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EXTENDING THE HYBRID SEIR MODEL WITH VITAL DYNAMICS: INSIGHTS FROM MONKEY POX OUTBREAKS IN THE US AND EUROPE

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ABSTRACT

The Mpox outbreak has ignited new interest in using infectious disease modeling to predict its future trajectory. Building on our previous study of the Mpox epidemic in the United States, this study applies an enhanced Susceptible-Exposed-Infectious-Recovered (SEIR) model to the outbreak in Europe. By incorporating vital dynamics, such as births and deaths, the model accounts for long-term population changes and offers a realistic long-term representation of infection dynamics. This follow-up analysis extends the insights from the US study to explore regional differences in transmission patterns, peak infection periods, and the eventual decline of the outbreak.Our findings provide a comparative perspective on the effectiveness of public health interventions in Europe versus the United States, highlighting the importance of early interventions and strategic planning for long-term epidemic control. This follow-up study validates the robustness of the enhanced SEIR model across regions and provides critical insights for health authorities to refine mitigation strategies.

Introduction

The SEIR model provides a foundational framework

for understanding the evolution of an epidemic by dividing the population into four compartments: Susceptible (S), Exposed (E), Infectious (I), and Recovered (R). To model infectious diseases like Monkeypox more realistically, particularly over an extended period, the inclusion of vital dynamics, such as birth and death rates, is essential [?].

This paper builds on previous research conducted on the US Monkeypox outbreak [1] by applying the enhanced SEIR model to the European outbreak. In addition to incorporating vital dynamics, the model introduces dynamic transmission rates, $\beta(t)$, that reflect changes due to public health interventions such as time-dependent public health interventions. Gaussian smoothing is applied to the raw epidemic data to reduce noise and improve model accuracy[2]. By optimizing key parameters and performing sensitivity analyses, this study identifies the optimal transmission rate, $\beta_{\max}$, for the Monkeypox outbreak in Europe and compares these findings with the US results. This comparative analysis highlights regional variations and validates the applicability of the enhanced SEIR model across different epidemiological settings.

1 Methodology Overview

The parameter δ represents the intervention strength, encompassing any time-dependent measures, such as interventions, vaccination campaigns, or other public health initiatives aimed at reducing the transmission rate.

Data Preprocessing

Primary data on Monkeypox cases was sourced from publicly available health repositories. Raw data was smoothed using a Gaussian filter to reduce irregularities caused by reporting delays and anomalies. This step helps ensure a more accurate representation of the epidemic curve.

SEIR Model with Vital Dynamics

The SEIR model incorporates vital dynamics to account for births and natural deaths, allowing for population turnover and realistic long-term epidemic projections. The governing differential equations include compartments for susceptible, exposed, infectious, and recovered populations. Dynamic transmission rates, $\beta(t)$, are modeled as time-dependent functions to reflect changes in disease spread due to interventions.

Parameter Optimization and Sensitivity Analysis

Key model parameters, including the transmission rate (β), recovery rate (γ), and incubation rate (σ), were optimized using numerical solvers to minimize the discrepancy between the modeled and observed data. Sensitivity analysis was conducted to evaluate the impact of varying $\beta_{\max}$ on the model's predictive accuracy.

2 SEIR Model with Gaussian Filtering and Optimization

The SEIR model was applied to simulate the Monkeypox outbreak dynamics in Europe, incorporating Gaussian filtering and parameter optimization to refine model predictions. Primary data on new cases was sourced from a publicly available Kaggle dataset. After cleaning for missing values and inconsistencies, a Gaussian filter with $\sigma = 3$ was applied to smooth the time-series data, minimizing noise and ensuring a realistic representation of the epidemic curve [2].

Model Setup: The SEIR model divides the population into compartments: Susceptible (S), Exposed (E), Infectious (I), and Recovered (R). Initial conditions were set as follows:

- $S_0 = N - E_0 - I_0$, where $N = 746{,}964{,}593$ is the total population.
- $E_0 = \max(20, 5 \times \text{firstsmoothedatapoint})$.
- $I_0 = \max(1, \text{firstsmoothedatapoint})$.
- $R_0 = 0$ (no recoveries initially).

