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VirusWarn: Mutation-based prioritization of concerning SARS-CoV-2 and Influenza virus variants from isolate and wastewater sequencing data

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The rapid evolution of respiratory viruses is characterized by the emergence of variants with concerning phenotypes that are efficient in antibody escape or show high transmissibility. This necessitates timely identification of such variants by surveillance networks to assist public health interventions.

Here we introduce *VirusWarn*, a comprehensive system designed for detecting, prioritizing, and warning of emerging virus variants from large genomic datasets. VirusWarn uses both manually-curated rules and machine-learning (ML) classifiers to generate and rank pathogen sequences based on mutations of concern and regions of interest.

Validation results for SARS-CoV-2 showed that VirusWarn successfully identifies variants of concern in both assessments, with manual- and ML-derived criteria from positive selection analyses. Although initially developed for SARS-CoV-2, VirusWarn has also been adapted to Influenza viruses and provides a robust performance, integrating a scheme that accounts for fixed mutations from past seasons. In addition, it features HTML reports that provide detailed results with searchable tables and visualizations, including mutation plots and heatmaps.

Because VirusWarn is written in Nextflow, it can be easily adapted to other pathogens, demonstrating its flexibility and scalability for genomic surveillance efforts. We are now applying VirusWarn to wastewater sequencing data, in order to provide timely surveillance of emerging variants on a broad scale.

Keywords

Warning system; SARS-CoV-2; Influenza virus; Genomic surveillance; Wastewater surveillance; Variant prioritization

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Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

Authors: KIRSCHBAUM, Christina (Robert Koch Institute); Mr KONGKITIMANON, Kunaphas (Hasso Plattner Institute); Mr FRANK, Stefan (Robert Koch Institute); Dr HÖLZER, Martin (Robert Koch Institute); Dr PARASKEVOPOULOU, Sofia (Robert Koch Institute); Dr RICHARD, Hugues (Robert Koch Institute)

Presenter: KIRSCHBAUM, Christina (Robert Koch Institute)

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