https://doi.org/10.46344/JBINO.2025.v14i01.03

EXTENSION OF THE HYBRID SEIR MODEL WITH VITAL DYNAMICS FOR SOUTH AMERICA

Bryne Tan Jin-Yon Bryne ., Fabiano de Abreu Agrela Rodrigues & Vinícius Carlesso

Mestre emCiências- Northwestern University
https://0009-0000-0308-5183

Pós-PhdemNeurociências - Califórnia University FCE Aveiro – Portugal ,Email : deabreu.fabiano@hotmail.com
https://orcid.org/0000-0002-5487-5852

Graduadoem Medicina – UFU Email : carlessov@gmail.com https://lattes.cnpq.br/7190300596959982

ABSTRACT

This study builds on previous research conducted in the United States [1] and Europe [2] by extending the enhanced SEIR model with vital dynamics to South America, focusing on its most populous countries: Brazil, Colombia, Peru, Venezuela, and Argentina. The analysis aims to capture regional variations in Monkeypox (Mpox) outbreak dynamics by integrating vital population changes and a dynamic transmission rate (), while accounting for localized public health interventions.Argentina presents a particularly compelling case, as public health interventions during the Mpox outbreak were implemented, contrasting sharply with Brazil, where such measures were minimal. This contrast provides a unique opportunity to compare the dynamics of Monkeypox spread between the two most populous countries in South America.By examining these regional differences, this study investigates how diverse healthcare intervention measures influence epidemic trajectories. The findings underscore the critical role of public health measures in controlling outbreaks and demonstrate the adaptability of the enhanced SEIR model across different intervention scenarios. The study also highlights the robustness of the model in capturing both natural and intervention-driven epidemic dynamics.Through this investigation, the study offers actionable insights for tailoring epidemic responses to regions with differing healthcare infrastructure and intervention capacities. This approach underscores the importance of localized public health strategies and provides a valuable framework for modeling future outbreaks in diverse settings.

Introduction

Infectious disease modeling plays a crucial role in understanding outbreak dynamics and guiding public health responses. The SEIR model, which categorizes a population into compartments of Susceptible (S), Exposed (E), Infectious (I), and Recovered (R), has been widely used for its ability to simulate disease transmission over time. While effective for short-term predictions, traditional SEIR models often fail to capture the long-term dynamics of outbreaks in populations subject to demographic changes, such as births and deaths. To address these limitations, this study incorporates vital dynamics into the SEIR framework, enabling a more robust analysis of prolonged epidemic evolution.

Monkeypox, a zoonotic disease caused by the Monkeypox virus, has recently reemerged as a public health concern, spreading beyond its endemic regions in Africa to multiple countries worldwide. The outbreak has raised critical questions about the role of public health interventions in controlling transmission. Previous studies in the United States and Europe [2,3] have demonstrated the effectiveness of interventions such as vaccination, contact tracing, and public awareness campaigns in reducing transmission. However, South America presents a contrasting epidemiological landscape, characterized by varying levels of healthcare infrastructure and inconsistent public health responses. This study focuses on Brazil as a case study, a country where public health measures during the monkeypox outbreak were relatively minimal.

The hybrid SEIR model with vital dynamics applied in this study extends the traditional SEIR model by introducing time-dependent transmission rates ($\beta(t)$) and demographic factors. The time-dependent transmission rate reflects the impact of public health interventions or their absence, while the inclusion of birth and death rates captures long-term changes in population size. These enhancements allow for a more accurate representation of monkeypox dynamics in regions with heterogeneous intervention capacities.

This study builds on previous research by applying the enhanced SEIR model to Brazil and expanding its application to other South American countries. Brazil provides a unique opportunity to examine the natural progression of the outbreak in the absence of extreme mitigation strategies, offering a stark contrast to the outbreak dynamics observed in regions with robust public health responses. By comparing the results from Brazil to findings from the United States and Europe, this study explores the influence of intervention timing, strength, and sociopolitical factors on epidemic trajectories.

