MIDAS
ANNUAL MEETING

Unveiling Key Factors in Disease Transmission through Explainable AI

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Introduction and Motivation

- Identifying the key factors driving disease propagation is paramount in reducing fatalities and addressing broader societal impacts.

- Infectious disease transmission is characterized by complex nonlinear dynamics making the analysis using conventional methods challenging.

- Integration of traditional modeling approaches in epidemiology with modern machine learning techniques can effectively identify the key factors influencing the outcomes of infectious disease transmission.

Research Objectives

This goal is comprised of three tasks:

- Develop models of transmission that account for multiple viral strains, multiple vaccines, vaccine preferences.

- Create novel architectures of AI-enabled algorithms that can learn the fundamental nonlinear dynamic features of outbreaks.

- Develop methods to identify what features of the trained algorithms from task 3 most impact disease outcomes.

Approach – Problem Formulation

- A multi-strain-vaccine disease dynamics model has been developed.

- Disease propagation starts with the first variant, and mutation in the variant occur and results in new variants of concern.

- We have integrated all vaccine-related components, such as the introduction date, lead time, and efficacy.

$$S(t+1) = S(t) - \sum_{l=1}^{K}\left[S(t)\frac{\beta^l(t)(I^l(t)+I_v^l(t))}{N}\right] - \sum_{l=1}^{K}\gamma_{SV}^l(1-\bar{\gamma})S(t)$$

$$V^k(t+1) = V^k(t) - \sum_{l=1}^{K}\left[V^k(t)\frac{\beta^{l,k}(t)(I^l(t)+I_v^l(t))}{N}\right] + \gamma_{SV}^k(1-\bar{\gamma})S(t)$$
$$+ \sum_{l=1}^{k-1}\left[\gamma_{VV}^{l,k}((1-\bar{\gamma})R^l(t)+V^l(t))\right] - \sum_{l=k+1}^{K}\gamma_{VV}^{k,l}V^k(t)$$

$$E^k(t+1) = E^k(t) + S(t)\frac{\beta^k(t)(I^k(t)+I_v^k(t))}{N} - \gamma_{EI}E^k(t)$$

$$E_v^k(t+1) = E_v^k(t) + \sum_{l\neq k}^{K}\left[R^l(t)\frac{\beta^{l,k}(t)(I^k(t)+I_v^k(t))}{N}\right] + \sum_{l=1}^{K}\left[V^l(t)\sum_j\frac{\beta^{k,l}(t)(I^k(t)+I_v^k(t))}{N}\right] - \gamma_{EI}E_v^k(t)$$

$$I^k(t+1) = I^k(t) + \gamma_{EI}E^k(t) - (\gamma_{IH}^k + \gamma_{IR}^k)I^k(t)$$

$$I_v^k(t+1) = I_v^k(t) + \gamma_{EI}E_v^k(t) - (\gamma_{vIH}^k + \gamma_{vIR}^k)I_v^k(t)$$

$$H^k(t+1) = H^k(t) + \gamma_{IH}^k I^k(t) - (\gamma_{HR}^k + \gamma_{HD}^k)H^k(t)$$

$$H_v^k(t+1) = H_v^k(t) + \gamma_{vIH}^k I_v^k(t) - (\gamma_{vHR}^k + \gamma_{vHD}^k)H_v^k(t)$$

$$R^k(t+1) = R^k(t) + \gamma_{IR}^k I_k(t) + \gamma_{vIR}^k I_{k,i}^v(t)) + \gamma_{HR}^k H_k(t) + \gamma_{vHR}^k H_v^k(t)$$
$$- \sum_{l\neq k}^{K}R^k(t)\frac{\beta^{l,k}(t)(I^l(t)+I_v^l(t))}{N} - \sum_{l=k+1}^{K}\gamma_{VV}^{k,l}(1-\bar{\gamma})R^k(t)$$