The transition rates for exposure ($\sigma = 1/6$) and recovery ($\gamma = 1/8$) were used, along with a mortality rate ($\mu = 1/(70 \times 365)$).

Dynamic Transmission Rates: The time-varying transmission rate, $\beta(t)$, was modeled as a function of key intervention phases: lock-downs, recovery periods, and potential second waves. The

function was parameterized to capture transitions between maximum and minimum transmission rates, reflecting real-world intervention impacts.

Optimization: Differential evolution was used to optimize key parameters, minimizing the root mean square error (RMSE) between the model output and smoothed actual data. Parameter bounds were defined, with $\beta_{\max}$ fixed at 0.236 to reflect realistic transmission limits.

Sensitivity Analysis: Sensitivity analysis was conducted on $\beta_{\max}$ to evaluate the impact of varying its value on model accuracy. This process ensured robustness of the optimized parameters across plausible ranges of transmission rates.

Results

Sensitivity Analysis of Max Beta

The sensitivity analysis for the maximum transmission rate, $\beta_{\max}$, demonstrated that model error is minimized at $\beta_{\max} = 0.236$ (Figure 1). Figure 2 shows the optimized SEIR model results with $\max\_\beta = 0.236$ compared to smoothed actual data.

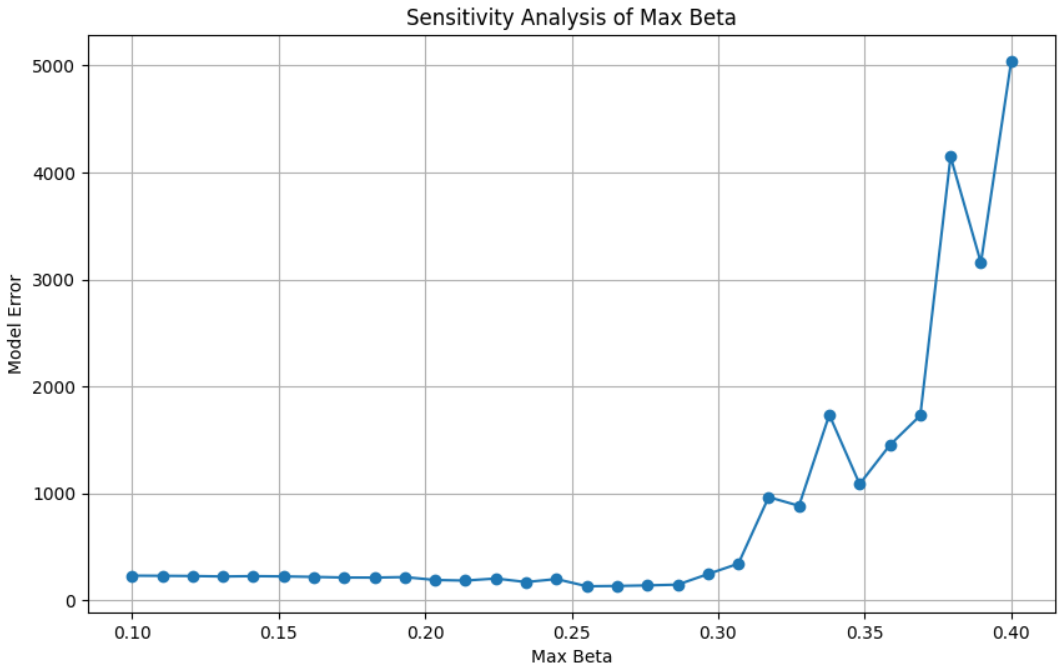

Figure 1: Sensitivity Analysis of the Maximum Beta Parameter

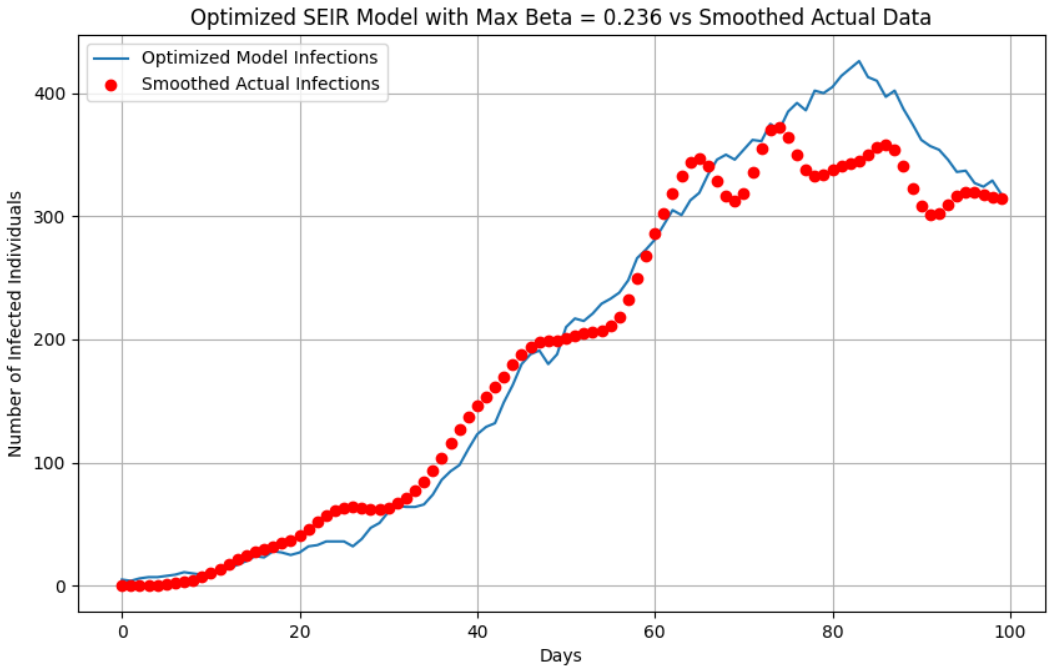

Figure 2: Optimized SEIR Model with $\max\_\beta = 0.236$ Compared to Smoothed Actual Infections

Discussion

The model captures the effect of time-dependent interventions through the parameter δ, which reflects the rate of reduction in transmission due to measures like Interventions, public awareness efforts, or vaccination programs. The sensitivity analysis highlighted the importance of selecting an optimal $\beta_{\max}$ value for model accuracy. Although $\beta_{\max} = 0.255$ initially appeared promising from the previous US optimization, the lower value of $\beta_{\max} = 