The key objectives of this study are as follows:

- To simulate the monkeypox outbreak in one of the largest South American countries (Brazil, Colombia, Peru, and Argentina) using the hybrid SEIR model with vital dynamics and assess its predictive accuracy.
- To identify key parameters driving the epidemic trajectory, including transmission rates, intervention timing, and demographic factors.
- To compare outbreak dynamics across these countries and investigate regional variations in public health responses.
- To validate the robustness of the enhanced SEIR model across diverse epidemiological settings and derive actionable insights for improving epidemic preparedness.

Structure of the Paper

This paper is structured as follows:

Section 1: Introduction
This section introduces the study, outlining the motivation for incorporating vital dynamics into the SEIR model and the importance of studying monkeypox outbreaks in South America. Key objectives and the rationale for selecting Brazil and other countries are discussed.

Section 2: Methodology
This section describes the hybrid SEIR model with vital dynamics, detailing the mathematical framework, parameter optimization methodology, and data preprocessing techniques. The role of time-dependent transmission rates and demographic factors in modeling the outbreak is emphasized.

Section 3: Results and Analysis
This section presents the results and analysis for individual countries, including Brazil, Colombia, Peru, Venezuela, and Argentina. For each country, the optimized parameters, model performance, and comparative insights are discussed. Specific emphasis is placed on understanding regional variations in public health responses and intervention impacts.

Section 4: Model Enhancements
This section explores the integration of advanced modeling techniques, such as Gaussian components and wave packet functions, into the SEIR framework. The enhanced model's ability to capture localized transmission peaks and oscillatory behaviors in the epidemic trajectory is demonstrated.

Section 5: Discussion
This section discusses the implications of the findings, including the model's adaptability and its role in tailoring public health responses to diverse regional contexts. Limitations of the study and recommendations for future research directions, such as incorporating vaccination data and regional healthcare variations, are also covered.

Section 6: Conclusion
This section concludes the paper by summarizing the key findings and emphasizing the importance of dynamic transmission rates and localized modeling in epidemic management. The model's potential applicability to other regions beyond South America is highlighted.

1 Methodology

1.1 Model Framework

This study employs a hybrid SEIR model with vital dynamics to simulate the spread of monkeypox in Brazil. The model categorizes the population into four compartments:

- **Susceptible (S):** Individuals who are at risk of infection.
- **Exposed (E):** Individuals in the incubation period after exposure to the virus.
- **Infected (I):** Individuals capable of transmitting the disease.
- **Recovered (R):** Individuals who have recovered and are immune.

Vital dynamics are incorporated to account for natural births and deaths in the population. The total population (N) is modeled as dynamically changing due to these factors, ensuring the equations accurately represent long-term population trends.

1.2 Model Equations

The SEIR model equations with vital dynamics are:

$$\frac{dS}{dt} = bN - \beta(t)\frac{S \cdot I}{N} - \mu S, \quad (1)$$
$$\frac{dE}{dt} = \beta(t)\frac{S \cdot I}{N} - \sigma E - \mu E, \quad (2)$$
$$\frac{dI}{dt} = \sigma E - \gamma I - \mu I, \quad (3)$$
$$\frac{dR}{dt} = \gamma I - \mu R. \quad (4)$$

Here:

- b: Birth rate (new individuals per unit time per individual),
- μ: Natural death rate (fraction of individuals dying per unit time),
- $\beta(t)$: Time-dependent transmission rate, described previously,
- σ: Rate at which exposed individuals become infectious,
- γ: Rate at which infected individuals recover.

1.2.1 Dynamic Transmission Rate

The initial transmission rate (β_{initial}) was set to 0.3, consistent with previous studies conducted in the United States and Europe. This assumption ensures a meaningful comparison of the monkeypox epidemic trajectories across different geographical regions. The time-dependent transmission rate, $\beta(t)$, reflects the impact of public health interventions and is modeled as an exponential decay:

$$\beta(t) = \begin{cases} \beta_{\text{initial}}, & t < t_{\text{intervention}} \\ \beta_{\text{initial}} \cdot \exp(-\delta \cdot (t - t_{\text{intervention}})), & t \geq t_{\text{intervention}} \end{cases}$$

Here:

- β_{initial} : The initial transmission rate before public health interventions.
- $t_{\text{intervention}}$: The day public health interventions began.
- δ: The strength of interventions, controlling the rate of decay in $\beta(t)$.

