

## How artificial intelligence (AI) can help prevent the next coronavirus from jumping from animals to humans

[New research by scientists at the University of Glasgow](#) suggests that machine learning (ML) models developed using viral genomes can be harnessed to predict the likelihood that any animal-infecting virus will migrate to infect humans, given biologically relevant exposure.

Most emerging infectious diseases of humans—such as [COVID-19](#)—are caused by viruses originating from other animal species, so identifying high-risk, potentially animal-to-human jumping zoonotic viruses earlier can help to improve research and surveillance priorities.

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To develop more accurate machine learning models using viral genome sequences, the researchers first compiled a dataset of 861 virus species from 36 families. They next built machine learning models, which assigned a probability of human infection based on virus taxonomy and/or relatedness to known human-infecting viruses.

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As the authors concluded,

Independently of the mechanisms involved, the performance of our models shows how increasingly ubiquitous and low-cost genome sequence data can inform decisions on virus research and surveillance priorities at the earliest stage of virus discovery with virtually no extra financial or time investment... Genome-based zoonotic risk assessment provides a rapid, low-cost approach to enable evidence-driven virus surveillance and increases the feasibility of downstream biological and ecological characterization of viruses.

**[This is an excerpt. Read the original post here.](#)**