Method for Detection of Virus Transmission Enhancing Mutations Using Population Samples of Genomic Sequences

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ABSTRACT

Researchers at the University of California, Davis have developed a computer-implemented method to identify viral mutations that enhance transmission and predict their prevalence in populations over time.

FULL DESCRIPTION

This technology uses genome sequence data aligned to a reference genome to build phylogenetic trees and applies advanced statistical methods to identify mutations that increase viral transmission rates. It further predicts the frequency of candidate genome sequences in populations by integrating mutation-specific transmission rates into deterministic epidemiological models.

APPLICATIONS

- Public health agencies for monitoring and controlling viral outbreaks.
- Pharmaceutical companies developing targeted antiviral therapies or vaccines.
- Research institutions studying viral evolution and epidemiology.
- Bioinformatics and computational biology service providers.
- Diagnostic companies offering genomic surveillance tools.
- Wildlife conversation agencies monitoring natural viral outbreaks in wild populations.
- Agricultural organizations monitoring diseases in agricultural plant and animal populations.
- Biosecurity agencies monitoring new/existing bioweapons.

FEATURES/BENEFITS

- Accurately identifies transmission-enhancing mutations (TEMs) through rigorous statistical modeling.
- Integrates phylogenetic data with epidemiological parameters for comprehensive analysis.
- Predicts mutation frequency dynamics in populations over time.
- Automates generation of reports detailing mutation impact on transmission rate (R0).
- Supports rapid response during viral epidemics by highlighting variants of concern.
- Distinguishes mutations that significantly affect viral transmissibility from neutral or deleterious mutations.
- Quantifies the impact of specific mutations on transmission rates in real-time.
- Forecasts the spread and prevalence of viral variants in populations.
- Provides actionable insights for epidemiological surveillance and public health interventions.

PATENT STATUS

Patent Pending

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OTHER INFORMATION

KEYWORDS

epidemiology, public health, vaccine, infectious disease, mutation detection, transmission-enhancing mutation, viral evolution, viral transmission

CATEGORIZED AS

- **Biotechnology**
  - Bioinformatics
  - Genomics
  - Health
- **Medical**
  - Disease: Infectious Diseases
  - Research Tools
- **Research Tools**
  - Bioinformatics

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