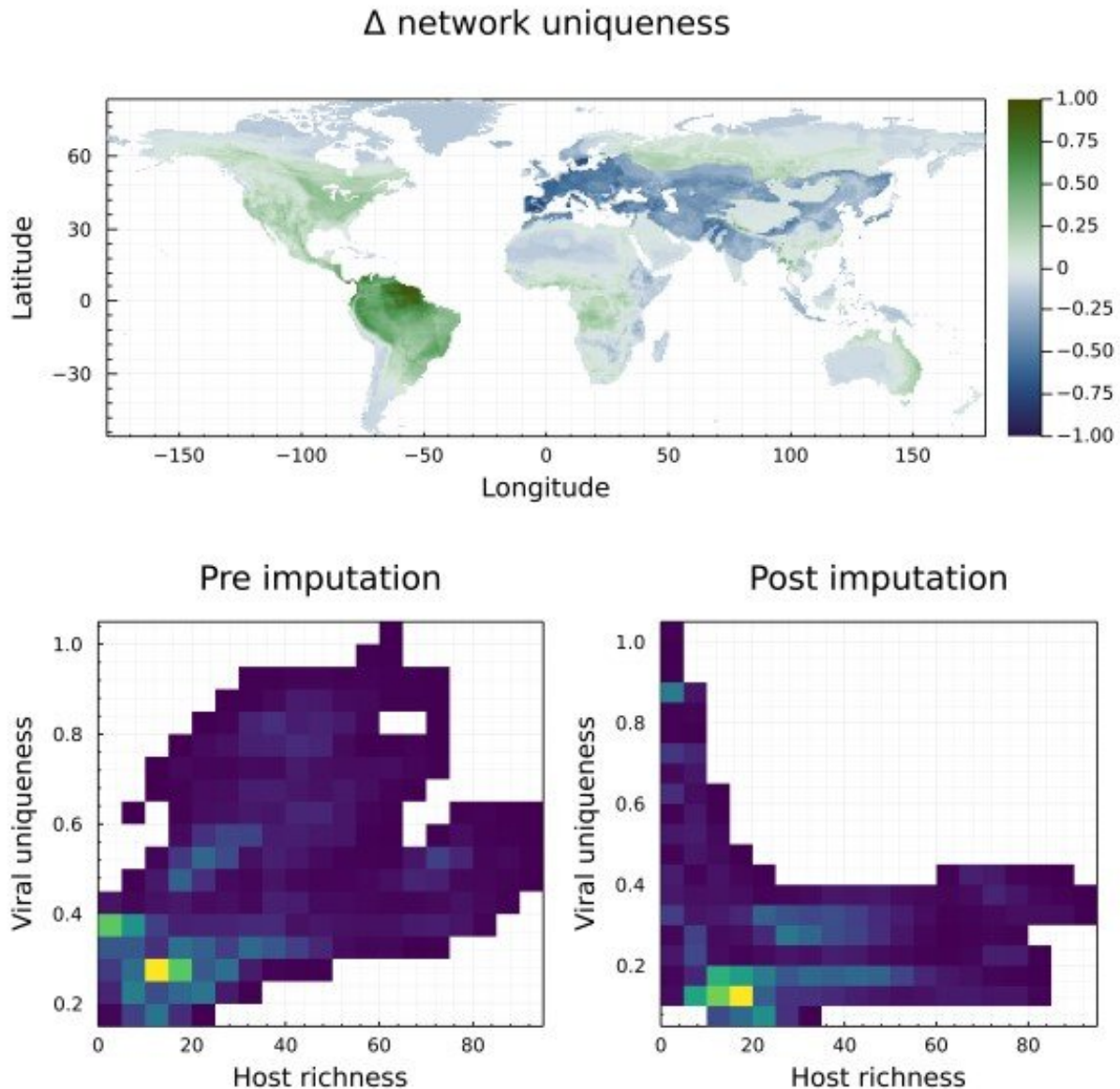


Where are the next zoonotic viruses lurking?