0.2236$ ultimately provided a better fit for the European data, as evidenced by the lower RMSE. This result diverges slightly from the optimal transmission rates in the US, reflecting regional variations in population density, social behavior, and healthcare response times. These findings underscore the necessity of tailoring epidemic models to specific regions to improve prediction accuracy.

Conclusion

Our findings suggest that the SEIR model, enhanced with Gaussian filtering and sensitivity analysis, effectively models the monkeypox outbreak in Europe when the optimal $\max\_\beta = 0.236$ is used. The model demonstrates the need to fine-tune parameters based on localized data to capture region-specific epidemic dynamics accurately. Future work may incorporate additional parameters like vaccination rates and regional healthcare response variations to enhance the model's robustness.

3 Hybrid SEIR Approach

Introduction

The hybrid SEIR approach combines the traditional Susceptible-Exposed-Infectious-Recovered (SEIR) model with Gaussian filtering and dynamic transmission rate (β) adjustments to model the Monkeypox outbreak in Europe. Two transmission rate values, $\beta_{\max} = 0.236$ and $\beta_{\max} = 0.3$, were evaluated using Root Mean Square Error (RMSE) analysis. While $\beta_{\max} = 0.236$ provided a reasonable fit, $\beta_{\max} = 0.3$ yielded a lower RMSE, suggesting a slightly better alignment with the observed epidemic data.

Methodology Overview

Data Cleaning and Preprocessing

Primary data on Monkeypox cases was sourced from publicly available datasets on Kaggle. The raw data included irregularities due to reporting delays, missing entries, and inconsistencies across regions. A rigorous data cleaning process was performed to ensure accuracy and reliability. This involved handling missing values, removing outliers, and standardizing formats. Gaussian filtering was subsequently applied to smooth the epidemic curve, minimizing noise and ensuring a clear representation of the disease progression.

