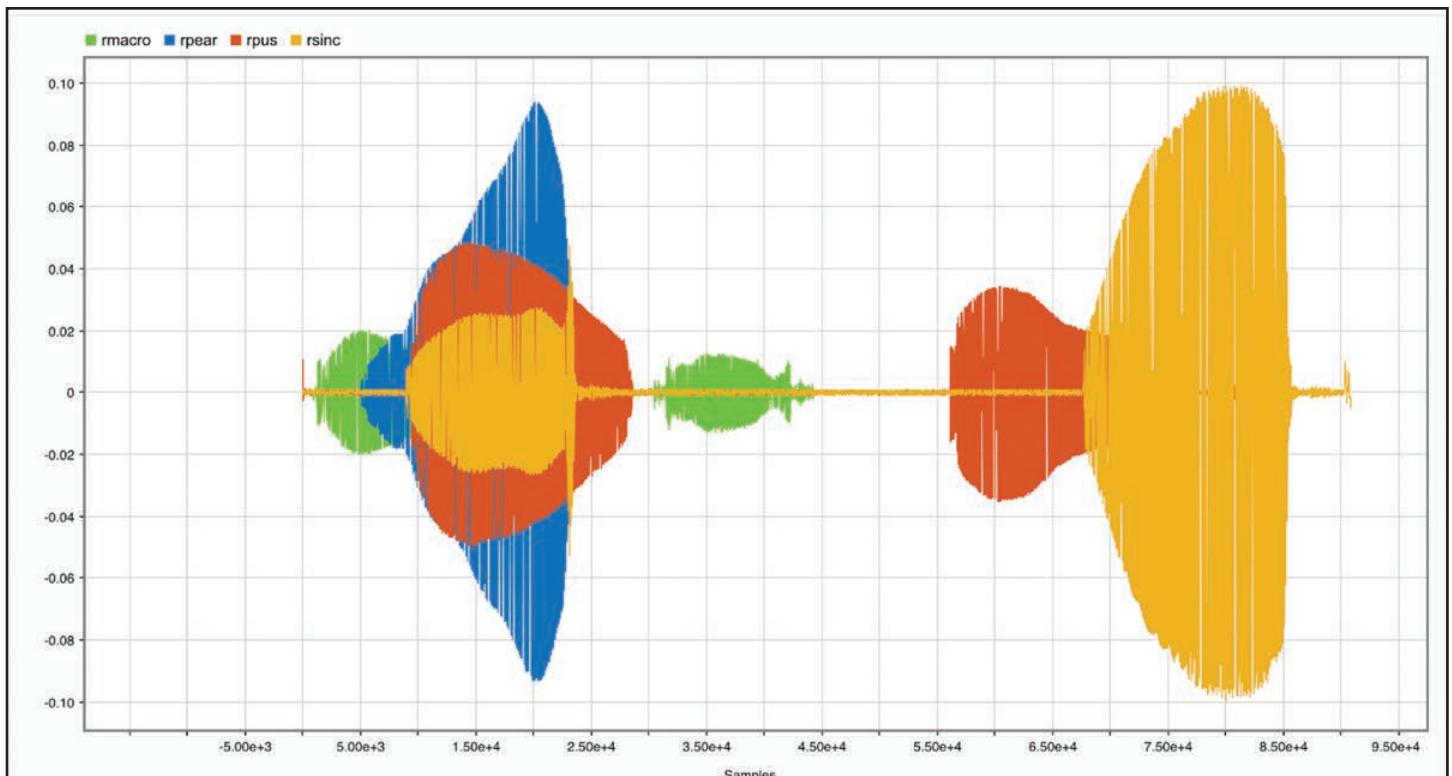


Figure 3. Visualization of Echolocation Signals of the *Rhinolophus* species: *pusillus* (red), *pearsoni* (blue), *macrotis* (green), and *sinicus* (yellow). Visualization by John Hessler using MATLAB Signal Processing Toolbox. Bioacoustic raw data from the Bat Ecology and Bioacoustics Lab, University of Bristol, UK.

continuous- and frequency-modulated signals, we often can decompose the signals into time-frequency spectrograms that are able to hint at probable species-level identifications. Several research programs, including the author's BIO-COMP Lab, currently employ deep- and machine-learning techniques, using convolutional neural networks, which have been trained to identify the particular traits of bat echolocations and to map them using traditional GIS.