$$D^k(t+1) = D^k(t) + \gamma_{HD}^k H_k(t) + \gamma_{vHD}^k H_v^k(t)$$
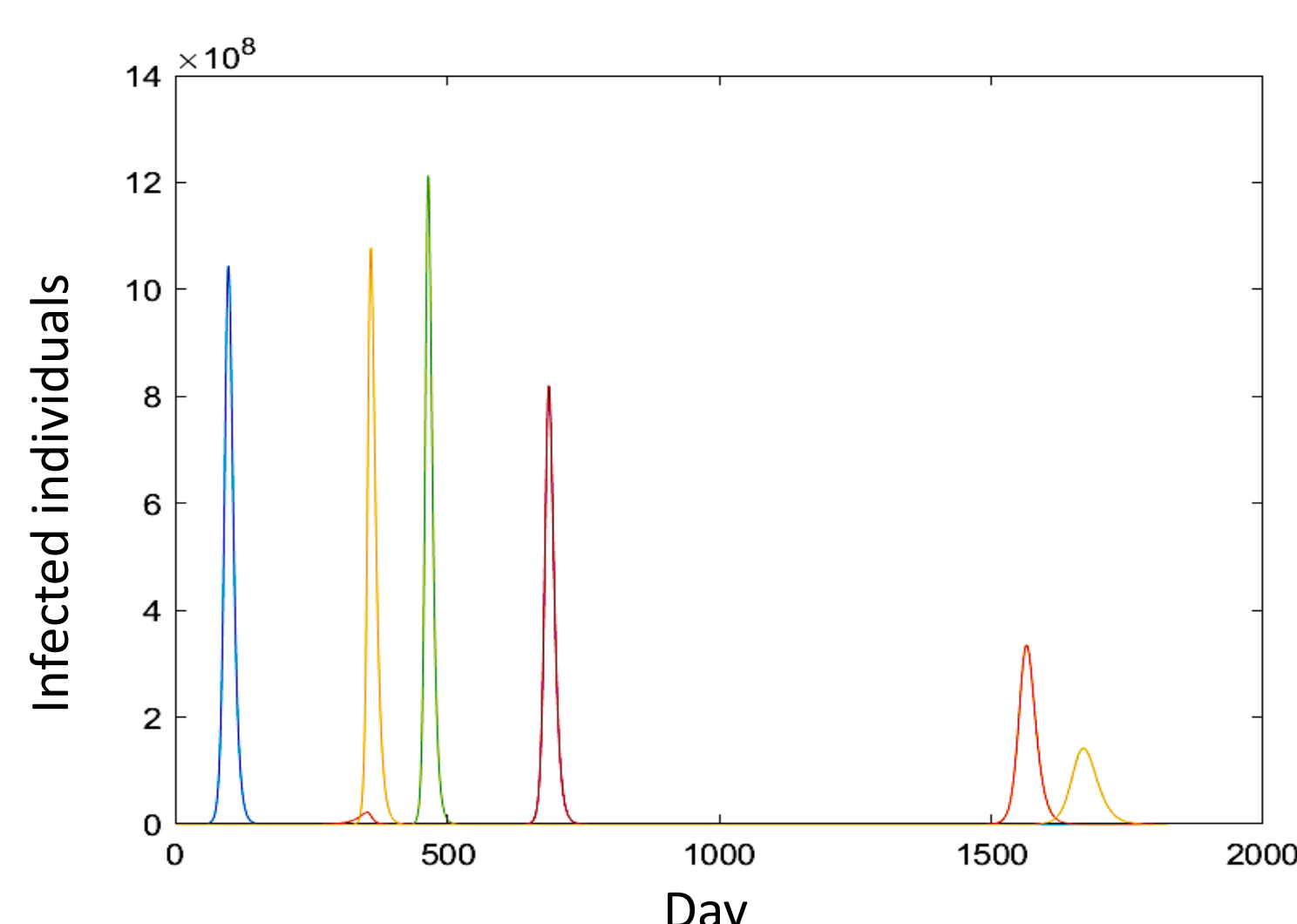
Multiple waves of transmission due to new variants

Approach – Explainable AI

- XAI algorithms specifically designed to provide human interpretability for complex decision making.

- A neural network algorithm is trained on the synthetic data generated from the multi-strain-vaccine model.