May 25 2022, by Béatrice St-Cyr-Leroux



Imputed network reveals undiscovered hotspots of unique host-virus associations in the Amazon. Top: Difference between (ranged) compositional uniqueness of

the viral community based on host presence (see ED Fig. 7). Dark green areas indicate that the imputed network suggests a higher originality of the viral community than available data would. Bottom: comparison between the number of hosts and the uniqueness of the viral community. Assuming random discovery of viruses through host sampling, this relationship would be overall linear and positive, as is the case pre-imputation. Adding imputed interactions removes some of the sampling biases, and shows how areas with lower host richness have more unique contributions to viral uniqueness, which suggests that they harbor viruses not shared by more speciose locations. Credit: arXiv:2105.14973v2 [q-bio.QM], <https://arxiv.org/abs/2105.14973>

Until recently, we knew of only two percent of the possible interactions between mammals and viruses, or the "virome." However, a new artificial intelligence (AI) technique has identified potential new host-virus interactions, increasing the size of the known virome by a factor of 15.

A new machine-learning-based approach to predicting host-virus interactions was applied and 35,000 hours of computer time was used on Calcul Québec computers to analyze data on interactions between a thousand mammals (the hosts) and as many viruses.

After 80,000 potential new host-virus interactions were identified, the network of host-virus associations was paired with a virus genome model to reassess the human infection potential of all the viruses in the database.

The result was a list of animal viruses that could cause zoonoses, i.e., infect humans.

The collaborative international research project was led by Timothée Poisot, a professor in the Department of Biological Sciences at the

University of Montreal who is interested in calculating pandemic risks. It was funded by IVADO, the Institute for Data Valorization, and carried out as part of the Viral Emergence Research Initiative.

Uncovering 'forgotten' viruses

To validate their predictions, Poisot and his team of experts in virology, AI and [public health](#) surveyed the literature for prior human outbreaks of the viruses they had tabbed as high risk. It turned out that of the 20 viruses with the strongest zoonotic potential, 11 have in fact made humans ill.

"Some of the viruses really surprised us; we didn't think they could be transmitted to humans," said Poisot. "For example, our system calculated that ectromelia, the virus responsible for smallpox in mice, has a 'very high' probability of infecting humans, and we discovered that there was indeed an outbreak in a Chinese school in 1987, but it was not listed in any of the databases."

Overall, the virus families that crop up most often on the high-risk list are bunyaviruses (one of which causes Rift Valley fever), rhabdoviruses (rabies), filoviruses (Ebola) and flaviviruses (dengue fever, yellow fever). "These are all families that are known to present significant zoonotic risk, but the model may enable us to measure the risk within these families more accurately," Poisot explained.

Monitoring hotspots, particularly the Amazon

This predictive research can help guide the efforts of virologists working to prevent zoonoses that could cause future epidemics and pandemics. The list of high-risk [viruses](#) can be used to target sampling campaigns on specific species and also on the basis of geographical distribution, as the

research team has mapped the results.

"As an ecologist doing biogeographical research, I want to know not only which virus will be compatible with which host, but also where those combinations can be found," said Poisot.

According to the computer model, the Amazon is the part of the world with the greatest potential for viral mutations. "The results are clear: the Amazon is a hotspot for novel host-virus interactions," said Poisot. "It's the region where we find the most interactions that don't usually occur."

According to Poisot, these novel contacts can be explained by the lack of data on the Amazonian virome, deforestation, [climate change](#) and [urban expansion](#), which increases contact between animals and humans.

More information: Timothée Poisot et al, Network embedding unveils the hidden interactions in the mammalian virome. arXiv:2105.14973v2 [q-bio.QM], arxiv.org/abs/2105.14973

Provided by University of Montreal

Citation: Where are the next zoonotic viruses lurking? (2022, May 25) retrieved 26 June 2024 from <https://phys.org/news/2022-05-zoonotic-viruses-lurking.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.