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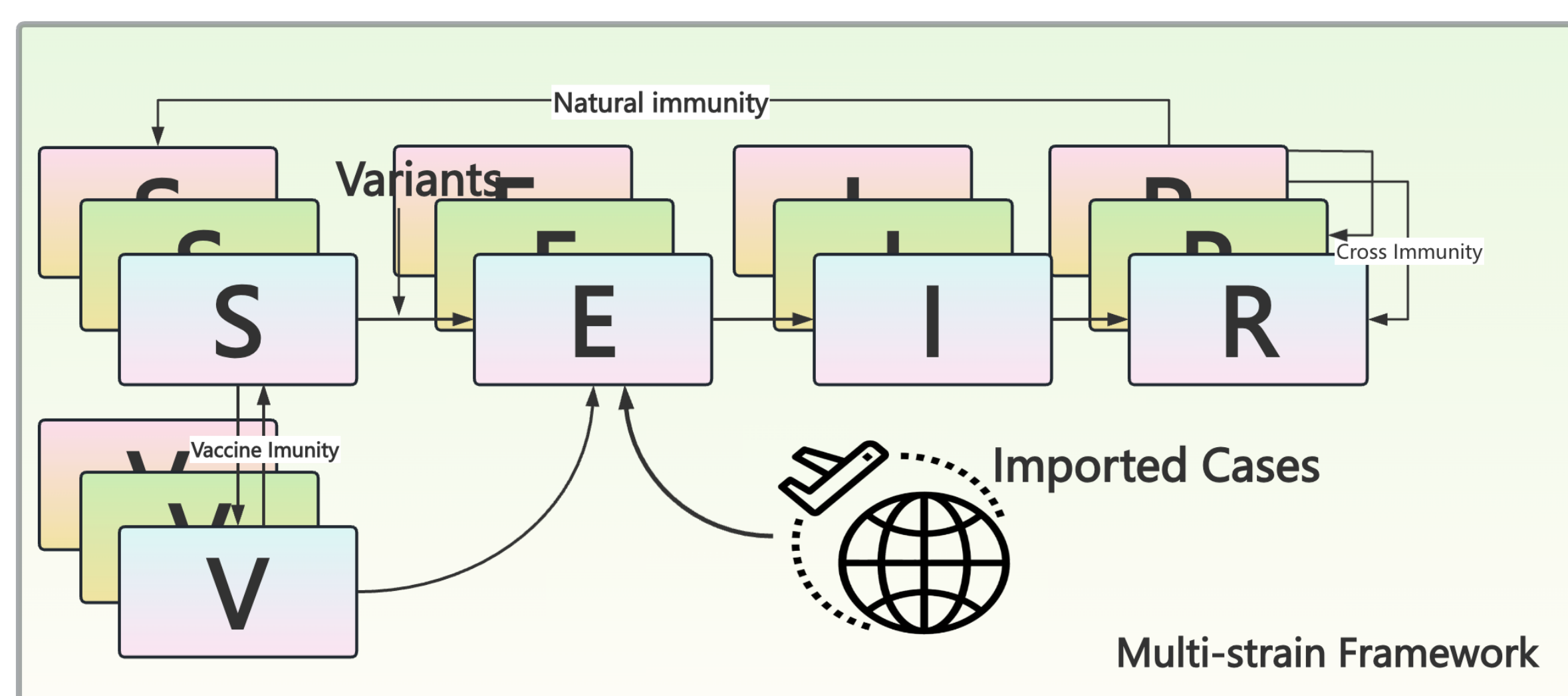
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Background

In early March 2025, the NB.1.8.1 variant of the SARS-CoV-2 virus rapidly emerged as the dominant variant across several Asian countries and regions, including China, Hong Kong, Thailand, and Singapore, causing a new wave of the COVID-19. By May 2025, the test positivity rate for SARS-CoV-2 in Hong Kong had escalated to 13.8%. Compared to the two prior pandemic waves in Hong Kong since 2024, this wave demonstrated the most rapid growth rate. Given the potential for widespread and unpredictable impacts on both Hong Kong and the global community, there is an urgent need to utilize mechanistic models to forecast the future dynamics of the outbreak and quantify the threat posed by the NB.1.8.1 variant.

Methods

We developed a data-driven multi-strain forecasting model integrating natural and vaccine-induced immunity, public health measures, 20 prevalent variants, and importation risks from 15 NB.1.8.1-dominant countries.