Deep learning is a computational architecture that uses artificial neural networks to learn to identify images and signals or to understand speech, and can classify huge amounts of data more accurately and much faster than humans.¹⁰ It is the same technology being developed for use in self-driving vehicles. These networks learn the echolocation signals of the various species of bats and then identify them from massive ambient sound files made using remote recorders placed in the field.

Because bats use several different forms of echolocation and have, in the case of *Rhinolophus* bats, particular frequencies at which they operate, computers using machine learning can highlight [Figure 4] the echolocation signals of bats from recordings and give biogeographers and cartographers an accurate indication of a species'

presence at a particular location, allowing their distribution to be mapped.

These recordings, when linked with field-checked data, are beginning to allow GIS analysts to start mapping the probable distribution of the genus in the most important parts of their range. Mapping the geospatial locations of the bat species linked to emerging disease outbreaks is critical to understanding the evolution of the disease, its genetic variations, and to gaining an idea of how they interact with humans. These maps are necessary tools in answering the important epidemiological questions of how, why, and where did a particular virus jump from animals to humans. The exact distribution of the three most important species of *Rhinolophus* bats—*affinis*, *malayanus*, and *sinicus*—for the understanding of SARS-CoV-2 spillover is still mostly unknown. The map shown in [Figure 5] was made by the author from the best currently available information.

Today, most cartography is driven by complex data. Sometimes those data are hard to come by; therefore, new methods must be invented to produce and analyze them—so it is with the mapping of the animal hosts of SARS-CoV-2. Geospatial acoustic fingerprinting techniques, paired with deep learning and GIS, hold out some