SEIR Model with Gaussian Filtering

The SEIR model was used as the foundational framework to simulate the Monkeypox outbreak. Gaussian filtering was integrated into the model to smooth daily case numbers and account for short-term fluctuations in reporting [2]. The filtered data allowed for the refinement of key parameters such as transmission rates (β), recovery rates (γ), and incubation rates (σ).

Hybrid Model without Vital Dynamics

A hybrid SEIR model was first constructed without incorporating vital dynamics (birth and death rates) to analyze the immediate impact of disease spread. This model focused on short-term projections by optimizing time-dependent transmission rates ($\beta(t)$) using numerical solvers. Sensitivity analyses were conducted to assess the impact of different transmission rate variations on outbreak dynamics.

Hybrid Model with Vital Dynamics

To model long-term epidemic trajectories, the hybrid SEIR model was extended to include vital dynamics. This addition accounted for population turnover due to births and natural deaths, providing a more comprehensive framework for simulating the progression of the Monkeypox outbreak over an extended period. The inclusion of vital dynamics enabled the evaluation of sustained public health interventions and their influence on disease control. Key parameters such as $\beta_{\max}$ and δ (intervention strength) were optimized, and comparisons were made between models with and without vital dynamics to highlight their respective implications.

3.1 Results

The optimal parameters identified are:

$$\sigma = 0.1923(\text{days}^{-1}),$$
$$\gamma = 0.0556(\text{days}^{-1}),$$
$$t_{\text{intervention}} = 29.7(\text{days}),$$
$$\delta = 0.0852.$$

3.1.1 Model Fit for $\beta_{\max} = 0.236$

The optimized transmission rate $\beta_{\max} = 0.236$ yielded an RMSE of 21.94. The comparison between the modeled infections and the smoothed actual data is shown in Figure 3.

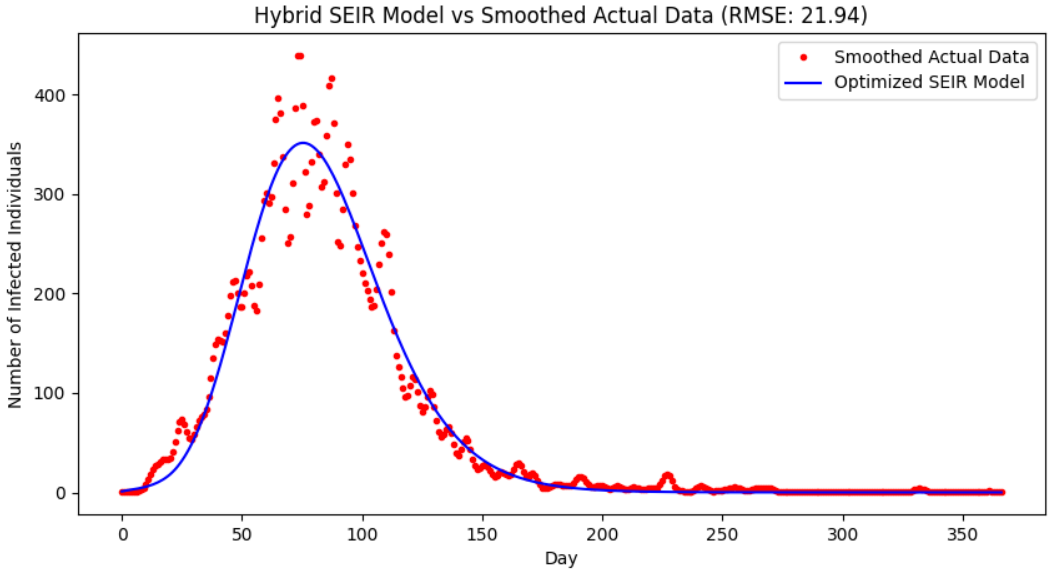

Figure 3: Hybrid SEIR Model with $\beta_{\max} = 0.236$ vs Smoothed Actual Data (RMSE: 21.94)

3.1.2 Model Fit for $\beta_{\max} = 0.3$

The transmission rate $\beta_{\max} = 0.3$ provided a better fit, with an RMSE of 21.46, as shown in Figure 4.