Mobility: $\Delta_i = \frac{1}{N_i} \sum_{k \neq i} (M_{ik} I_k - M_{ki} I_i)$

Genetic diversity: $v(t) = v_0(t) e^{a \cdot \text{div}(t)}$

$\beta_t = \beta_{\text{spline}} \cdot \exp(\sum_{v=1}^V \delta_v \cdot p_{t,v})$

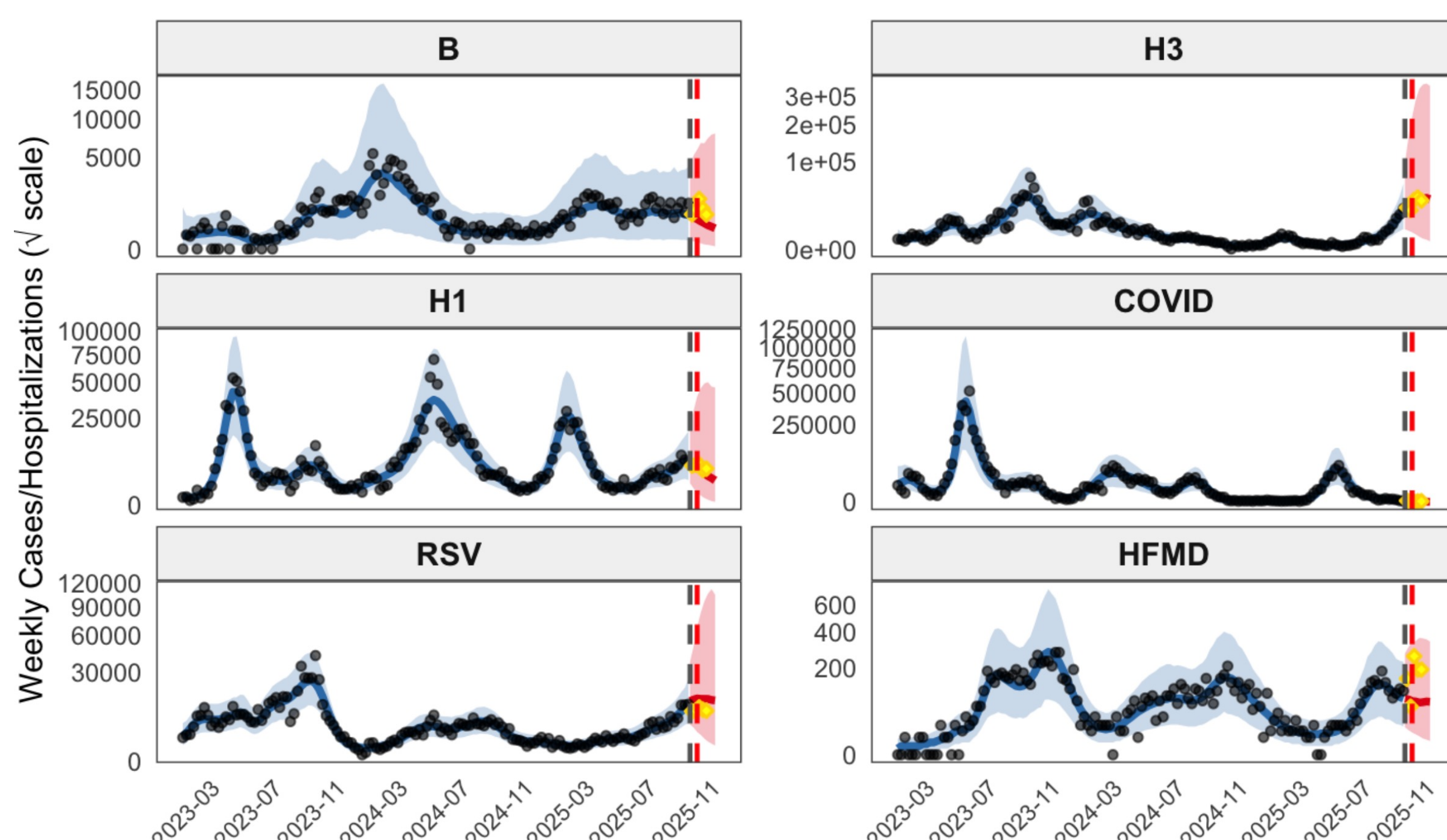


Figure 1. Fitting and Forecasting Results for Multi-strain Dynamics.