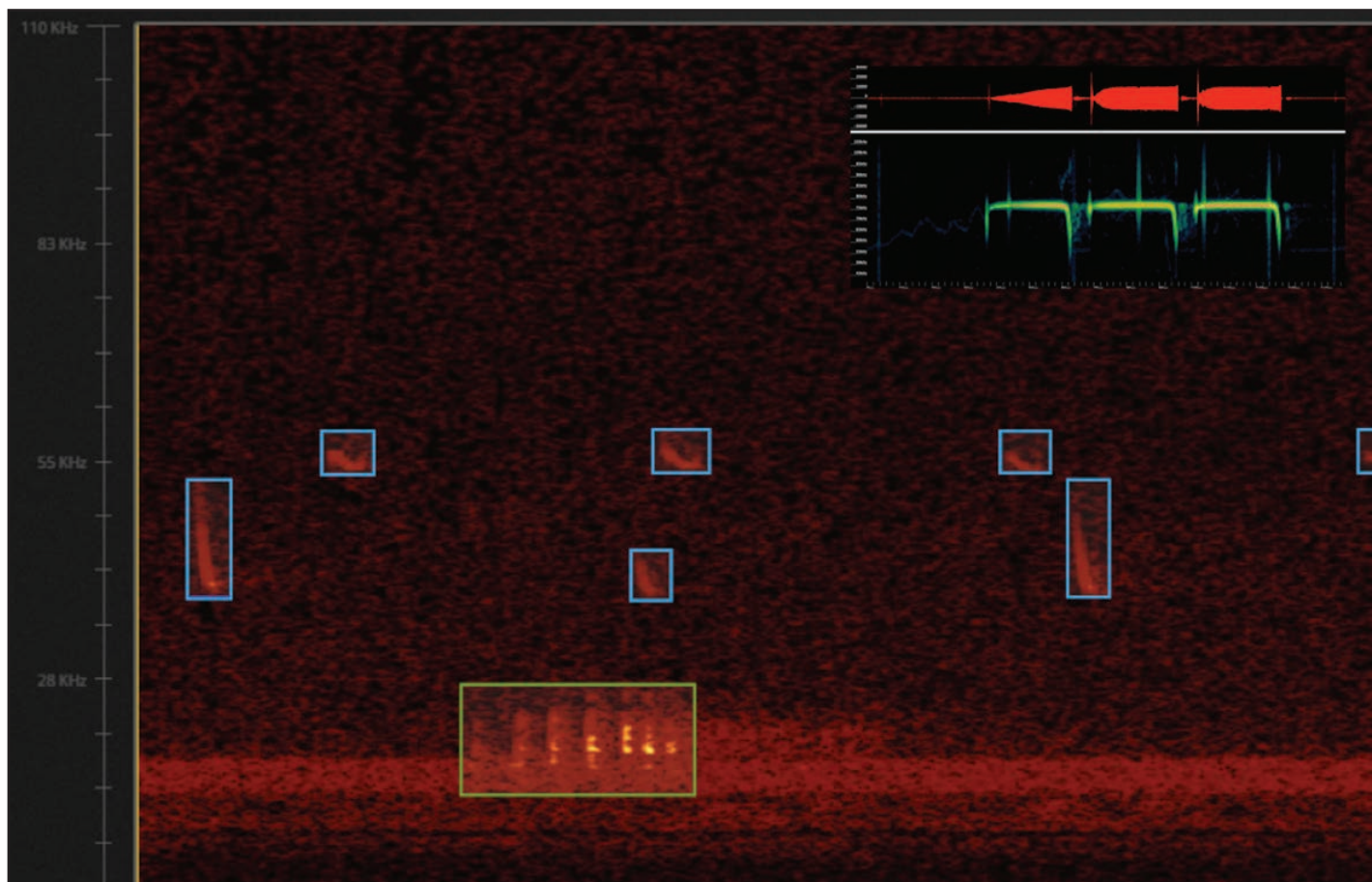


Figure 4. Neural network identification of various bat frequency modulated TFRs from ambient sound recordings. The inset shows the shape of the constant frequency spectrogram of *Rhinolophus affinis*, a possible host for SARS-CoV-2, which is not present in the ambient signal and therefore is not living in the area of the recording. Diagram from Oisín Mac Aodha, et al., "Bat Detective: Deep Learning Tools for Bat Acoustic Signal Detections," *PloS: Computational Biology* 14, no. 3 (2018).¹¹

promise that in the future the biogeography of these animals, and how they interact with humans, will be better understood and finally mapped in detail.

ABOUT THE AUTHOR

John Hessler is a Specialist in Computational Geography and Geographic Information Science at the Library of Congress. He is a Lecturer of Evolutionary Computation at the Johns Hopkins University and founder of the New Geometries Laboratory whose research uses geospatial data in conjunction with evolutionary computation to solve complex spatial analysis problems, like mapping COVID-19. This is his second article in a series on various mapping that supports understanding of the pandemic.

ENDNOTES

1 This article is the third in a series about the way new techniques in GIS, combined with methods from

artificial intelligence and new data sources to help understand and to fight the SARS-CoV-2 / COVID-19 pandemic.

- 2 Thomas Nagel, "What Is It Like To Be a Bat?," *The Philosophical Review* 83 (1974): 435–50.
- 3 For more information about Zoonotic transmission of viruses, see David Quammen's *Spillover: Animal Infections and the Next Human Pandemic* (New York: W.W. Norton, 2013).
- 4 Patrick T. Dolan, "Mapping the Evolutionary Potential of RNA Viruses," *Cell Host & Micro Review* 23 (2018): 435–46.
- 5 Lin-Fa Wang and Christopher Coaled, eds., *Bats and Viruses: A New Frontier of Emerging Infectious Diseases* (Hoboken, NJ: John Wiley & Sons, 2015).
- 6 Michael Leko, "Bat-Bourne Virus Diversity, Spillover and Emergence," *Nature Reviews Microbiology* 18 (2020): 461–71.

