

# Cheriton researchers and their colleagues at Western University use machine learning to identify and classify deadly astroviruses

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A team of researchers at the Cheriton School of Computer Science, along with their colleagues at Western University, have successfully classified 191 previously unidentified astroviruses using a new machine learning-enabled classification process.

Astroviruses are some of the most damaging and widespread viruses in the world. These viruses cause severe diarrhea, which kills more than 440,000 children under the age of five annually. In the poultry industry, astroviruses like avian flu have an 80 per cent infection rate and a 50 per cent mortality rate among livestock, leading to economic devastation, supply chain disruption, and food shortages.

Astroviruses mutate quickly and can spread easily across their more than 160 host species, putting researchers and public health officials in a constant race to classify and understand new astroviruses as they emerge. In 2023, there were 322 unidentified astroviruses with distinct genomes. This year, that number has risen to 479.

“At any given point, between two and nine per cent of humans carry one of these viruses,” said Fatemeh Alipour, PhD candidate at the Cheriton School of Computer Science and the lead computer science author of the research study. “That number can be as high as 30 per cent in some countries. “Understanding and classifying these viruses effectively is essential for developing vaccines.”



Left to right: Cheriton School of Computer Science Professor Lila Kari and PhD candidate Fatemeh Alipour. (Study collaborators Professor Yang Lu from the Cheriton School of Computer Science, and Connor Holmes and Professor Kathleen A. Hill from the University of Western Ontario were unavailable for the photo.)

Professor [Lila Kari](https://cs.uwaterloo.ca/~lila/) is an author of more than 200 peer-reviewed articles, and is regarded as one of the world's experts in biomolecular computation.

PhD candidate [Fatemeh Alipour](#) works on DNA sequence classification using alignment-free methods with applications to the study of virus-host co-evolution.

Professor [Yang Lu](#) and his students develop interpretable machine learning models to make sense of complex biological data and discover scientifically interesting and statistically confident hypotheses by interpreting these models.

Read the [full article on Waterloo News](https://uwaterloo.ca/news/media/identifying-next-deadly-virus).

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To learn more about this research, please see Fatemeh Alipour, Connor Holmes, Yang Young Lu, Kathleen A. Hill, Lila Kari, [Leveraging machine learning for taxonomic classification of emerging astroviruses](https://www.frontiersin.org/articles/10.3389/fmolb.2023.1305506/full), *Frontiers in Molecular Biosciences*, Vol 10, 2024.