Results

Estimated Effective Reproduction Number (Rt)

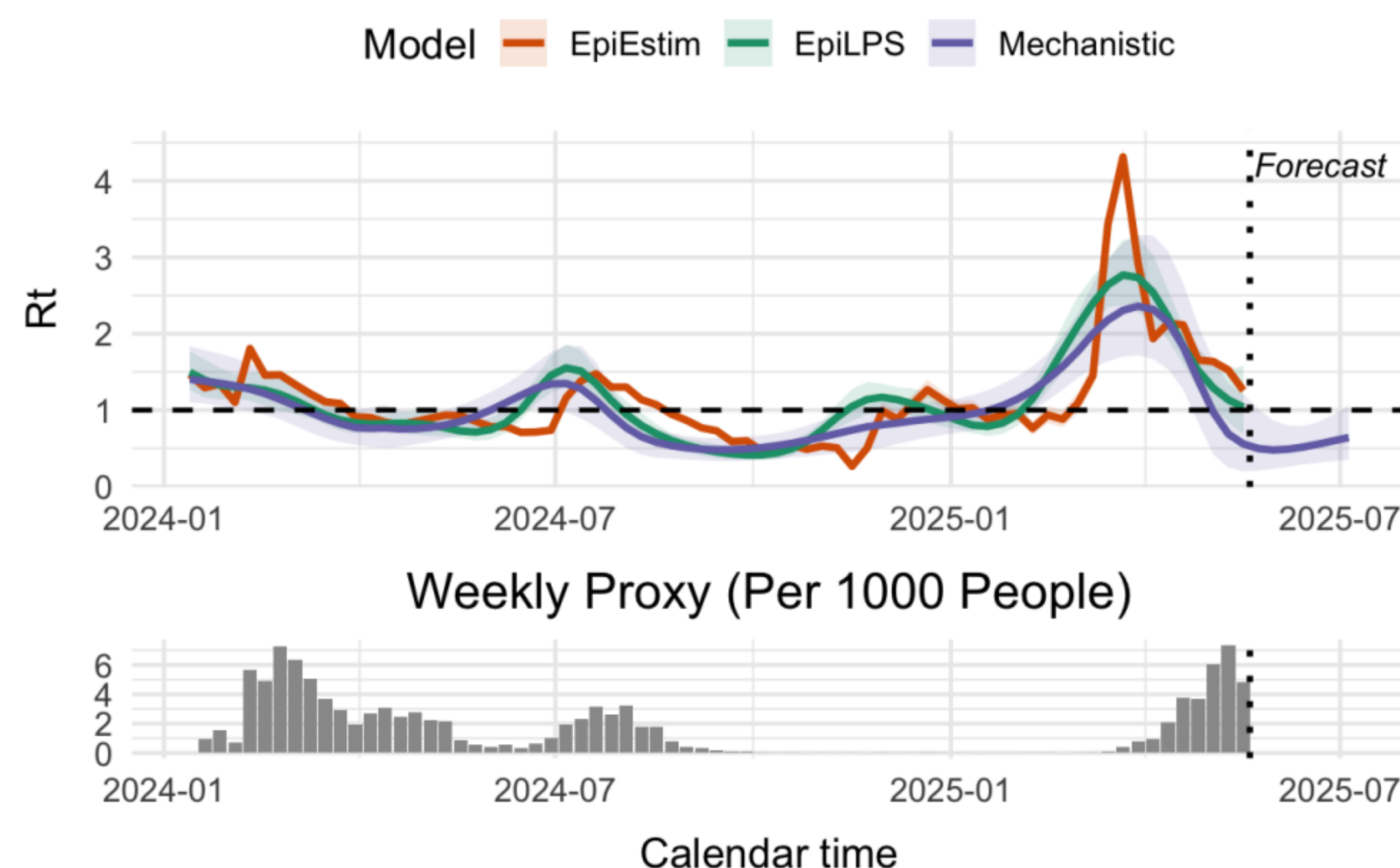


Figure 2. Comparison of Rt Estimates Across Different Models.