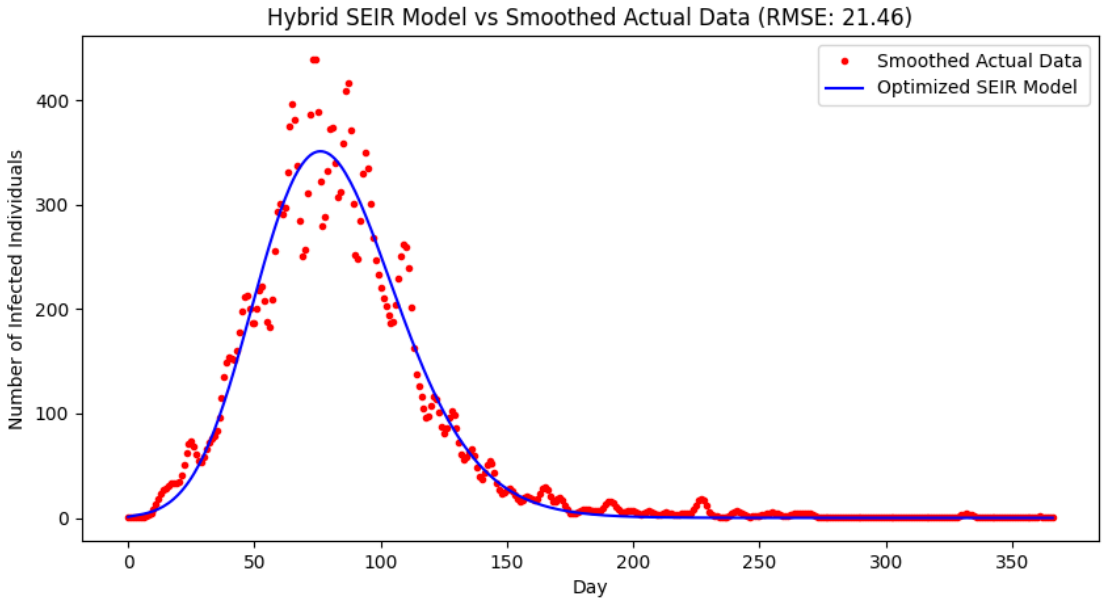

Figure 4: Hybrid SEIR Model with $\beta_{\max} = 0.3$ vs Smoothed Actual Data (RMSE: 21.46)

3.2 Discussion

The model captures the effect of time-dependent interventions through the parameter δ, which reflects the rate of reduction in transmission due to measures like Interventions, public awareness efforts, or vaccination programs. The analysis revealed that $\beta_{\max} = 0.3$ provided a better fit to the observed data compared to $\beta_{\max} = 0.236$, as indicated by a lower RMSE (21.46 vs. 21.94). This suggests that $\beta_{\max} = 0.3$ captures the transmission dynamics more accurately, potentially due to region-specific variations in social behavior and intervention measures. However, both values demonstrated strong alignment with the

epidemic's growth, plateau, and decline phases, highlighting the robustness of the hybrid SEIR approach.

3.3 Conclusion

The hybrid SEIR model successfully integrates dynamic transmission rates and Gaussian filtering to model the Monkeypox outbreak in Europe. While $\beta_{\max} = 0.3$ provided a slightly better fit, $\beta_{\max} = 0.236$ remains a valid alternative for capturing key epidemic dynamics. Future work can extend this methodology to incorporate vaccination rates, mobility indices, and other real-world factors to enhance predictive accuracy.

4 Impact of Vital Dynamics on the hybrid SEIR Model

4.1 Introduction

To assess the role of vital dynamics (births and natural deaths) in epidemic modeling, we incorporated these dynamics into the hybrid SEIR model. Vital dynamics account for the natural population turnover, introducing new susceptible individuals through births (μN) and removing individuals from all compartments due to natural deaths ($-\mu S, -\mu E, -\mu I, -\mu R$). This section compares the model's performance with and without vital dynamics in terms of root mean square error (RMSE) and epidemic trajectory.

4.2 Results Without Vital Dynamics for Europe

In the initial hybrid SEIR model without vital dynamics, the population was assumed to remain constant. The optimized parameters were:

- $\sigma = 0.333$ (~ 3days incubation period),
- $\gamma = 0.077$ (~ 13days infectious period),
- $t_{\text{intervention}} = 10.05$days,
- $\delta = 0.0215$ (intervention strength).