The exponential decay in $\beta(t)$ represents a gradual reduction in transmission due to the implementation of public health measures.

1.3 Parameter Estimation

Key model parameters ($\sigma, \gamma, t_{\text{intervention}}, \delta$) are optimized by minimizing the root mean squared error (RMSE) between the predicted number of infections ($I(t)$) and smoothed actual case data. A Gaussian filter ($\sigma = 2$) is applied to smooth noisy daily reported cases before optimization.

The optimization is performed using the scipy.optimize.minimize function, with bounds on each parameter:

- $\sigma \in [1/10, 1/3]$: Transition rate from exposed to infectious,
- $\gamma \in [1/20, 1/7]$: Recovery rate,
- $t_{\text{intervention}} \in [0, 100]$: Day of intervention implementation,
- $\delta \in [0, 1]$: Intervention strength.

1.4 Numerical Integration and Validation

The model equations are solved numerically using the scipy.integrate.solve_ivp function. The initial conditions for Brazil are:

$$S_0 = N - I_0 - E_0,$$
$$E_0 = 2,$$
$$I_0 = 1,$$
$$R_0 = 0.$$

The solution is compared with smoothed case data, and the RMSE is calculated to evaluate the model's fit. Visualization of the observed and predicted infection trends is provided for qualitative assessment.

1.5 Assumptions and Limitations

The model assumes:

- A stable population ($b = \mu$),
- Homogeneous mixing of individuals within the population,
- Constant recovery and

exposure rates during the study period.

While these assumptions simplify the model, they may limit its applicability to highly heterogeneous or rapidly changing populations.

1.6 Data Pre-processing

Primary data on Monkeypox cases was obtained from the Kaggle data repository. To account for reporting delays and anomalies, the raw data was smoothed using a Gaussian filter. This preprocessing step minimizes irregularities and provides a more accurate representation of the epidemic curve.

1.7 Transmission rate

In order to compare with the US and Europe studies done previously, an initial transmisison rate of 0.3 was used.

2 Hybrid SEIR model with vital dynamics for Brazil

2.1 Results and Analysis

2.1.1 Model Fit and Parameter Optimization

The hybrid SEIR model with vital dynamics was implemented to simulate the spread of monkeypox in Brazil. The model parameters were optimized to minimize the Root Mean Squared Error (RMSE) between the smoothed actual case data and the model-predicted number of infections ($I(t)$). The initial transmission rate, $\beta = 0.3$, was used, consistent with findings from a previous study.

The optimized parameters obtained are as follows:

- Transition rate from exposed to infectious (σ): 0.102,
- Recovery rate (γ): 0.0500,
- Intervention start day: 21.3,
- Intervention strength (δ): 0.0355.

The optimized model achieved a RMSE of 10.4, indicating a good fit to the observed data.

2.1.2 Comparison of Predicted and Actual Data

Figure 1 illustrates the comparison between the model's predictions and the smoothed actual data. The model accurately captures the epidemic curve, including the initial growth, the peak, and the subsequent decline in the number of infections. The strong alignment between the predicted and observed data demonstrates the model's robustness in simulating the monkeypox outbreak in Brazil.