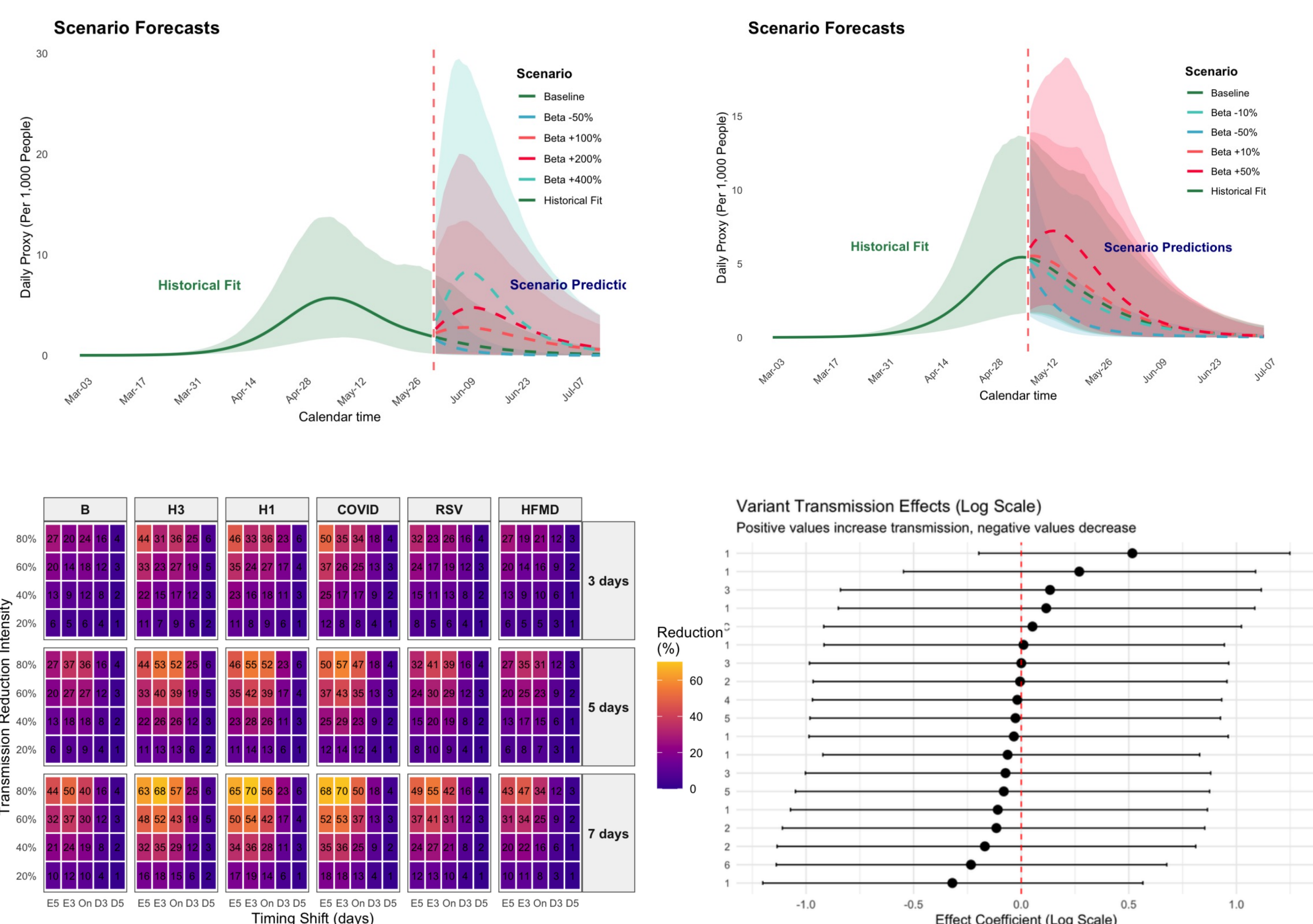


Figure 3. Counterfactual Analyses and Identification of Critical Variants.

Discussion

We developed a data-driven forecasting model incorporating immunity, interventions, variant dynamics, and importation risks, revealing that strict measures can substantially reduce the projected attack rate and that variants XDV.1 and NB.1.8.1 exhibit markedly higher transmissibility.

References

[1] Nickbakhsh, S., Mair, C., Matthews, L., Reeve, R., Johnson, P. C., Thorburn, F., ... & Murcia, P. R. (2019). Virus–virus interactions impact the population dynamics of influenza and the common cold. *Proceedings of the National Academy of Sciences*, 116(52), 27142-27150.

Acknowledgements

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