



Conference Abstract

How much time have we got?

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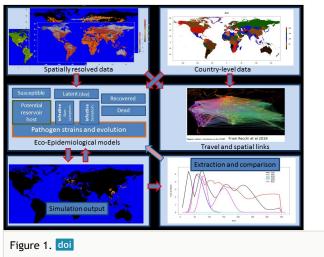
Abstract

Here we present a developing probabilistic simulation model and tool to assess likely lead times from emergence to detection and arrival for new emerging infectious diseases (EIDs). Key aspects include combining real-world data available on multiple scales with a flexible underlying disease model.

As demonstrated by the SARS-CoV-2 pandemic and other emerging infectious diseases, there is a need for scenario exploration for mitigation, surveillance and preparedness strategies. Existing simulation engines have been assessed but found to offer an insufficient set of features with regards to flexibility and control over processes, disease model structure and data sets incorporated for a wider enough range of diseases, circumstances, cofactors and scenarios (Heslop et al. 2017) to suit our aims.

We are therefore developing the first version of a simulation model designed to be able to incorporate a diverse range of disease models and data sources including multiple transmission and infectivity stages, multiple host species, varying and evolving virulence, socioeconomic differences, climate events and public health countermeasures. It is designed to be flexible with respect to implementing both improvements in the model structure and data as they become available. It is based on a discrete-time (daily) structure where spatial movement and transition between categories and detection are stochastic

rates dependent on spatial data and past states in the model, while being informed by the most suitable data available (Fig. 1).



Schematic overview of model structure.

The probability of detection is in itself treated as a probabilistic process and treated as a variable dependent on socioeconomic factors and parameterized by past performance, yet open for manipulation in scenario exploration regarding surveillance and reporting effectiveness.

Pathogen hotspot data are sourced from literature and included as a probabilistic assessment of emergence as well as a source of cofactor data (Allen et al. 2017), population data are adressed (Leyk et al. 2019) for utility and combined with data on local connectivity (Nelson et al. 2019) and transnational movement patterns (Recchi et al. 2019Fig. 1), as well as an increasing set of ecological and socioeconomic candidate variables.

Model parameterization relies on a machine learning framework with matching to the often partial data available for known relevant disease cases as the training data, and assessing them for plausible ranges of input for new, hypothetical EIDs.

As parameterizations improve, the range of scenarios to explore will incorporate effects of climate change and multiple stressors. When a suitable version becomes available it will be shared under a MIT license.

Keywords

Simulation models, GIS, Predictive models, Emerging threats

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Grant title

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Norwegian Veterinary Institute

Ethics and security

The project uses openly available published data in a open-source platform to improve public health and security.

Author contributions

JW and NCS wrote the initial project description and grant proposal, KK wrote and implemented the first version of the model, MF aggregated training data, all authors have contributed discussions and input at various stages of the project.

Conflicts of interest

The authors declare no conflict of interest.

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