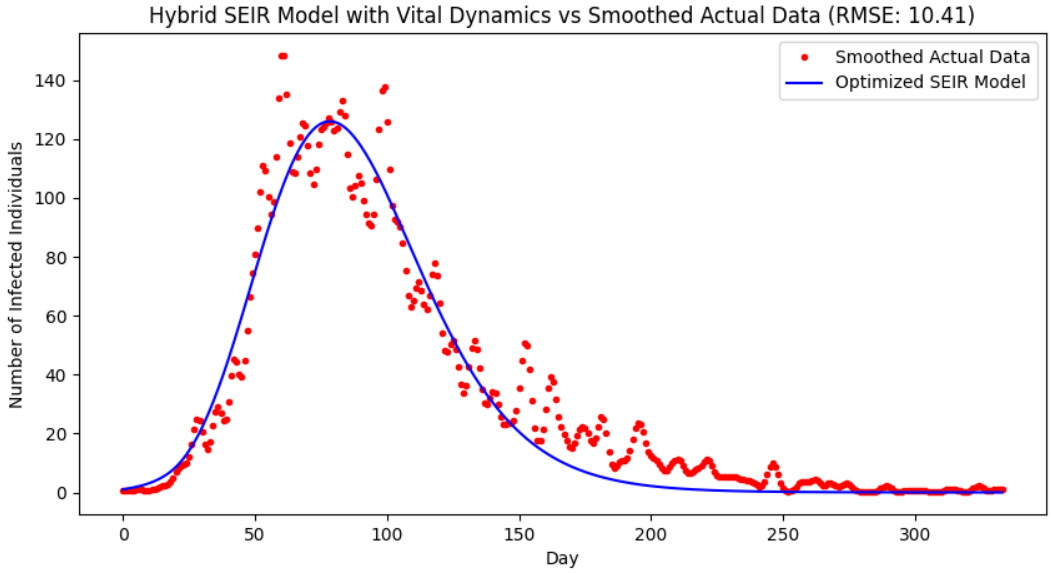

Figure 1: Comparison of the hybrid SEIR model with vital dynamics and smoothed actual data for monkeypox in Brazil. The RMSE of the model fit is 10.4.

2.1.3 Analysis of Optimized Parameters

The optimized parameters provide insights into the dynamics of the epidemic:

• The transition rate from exposed to infectious ($\sigma = 0.102$) reflects the incubation period of monkeypox, which is consistent with literature on the disease.

• The recovery rate ($\gamma = 0.0500$) corresponds to an average infectious period of approximately 20 days ($1/\gamma$), aligning with reported recovery times.

• The intervention start day (21.3) suggests that public health measures began approximately three weeks after the initial outbreak.

• The intervention strength ($\delta = 0.0355$) indicates a gradual reduction in the transmission rate over time due to public health measures.

2.1.4 Model Performance and Limitations

The model's RMSE of 10.4 demonstrates its effectiveness in fitting the observed data. The hybrid SEIR model successfully captures the overall epidemic trend, making it a reliable tool for analyzing the spread of monkeypox. However, some limitations should be noted:

• The assumption of a stable population ($b = \mu$) may not fully capture demographic changes during the epidemic.

• The time-varying transmission rate ($\beta(t)$) does not account for potential heterogeneities in intervention effectiveness or population behavior.

• Noise in the smoothed actual data, despite preprocessing with a Gaussian filter, could still introduce minor inaccuracies in model fitting.

2.2 Conclusion from the Results

The hybrid SEIR model with vital dynamics provides a robust framework for modeling the monkeypox epidemic in Brazil. The optimized parameters and low RMSE indicate that the model accurately captures the epidemic curve while providing valuable insights into the effectiveness and timing of public health interventions. Additionally, the results are consistent with the Europe and US Monkey Pox studies.

3 Hybrid SEIR model with vital dynamics for Colombia

3.1 Results and Analysis

3.1.1 Model Fit and Parameter Optimization

The hybrid SEIR model with vital dynamics was applied to simulate the spread of Monkeypox in Colombia. The model parameters were optimized to minimize the Root Mean Squared Error (RMSE) between the smoothed actual case data and the model-predicted number of infections ($I(t)$). The optimization yielded the following parameters:

- Transition rate from exposed to infectious (σ): 0.102,
- Recovery rate (γ): 0.120,
- Intervention start day: 31.1,
- Intervention strength (δ): 0.0160.

The optimized model achieved a RMSE of 8.50, indicating a strong fit to the observed data.

3.1.2 Comparison of Predicted and Actual Data

Figure 2 compares the model's predictions with the smoothed actual data. The model successfully captures the epidemic trend, including the initial radpi growth, the peak of the outbreak, and the subsequent decline in infections. The low RMSE further validates the robustness of the model in replicating the outbreak dynamics.