This configuration resulted in an RMSE of 21.46. The model provided a strong fit to the smoothed actual data, accurately capturing the outbreak's growth, peak, and decline phases (refer to the previous figure of the hybrid SEIR model without vital dynamics, with $\beta_{\max} = 0.3$).

4.3 Results With Vital Dynamics for Europe

When vital dynamics were incorporated into the model, the same optimized parameters were achieved ($\sigma = 0.333, \gamma = 0.077, t_{\text{intervention}} = 10.05, \delta = 0.0215$), with an RMSE of 21.46 (Figure 5). This suggests that the inclusion of births and natural deaths does not impact the model's short-term fit.

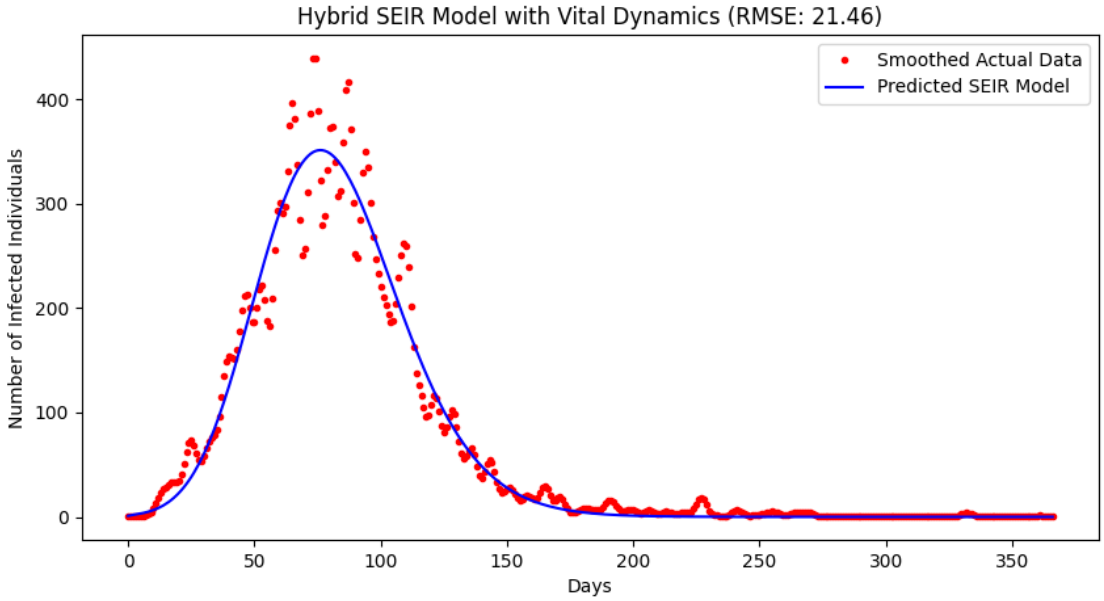

Figure 5: Hybrid SEIR Model With Vital Dynamics ($\beta_{\max} = 0.3$) vs Smoothed Actual Data (RMSE: 21.46) for Europe

4.4 Comparison of Results of hybrid SEIR model with and without dynamics for Europe

The comparison of the two models reveals the following:

• **RMSE:** Both models achieve identical RMSE values (21.46), indicating no improvement in the model's ability to fit the observed data by adding vital dynamics.

• **Epidemic Trajectory:** The visual fits of the two models to the smoothed data are nearly indistinguishable, capturing the growth, peak, and decline phases effectively in both cases.

• **Short-Term vs Long-Term Dynamics:**

In the short term, the natural birth and death rates ($\mu \sim 3.42 \times 10^{-5}$) are too small to significantly affect the population and, consequently, the epidemic trajectory.

Over the long term, vital dynamics prevent the susceptible population (S) from unrealistically depleting to zero and introduce population renewal through births, making the model more realistic for extended projections.

4.5 Discussion

The model captures the effect of time-dependent interventions through the parameter δ, which reflects the rate of reduction in transmission due to measures like Interventions, public awareness efforts, or vaccination programs. The inclusion of vital dynamics does not impact the short-term prediction of the epidemic, as evidenced by the unchanged RMSE and similar visual fits. However, vital dynamics are crucial for long-term simulations where population turnover influences the epidemic trajectory. This extension enhances the realism of the model by:

• Accounting for population replenishment through births,

• Ensuring a non-zero susceptible population over time,

• Providing a more realistic framework for evaluating recurrent outbreaks or endemic equilibria.

