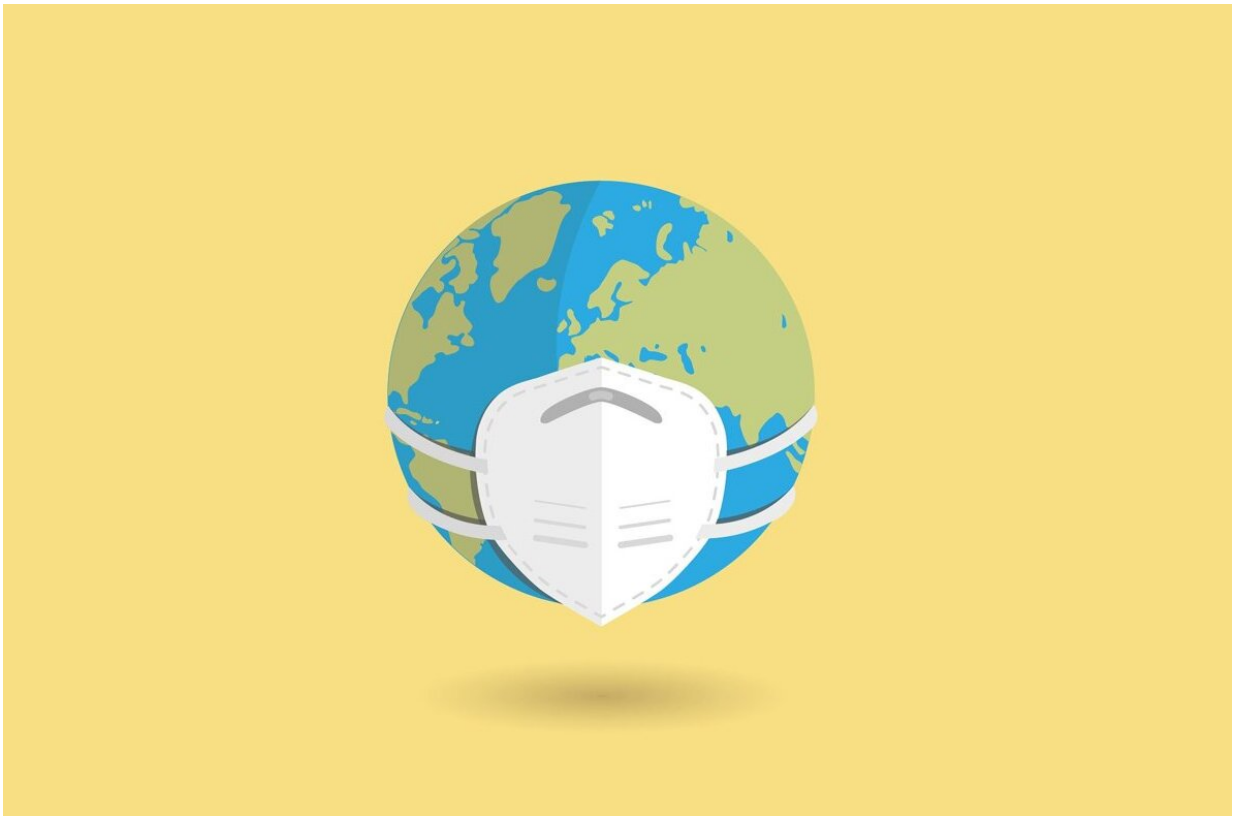# Predicting new pandemics through data analysis of recombinant virus genomes

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A study published in *Nature Communications* presents the promising results of RecombinHunt, a new data-driven method developed by the Department of Electronics, Information and Bioengineering of the

Politecnico di Milano and the University of Milan, which can identify, with high accuracy and computational efficiency, recombinant SARS-CoV-2 genomes with one or two breakpoints.

Recombination, that is, the composition of two or more viral genomes to form a new [genome](link), is an efficient molecular mechanism for [virus](link) evolution and adaptation.

Exploiting the incentive of the COVID-19 [pandemic](link), several methods have been proposed to detect recombinant genomes of SARS-CoV-2 virus; however, so far, none has been able to faithfully confirm the manual analyses of experts in the field.

RecombinHunt shows [high specificity](link) and sensitivity, is more effective than all other methods already developed, and faithfully confirms manual expert analyses.

The method, developed under the PRIN PNRR 2022, SENSIBLE project (Small-data Early warNing System for [viral pathogens](link) In puBLic hEalth), also identifies recombinant viral genomes from the recent monkeypox epidemic with high concordance with analyses manually curated by experts, suggesting that the approach is robust and can be applied to any epidemic or pandemic virus, representing an important tool to combat future pandemics.

Prof. Stefano Ceri notes that "the research was possible thanks to the extraordinary contribution of laboratories from all over the world, which made more than 15 million viral sequences available to the international community," Dr. Anna Bernasconi, SENSIBLE project leader, notes, "Our goal is to build warning tools to anticipate and combat new viral epidemics and pandemics."

"The study demonstrates how the development of innovative and

efficient computational methods allows us to more accurately and rigorously appreciate the evolution of pathogens, and any implications for human health," adds Prof. Matteo Chiara, professor of Molecular Biology at the University of Milan and co-leader of the SENSIBLE project.

Dr. Tommaso Alfonsi, who recently earned a doctorate "cum laude" in Information Engineering, is the first author of this study.

Provided by Polytechnic University of Milan