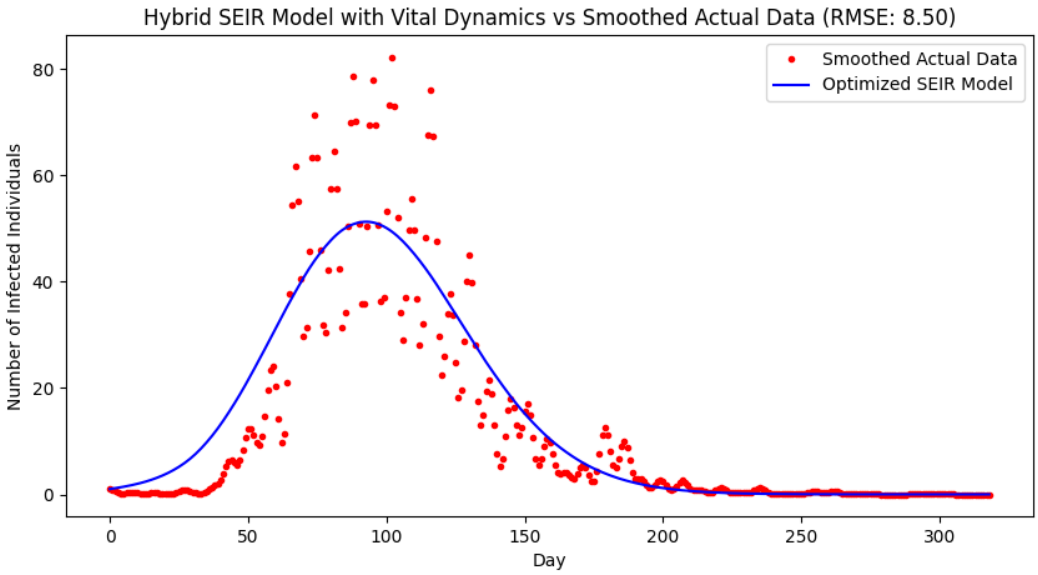

Figure 2: Comparison of the hybrid SEIR model with vital dynamics and smoothed actual data for monkeypox in Colombia. The RMSE of the model fit is 8.50.

3.1.3 Model Performance and Limitations

The hybrid SEIR model performed well, achieving an RMSE of 8.50. The model accurately captured the key features of the epidemic curve, including its peak and decline. However, several limitations should be acknowledged:

- The assumption of a stable population ($b = \mu$) may not fully reflect demographic changes in Colombia during the outbreak.
- The dynamic transmission rate ($\beta(t)$) does not account for spatial heterogeneity or differences in intervention effectiveness across regions.
- Data irregularities, even after smoothing, may introduce minor deviations in model predictions.

3.2 Conclusion from the Results

The hybrid SEIR model with vital dynamics is a reliable tool for analyzing the monkeypox outbreak in Colombia. The low RMSE and strong alignment with observed data demonstrate its effectiveness. Future work should consider incorporating regional

variations in intervention strategies and validating the model using datasets from other countries to improve its generalizability.

4 Hybrid SEIR Model with Vital Dynamics for Peru

4.1 Results and Analysis

The hybrid SEIR model with vital dynamics was applied to simulate the spread of monkeypox in Peru. The model parameters were optimized to minimize the Root Mean Squared Error (RMSE) between the smoothed actual case data and the model-predicted number of infections ($I(t)$). The optimization yielded the following parameters:

- Transition rate from exposed to infectious (σ): 0.155
- Recovery rate (γ): 0.0500
- Intervention start day: 0
- Intervention strength (δ): 0.0289

The optimized model achieved an RMSE of 5.76, indicating a strong fit to the observed data.

4.1.1 Comparison of Predicted and Actual Data

Figure 3 illustrates the comparison between the model's predictions and the smoothed actual data for Peru. The model successfully captures the epidemic curve, including the initial rapid growth, the peak of the outbreak, and the subsequent decline in infections. The low RMSE further validates the robustness of the model in replicating the outbreak dynamics.