The results suggest that while vital dynamics are not critical for modeling the 2022 Monkeypox outbreak in Europe due to its relatively short duration, they are essential for modeling epidemics

with longer time scales or for studying post-outbreak dynamics.

4.6 Conclusion

Incorporating vital dynamics into the hybrid SEIR model provides no immediate improvement in the model fit for short-term epidemic prediction. However, for long-term epidemic modeling, vital dynamics enhance the realism and applicability of the model. Future work could explore the interaction of vital dynamics with other factors, such as vaccination and mobility, to assess their combined effects on epidemic trajectories.

5 Comparative Analysis of the US SEIR Model with and without Vital Dynamics

The Susceptible-Exposed-Infectious-Recovered (SEIR) model provides a robust framework for understanding epidemic dynamics. This section compares the hybrid SEIR model for the US Monkeypox outbreak with and without vital dynamics, focusing on short-term predictions and long-term modeling.

5.1 Optimized Parameters for the SEIR Model

• **Incubation Rate (σ):**
- Without vital dynamics: 0.1201 (approx. 8.33 days).
- With vital dynamics: 0.1202 (approx. 8.33 days).

• **Recovery Rate (γ):** Identical at 0.0500 (approx. 20 days) for both models.
• **Intervention Start Day ($t_{\text{intervention}}$):**
- Without vital dynamics: 38.83 days.
- With vital dynamics: 38.82 days.

• **Intervention Strength (δ):**
- Without vital dynamics: 0.06087.
- With vital dynamics: 0.06082.

5.2 Key Observations

• **Parameter Comparison:** The inclusion of vital dynamics leads to minimal differences in the optimized parameters, with negligible impact on short-term dynamics.
• **RMSE Comparison:** Both models achieve identical Root Mean Square Error (RMSE) values of 21.46, demonstrating equivalent short-term predictive accuracy.
• **Graphical Fit:**
- Both models closely align with the epidemic data during growth, peak, and decline phases.
- Post-peak fluctuations are slightly smoother with vital dynamics due to population replenishment effects.

• **Long-Term Dynamics:** The model with vital dynamics projects more realistic long-term behavior by accounting for population replenishment, whereas the model without vital dynamics risks unrealistic depletion of the susceptible population.

5.3 Conclusion

The inclusion of vital dynamics has negligible impact on the short-term predictions of the SEIR model but is essential for accurate long-term projections.

6 Comparison Between US and Europe Results

6.1 US Optimization Parameters and Graph

The optimization of the hybrid SEIR model with vital dynamics for the US outbreak yielded the following parameters:

• **Sigma (σ)**: 0.1202 $(\sim 8.3\text{days})$.
• **Gamma (γ)**: 0.05 $(\sim 20\text{days})$.
• **Intervention Start Day ($t_{\text{intervention}}$)**:

38.82days.

- **Intervention Strength (δ)**: 0.0608.

The corresponding model fit is shown in Figure 6.

The model captures the epidemic features effectively, with an RMSE of 20.12, demonstrating a strong agreement between the modeled and observed data.

