



# *In Silico* Prediction of Pandemics: A Computational Tool to Complement Real-World Assessment

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## To the Editor,

Predicting pandemics is an intricate challenge that requires constant monitoring of several variables, including global travel patterns, the spread of infectious diseases, and the possibility of zoonotic (animal-to-human) transmission.<sup>1</sup> Scientists and public health experts employ risk assessments, modeling approaches, and surveillance systems, among other tools, to identify potential risks. While making precise early forecasts is complex, numerous agencies such as the Centers for Disease Control and Prevention (CDC) and the World Health Organization (WHO) closely monitor disease outbreaks and evaluate pandemic risks. They analyze information on disease transmission, pathogen properties, and other pertinent factors to make well-informed decisions. One promising technique that may be employed is the *in silico* prediction of pandemics.<sup>1,2</sup>

Pandemics can be predicted and analyzed *in silico*, which refers to the use of computer models and simulations to forecast and analyze the spread of infectious illnesses before they occur. This method evaluates potential risk factors, simulates and comprehends disease transmission dynamics, and explores outbreak scenarios using various computational tools, algorithms, and mathematical models.<sup>3</sup> The significant methods and protocols involved in *in silico* prediction of pandemics include epidemiological modeling, data-driven approaches, network analysis, phylogenetic analysis, geospatial modeling, climate and environmental analysis, and simulation and scenario analysis.<sup>3</sup>

The first method involves preparing epidemiological models, which include agent-based and compartmental models. Agent-based models simulate the interactions of individual agents (e.g., humans) within a virtual environment, facilitating the capture of local dynamics of disease propagation and population variability. In contrast, compartmental models use differential equations to describe transitions between compartments, which divide the population into categories such as

susceptible, infected, and recovered.<sup>3</sup> An example of this is the susceptible-infectious-recovered model. Following the development of these models, large datasets are analyzed using machine learning and analysis software. In machine learning, large data sets can be analyzed using various algorithms, allowing for the identification of trends and correlations in the spread of a particular disease.<sup>4</sup> In the second method, large datasets are analyzed using big data analytics software, which includes information related to demographics, travel patterns, and environmental factors.<sup>5</sup> Both methods help recognize risk indicators, forecast outbreaks, and maximize intervention tactics.

Thirdly, network analysis involves examining the social network of a particular population to understand the potential for disease transmission. Furthermore, transport network analysis is performed to forecast the geographic spread of diseases and the movement of people and goods.<sup>6</sup>

This is followed by phylogenetic analysis, where the genome data is analyzed to understand the genetic composition of pathogens. This can help understand their evolution, modes of transmission, and potential for causing pandemics.<sup>7</sup>

Next, geospatial modeling uses geographic information systems to examine geographic data and assess the potential for disease transmission between various locations.<sup>8</sup> Climate and environmental factors are analyzed through climate modeling to understand how various climate conditions can affect the survival and transmission of pathogens.<sup>9</sup>

Finally, simulation and scenario analysis are performed using Monte Carlo simulations, which run several simulations under different conditions to evaluate potential outcomes. Then, scenario planning is done to analyze the effects of different interventions and policies by considering different theoretical scenarios.<sup>10</sup>

In summary, the accuracy of *in silico* predictions relies on the quality of data, the assumptions underlying the models, and the dynamic nature of real-world scenarios. These predictions, which are based on models and

simulations, often support established epidemiological research and surveillance initiatives.

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None

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None.

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