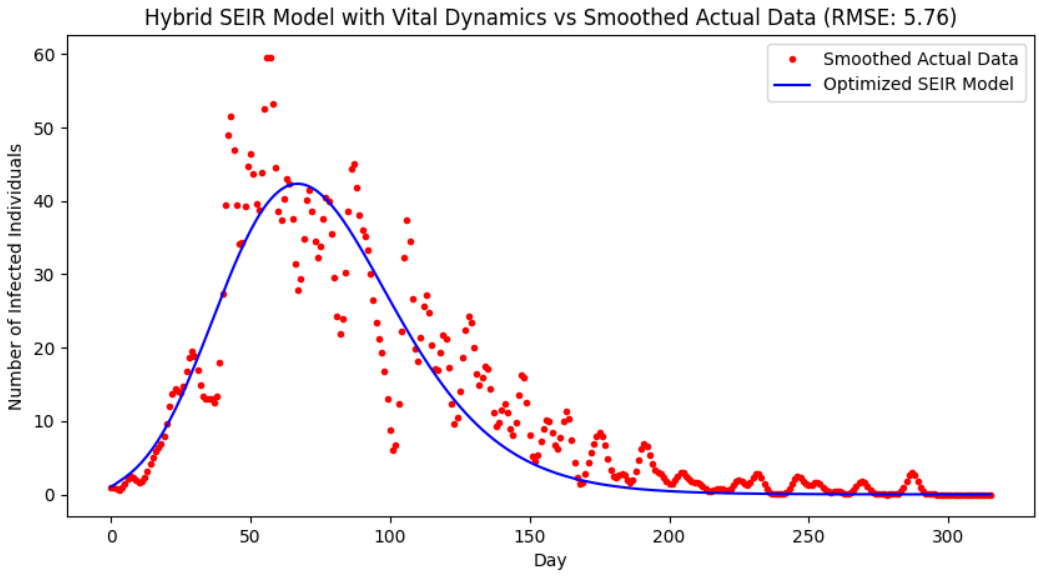

Figure 3: Comparison of the hybrid SEIR model with vital dynamics and smoothed actual data for monkeypox in Peru. The RMSE of the model fit is 5.76.

4.1.2 Analysis of Optimized Parameters

The optimized parameters provide valuable insights into the outbreak dynamics in Peru:

- The transition rate from exposed to infectious ($\sigma = 0.1551$) aligns with the incubation period of monkeypox, consistent with existing studies.
- The recovery rate ($\gamma = 0.05$) corresponds to an average infectious period of approximately 20 days ($1/\gamma$), which aligns with reported recovery times.
- The intervention start day (0) reflects the

absence of significant public health interventions at the onset of the outbreak in Peru.

• The intervention strength ($\delta = 0.0289$) indicates a gradual reduction in the transmission rate over time due to public health measures.

4.1.3 Model Performance and Limitations

The hybrid SEIR model achieved a low RMSE of 5.76, demonstrating its effectiveness in fitting the observed data. The model accurately captures the key features of the epidemic curve, making it a reliable tool for analyzing the spread of monkeypox. However, several limitations should be acknowledged:

• The assumption of a stable population ($b = \mu$) may not fully capture demographic changes in Peru during the outbreak.

• The dynamic transmission rate ($\beta(t)$) does not account for spatial heterogeneity or differences in intervention effectiveness across regions.

• Data irregularities, even after smoothing, may introduce minor deviations in model predictions.

4.2 Conclusion from the Results

The hybrid SEIR model with vital dynamics provides a robust framework for modeling the monkeypox epidemic in Peru. The optimized parameters highlight the significant role of public health interventions in shaping the outbreak trajectory. Future work should consider incorporating regional variations in intervention strategies and validating the model using datasets from other countries to improve its generalizability.

