

New methodology predicts coronavirus and other infectious disease threats to wildlife

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The rate at which emerging wildlife diseases infect humans has steadily increased over the last three decades. Viruses, such as the global coronavirus pandemic and recent monkeypox outbreak, have heightened

the urgent need for disease ecology tools to forecast when and where disease outbreaks are likely. A University of South Florida assistant professor helped develop a methodology that will do just that—predict disease transmission from wildlife to humans, from one wildlife species to another and determine who is at risk of infection.

The [methodology](#) is a [machine-learning approach](#) that identifies the influence of variables, such as location and climate, on known pathogens. Using only small amounts of information, the system is able to identify community hot spots at risk of infection on both global and local scales.

"Our main goal is to develop this tool for [preventive measures](#)," said co-principal investigator Diego Santiago-Alarcon, assistant professor of integrative biology. "It's difficult to have an all-purpose methodology that can be used to predict infections across all the diverse parasite systems, but with this research, we contribute to achieving that goal."

With help from researchers at the Universidad Veracruzana and Instituto de Ecología, located in Mexico, Santiago-Alarcon examined three host-pathogen systems—avian malaria, birds with West Nile virus and bats with coronavirus—to test the reliability and accuracy of the models generated by the methodology.

The team found that for the three systems, the species most frequently infected was not necessarily the most susceptible to the disease. To better pinpoint hosts with higher risk of infection, it was important to identify relevant factors, such as climate and evolutionary relationships.

By integrating geographic, environmental and evolutionary development variables, the researchers identified [host species](#) that have previously not been recorded as infected by the parasite under study, providing a way to identify susceptible species and eventually mitigate pathogen risk.

"We feel confident that the methodology is successful, and it can be applied widely to many host-pathogen systems," Santiago-Alarcon said. "We now enter into a phase of improvement and refinement."

The results, published in the *Proceedings of the National Academy of Sciences*, prove the methodology is able to provide reliable global predictions for the studied host–pathogen systems, even when using a small amount of information. This new approach will help direct infectious disease surveillance and field efforts, providing a cost-effective strategy to better determine where to invest limited disease resources.

Predicting what kind of pathogen will produce the next medical or veterinary infection is challenging, but necessary. As the rate of human impact on [natural environments](#) increases, opportunity for novel diseases will continue to rise.

"Humanity, and indeed biodiversity in general, are experiencing more and more infectious disease challenges as a result of our incursion and destruction of the natural order worldwide through things like deforestation, [global trade](#) and climate change," said Andrés Lira-Noriega, research fellow at the Instituto de Ecología. "This imposes the need of having tools like the one we are publishing to help us predict where new threats in terms of new pathogens and their reservoirs may occur or arise."

The team plans to continue their research to further test the methodology on additional host-pathogen systems and extend the study of [disease transmission](#) to predict future outbreaks. The goal is to make the tool easily accessible through an app for the scientific community by the end of 2022.

More information: Ángel L. Robles-Fernández et al, Wildlife

susceptibility to infectious diseases at global scales, *Proceedings of the National Academy of Sciences* (2022). [DOI: 10.1073/pnas.2122851119](https://doi.org/10.1073/pnas.2122851119)

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