

BIO-FI: LEVERAGING THE POWER OF BIOLOGICAL BIG DATA FOR ADVANCED ANALYTICS AND MODELING OF CHEMICAL AND BIOLOGICAL THREATS

Predicting Early Warning Signals In Disease Systems For Forecasting Emerging Viral Threats.

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In the past two decades, several novel-life-threatening viruses have been identified and spread globally. Predicting the next disease emergence event either in, or between, animal and human populations, remains a paramount bio-security challenge to prevent and facilitate early control. The pathway for disease emergence can be broadly differentiated into three distinct phases: 1. the pre-emergence transmission in animal populations, 2. transmission at human-animal interfaces, and 3. the early human-to-human spread. We present a suite of tools that leverage biological, surveillance, and ecological data to identify early warning signals in disease systems at each of the three phases of disease emergence.

A key component of these analytical techniques includes a network-based approach for understanding the zoonotic potential of novel viruses even before they have spilled into people. We have been able to quantify the risk of zoonotic transmission for 531 novel animal viruses with models predicting cryptic links in host-virus networks. Based on spillover risk, present a metric to prioritize novel viruses not only for further surveillance efforts but also for further genetic and in-vivo characterization. Using these models, we were able to identify novel coronaviruses with the highest risk prioritization scores that are detected in bats and rodent species from Southeast Asia, Africa, and South America.

We have developed tools that can predict the global vulnerability of spillover by predicting yet-unknown wildlife hosts of emerging viruses, specifically focusing on Flaviviruses including Zika, dengue, and Japanese encephalitis virus. These supervised-learning models used biogeographical characteristics of known Flavivirus hosts and predicted yet undetected hosts that show similar ecological characteristics. For example, our models identified 173 species as possible sylvatic hosts for the dengue virus, 139 had not previously been detected as carriers. We were able to highlight regions with a high diversity of species that should be prioritized for flavivirus surveillance through the generation of maps showing hotspots. In South Asia, models identified three primate species with a high likelihood of being hosts of Zika virus. At the time of data collection for this study, there were no reported outbreaks of Zika in South Asia. Since then, Asia has seen the emergence of Zika virus, indicating the need to strengthen wildlife surveillance for flaviviruses in the region.

Identifying anomalous trends is key to the early detection of warning signs for all disease surveillance systems. We have implemented novel methods for passive surveillance systems that can standardize a wide variety of data using rule-based and supervised algorithms to identify anomalous trends significantly earlier than other active surveillance systems. These algorithms are already implemented in Wildlife Morbidity and Mortality Event Alert system and are being used by analysts, conservation, and public health specialists. Over the last couple of years, the system has led to the discovery of emerging wildlife pathogens such as Pigeon Paramyxovirus Type 1, Sarcocystis calchasi, and Mycoplasmosis in California.

These tools provide next-generation predictive intelligence informing pandemic preparedness useful for identifying agent as well as host-related risk and help generate a holistic ecosystem of decision support software for mitigating biological threats.

The work has been supported by the United States Agency for International Development 584(USAID) Emerging Pandemic Threat PREDICT program (Cooperative Agreement nos. GHN-A-58500-09-00010-00 and AID-OAA-A-14-00102), National Institute Of Allergy And Infectious Diseases of the National Institutes of Health under 587Award Number U01AI151814, Defense Threat Reduction Agency, United States Department of Defense for a contract: Data-Driven Framework for Zoonotic Disease Prediction (Contract number: HDTRA1-15-C-0017), and State Wildlife Grant (Agreement no. F14AF00639).

Abstract contains work presented in the following journal articles that are available publically.

1. Pandit, Pranav, Simon Anthony, Tracey Goldstein, Kevin Olival, Megan Doyle, Nicole Gardner, Brian Bird et al. "Predicting the potential for zoonotic transmission and host associations for novel viruses." (2022).
2. Pandit, Pranav S., Megan M. Doyle, Katrina M. Smart, Cristin CW Young, Gaylen W. Drape, and Christine K. Johnson. "Predicting wildlife reservoirs and global vulnerability to zoonotic Flaviviruses." Nature communications 9, no. 1 (2018): 1-10.
3. Kelly, Terra R., Pranav S. Pandit, Nicole Carion, Devin F. Dombrowski, Krysta H. Rogers, Stella C. McMillin, Deana L. Clifford et al. "Early detection of wildlife morbidity and mortality through an event-based surveillance system." Proceedings of the Royal Society B 288, no. 1954 (2021): 20210974.