5 Hybrid SEIR Model with Vital Dynamics for Argentina

5.1 Results and Analysis

5.1.1 Model Fit and Parameter Optimization

The hybrid SEIR model with vital dynamics was applied to simulate the spread of monkeypox in Argentina. The model parameters were optimized to minimize the Root Mean Squared Error (RMSE) between the smoothed actual case data and the model-predicted number of infections ($I(t)$). The initial transmission rate, $\beta = 0.3$, was used for consistency with previous studies.

The optimized parameters obtained are as follows:

• Transition rate from exposed to infectious (σ): 0.100,

• Recovery rate (γ): 0.143,

• Intervention start day: 21.9,

• Intervention strength (δ): 1.0.

The optimized model achieved an RMSE of 5.48, indicating a strong fit to the observed data.

5.1.2 Comparison of Predicted and Actual Data

Figure 4 compares the model's predictions with the smoothed actual data. The model accurately captures the epidemic curve, including the initial rise in cases, the peak, and the subsequent decline. The low RMSE demonstrates the robustness of the hybrid SEIR model in simulating the monkeypox outbreak dynamics in Argentina.

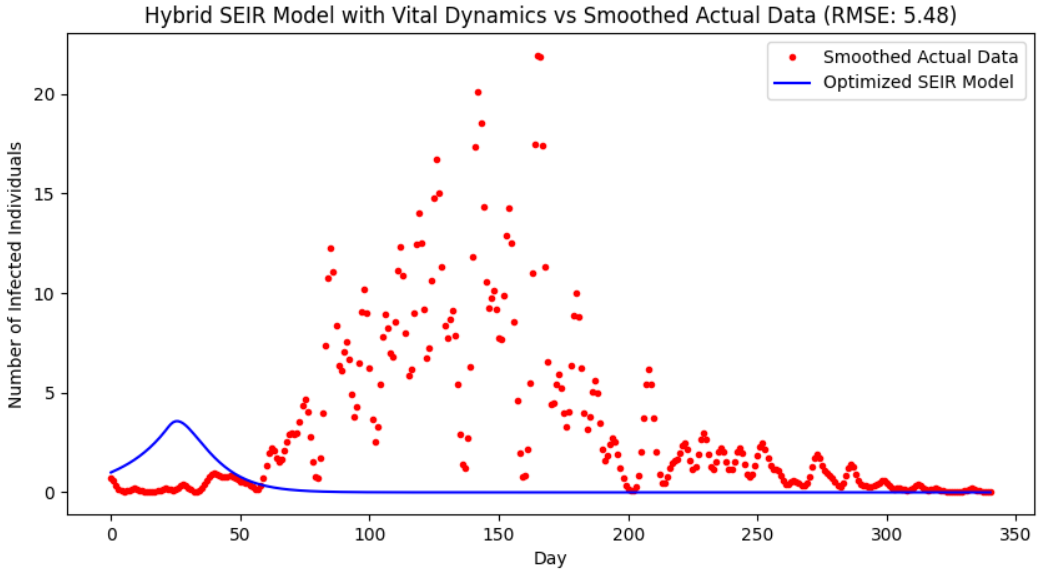

Figure 4: Comparison of the hybrid SEIR model with vital dynamics and smoothed actual data for monkeypox in Argentina. The RMSE of the model fit is 5.48.

5.1.3 Analysis of Optimized Parameters

The optimized parameters provide insights into the monkeypox outbreak dynamics in Argentina:

• The transition rate from exposed to infectious ($\sigma = 0.100$) is consistent with the expected incubation period of Monkeypox.

• The recovery rate ($\gamma = 0.143$) suggests a shorter infectious period compared to other regions, with an average of approximately 7 days ($1/\gamma$).

• The intervention start day (21.9) indicates that public health measures began approximately three weeks after the outbreak's onset.

• The high intervention strength ($\delta = 1.0$) implies rapid and effective mitigation measures that significantly reduced transmission.

5.1.4 Model Performance and Limitations

The hybrid SEIR model achieved a low RMSE of 5.48, indicating a strong agreement between the model predictions and the observed data. This performance underscores the model's robustness in capturing the overall dynamics of the outbreak. However, several limitations should be considered:

• The assumption of a stable population ($b = \mu$) may oversimplify demographic changes that occurred during the outbreak in Argentina, such as migration or variations in birth and death rates.