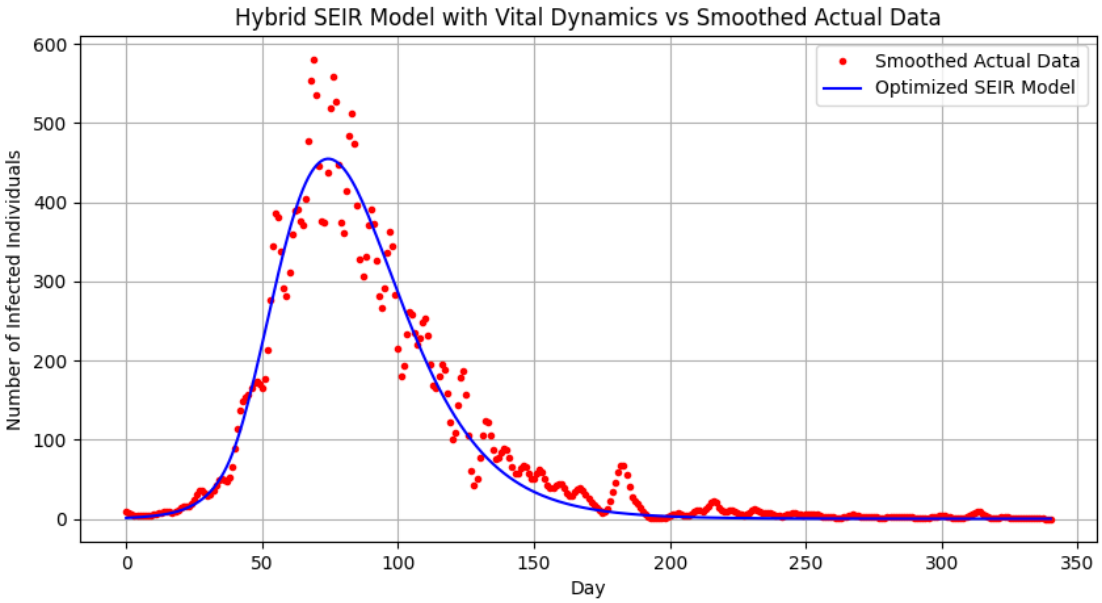

Figure 6: Hybrid SEIR Model with Vital Dynamics for the US ($\beta_{\max} = 0.3$)

6.2 Europe Optimization Parameters and Graph

For the European outbreak, the optimized parameters of the hybrid SEIR model with vital dynamics are as follows:

- **Sigma (σ)**: 0.3333 ($\sim$ 3days).
- **Gamma (γ)**: 0.0766 ($\sim$ 13days).
- **Intervention Start Day ($t_{\text{intervention}}$)**: 10.05days.
- **Intervention Strength (δ)**: 0.0215.

The model fit for Europe is shown in Figure 5, with an RMSE of 21.46, indicating strong alignment with the observed data.

6.3 Parameter Comparison

The comparison of the key parameters reveals regional variations:

- **Transmission Rate ($\beta_{\max}$)**: Both regions had an approximate starting $\beta_{\max} = 0.3$, indicating similar initial transmission dynamics.
- **Intervention Timing and Strength:**

- US: $t_{\text{intervention}} = 38.82$days, $\delta = 0.0608$ (stronger intervention).
- Europe: $t_{\text{intervention}} = 10.05$days, $\delta = 0.0215$ (milder intervention).

- **Recovery Rate (γ)**: The US had a longer recovery period (20days) compared to Europe (13days).
- **Incubation Rate (σ)**: The incubation period was shorter in Europe (3days) compared to the US (8.3days).

The following results can be summarised in the table below:

Parameter	Europe	US
Incubation Rate (σ)	0.333 ($\sim$ 3days)	0.120 ($\sim$ 8.3days)
Recovery Rate (γ)	0.077 ($\sim$ 13days)	0.050 ($\sim$ 20days)
Intervention Timing ($t_{\text{intervention}}$)	10.05 days	38.82 days
Intervention Strength (δ)	0.0215	0.0608
Maximum Transmission Rate ($\beta_{\max}$)	0.3	0.3

Table 1: Optimized Parameters for Europe and the US

6.4 Discussion

The model captures the effect of time-dependent interventions through the parameter δ, which reflects the rate of reduction in transmission due to measures like Interventions, public awareness efforts, or vaccination programs. The results demonstrate the adaptability of the hybrid SEIR model with vital dynamics to both regions. Key observations include:

• **RMSE:** Both models achieved low RMSE values (20.12 for the US, 21.46 for Europe), validating the model's accuracy.

• **Intervention Timing:** Europe implemented earlier but milder interventions, while the US had delayed but stronger measures.

• **Disease Characteristics:** Differences in recovery and incubation rates could reflect variations in healthcare systems, data reporting standards, or disease progression.

6.5 Conclusion

The comparison highlights the robustness of the hybrid SEIR model with vital dynamics across regions. While short-term dynamics are similar, regional differences in intervention strategies and recovery rates underscore the need for localized modeling approaches. These findings can guide future studies and public health interventions to improve epidemic control strategies.

References

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