- SHAP (SHapley Additive exPlanations) algorithm within XAI is considered to analyze the important features contributing to an increased number of fatalities during a pandemic.
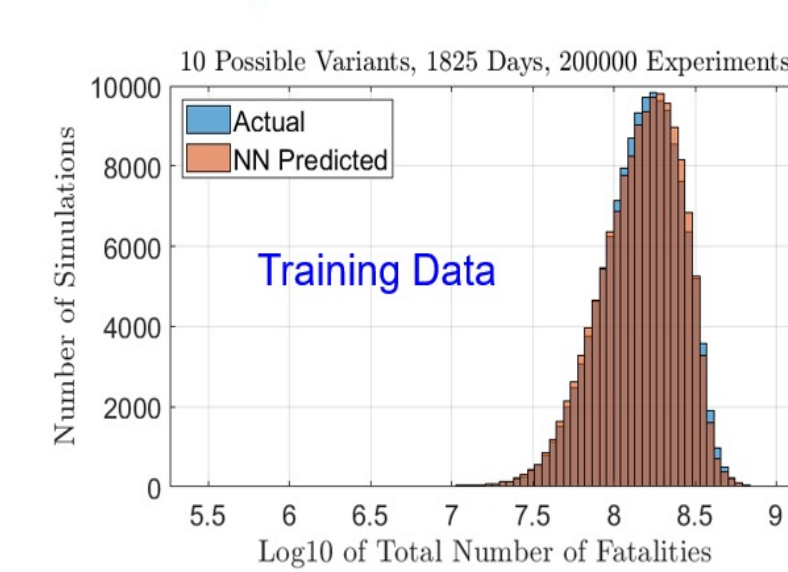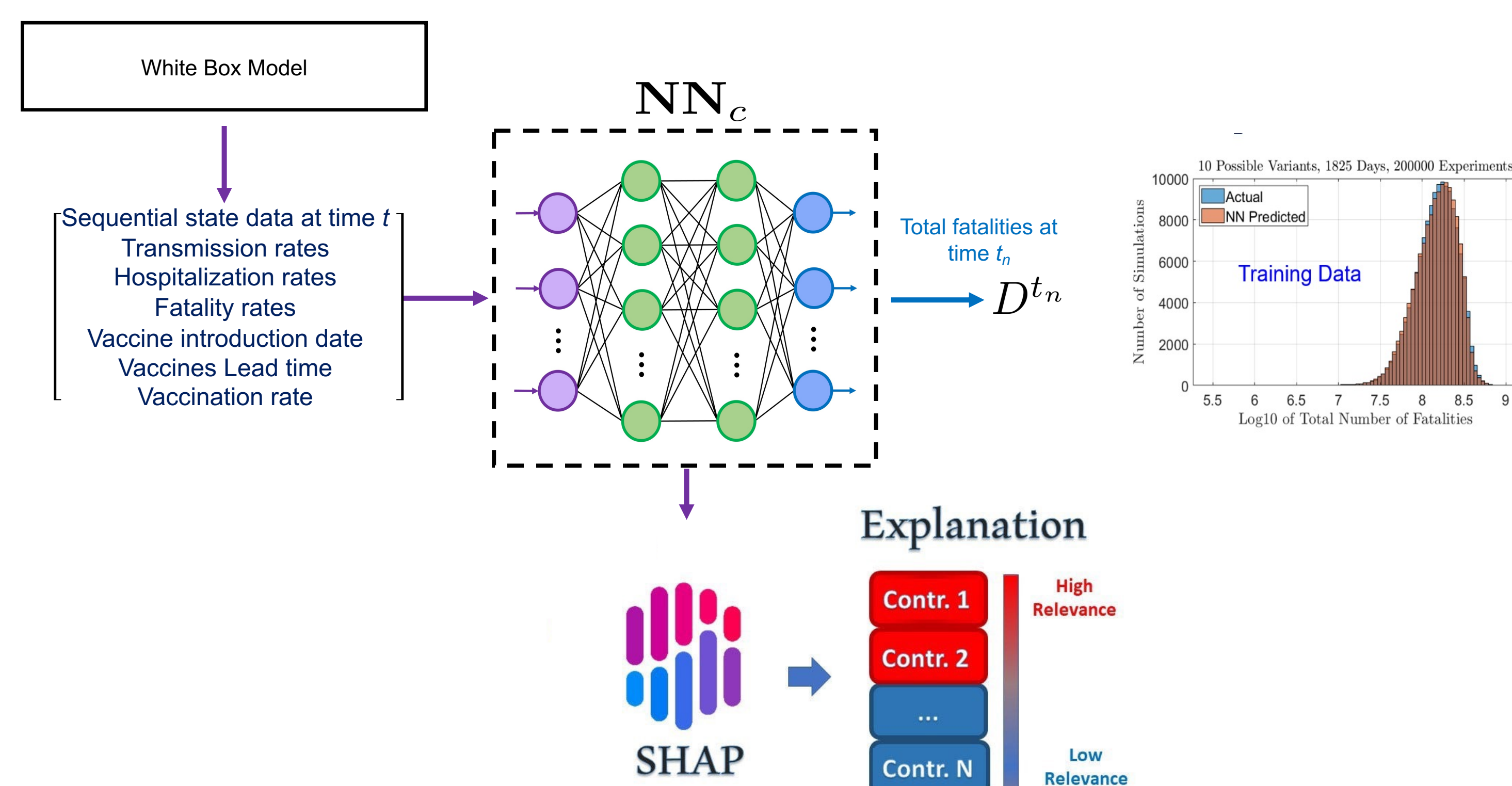
Results