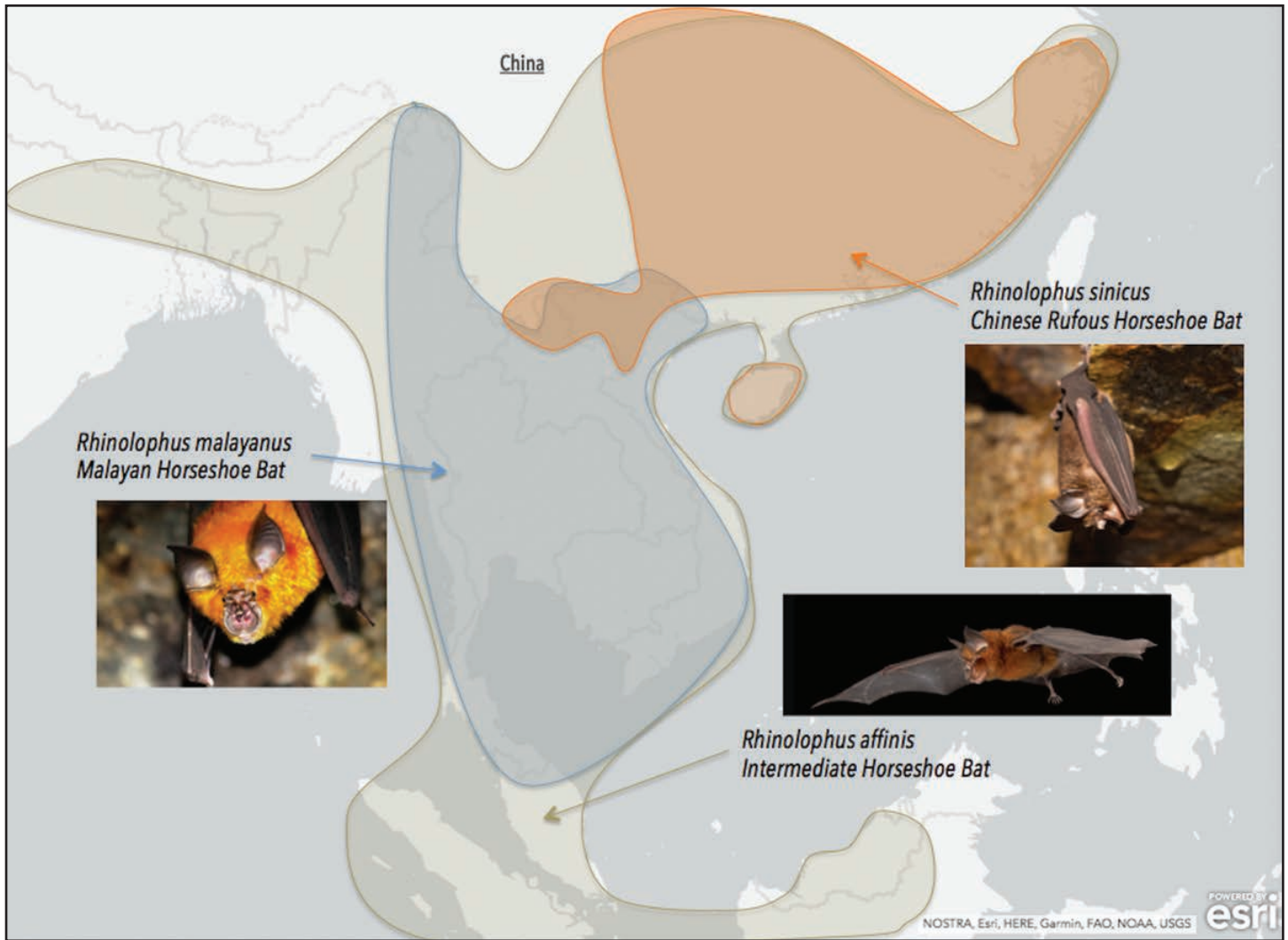


Figure 5. Map of the probable and little understood distribution of *Rhinolophus* bats associated with SARS-CoV-2, made by author based on best available data.

- 7 Kristen Anderson, et al., "The Proximal Origin of SARS-CoV-2," *Nature Medicine* 26 (2020): 450–55.
- 8 Kevin J. Olival, et al., "Possibility for Reverse Zoonotic Transmission of SARS-CoV-2 to Free-Ranging Wildlife: A Case Study of Bats," *PLoS Pathogens* 16, no. 9 (2020), <https://doi.org/10.1371/journal.ppat.1008758>.
- 9 *Ibid.*, "Fig 2. Old-World and New-World bats."
- 10 For an introduction to *Deep Learning*, see Terrence J. Sejnowski, *The Deep Learning Revolution* (Cambridge, MA: MIT Press, 2018).
- 11 Oisín Mac Aodha, et al., "Bat Detective: Deep Learning Tools for Bat Acoustic Signal Detections," *PLoS: Computational Biology* 14, no. 3 (2018), <https://doi.org/10.1371/journal.pcbi.1005995>. See "Fig 1. Detection Pipeline for Search-Phase Bat Echolocation Calls." 