- The factors that have the greatest impact on the fatality rate during a 5-year simulation of disease dynamics are identified.
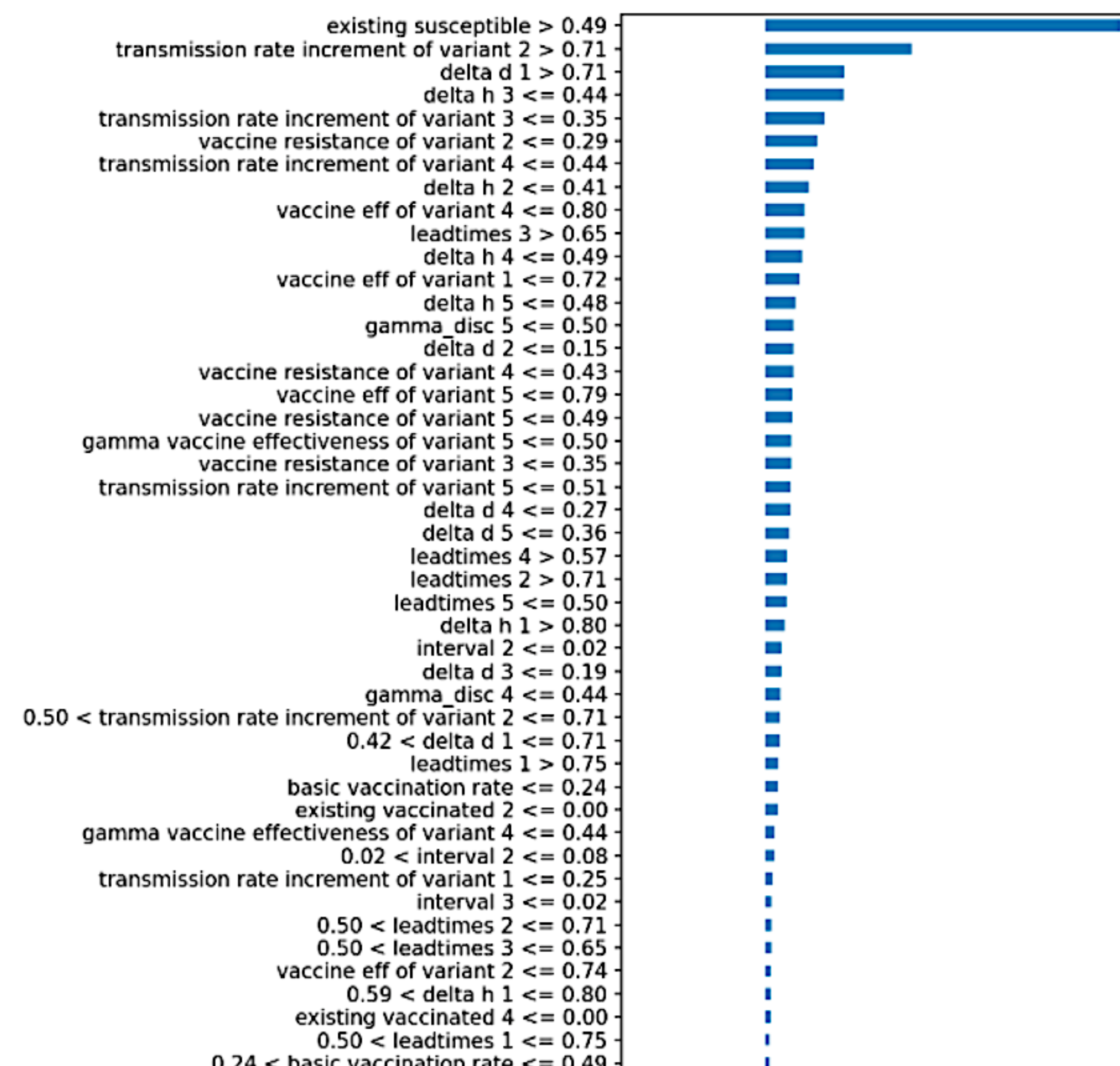
Conclusions

- An AI-enabled algorithm combined with compartmental modeling methods is proposed to detect the features that affect disease outcomes the most

- The parameters that affect the disease outcome depend on the current state of a pandemic, and might vary as time evolves

- The analysis results will guide health officials in prioritizing actions and policies to prevent disease transmission consequences.