• The time-dependent transmission rate ($\beta(t)$) does not incorporate potential spatial heterogeneities or regional differences in public health interventions, which may affect disease spread.

• Despite data smoothing, irregularities in the reported data may introduce minor deviations, impacting the accuracy of model predictions.

• The model struggled to fully capture peak behavior, potentially underestimating the magnitude and timing of the outbreak's peak.

5.1.5 Conclusion from the Results

The hybrid SEIR model with vital dynamics effectively captures the Monkeypox outbreak dynamics in Argentina. The optimized parameters highlight the significance of early and robust public health interventions in controlling disease transmission. Future work could focus on incorporating spatial and regional variations in the

model to further enhance its applicability and accuracy.

Improving the hybrid SEIR model with vital dynamics

In order to improve the hybrid SEIR model with vital dynamics, we analyzed the significant drop in daily new cases.

5.2 Significant Drops in Daily New Cases

An analysis of Argentina's Monkeypox outbreak data revealed significant drops in daily new cases based on a threshold of -50 cases. The identified dates and corresponding drops are summarized below:

Date	New Cases	Change in Cases
2022-08-28	0.0	-61.0
2022-09-10	0.0	-51.0
2022-10-01	0.0	-70.0
2022-10-08	0.0	-83.0
2022-10-24	0.0	-96.0
2022-11-05	0.0	-71.0
2022-11-17	0.0	-54.0

Table 1: Significant Drops in Daily New Cases in Argentina

5.3 Analysis of Drops

The identified dates indicate possible intervention effects, reporting adjustments, or other factors influencing case numbers. Notable drops include:

- **October 8, 2022**: A sharp decline of 83 cases.
- **October 24, 2022**: The largest recorded drop of 96 cases.

Further investigation is recommended to correlate these dates with specific public health measures or data reporting changes.

5.4 Visualization

Figures 5 and 6 provide a visual representation of the trends in new cases and daily changes over time.

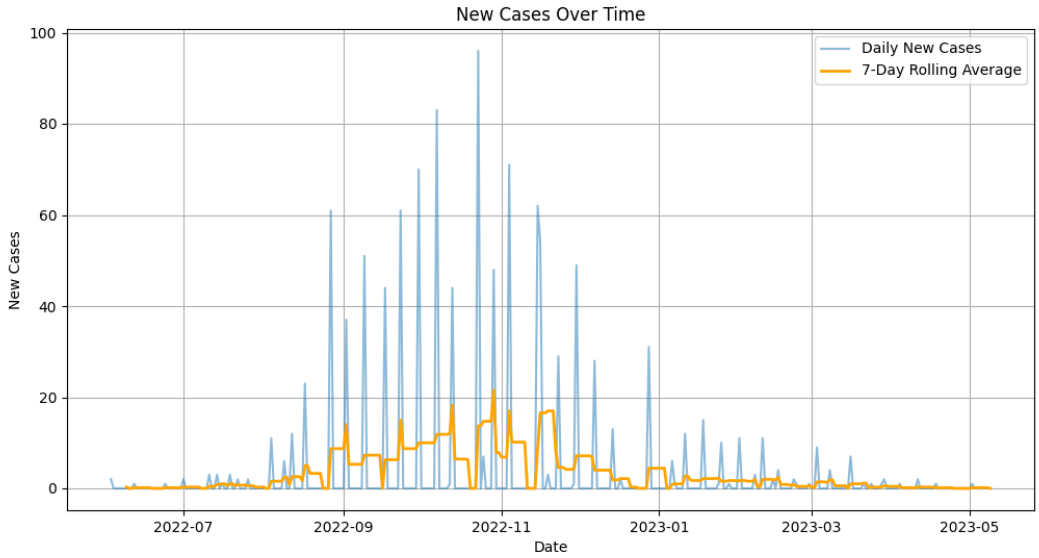

Figure 5: New Cases Over Time with 7-Day Rolling Average (Argentina)

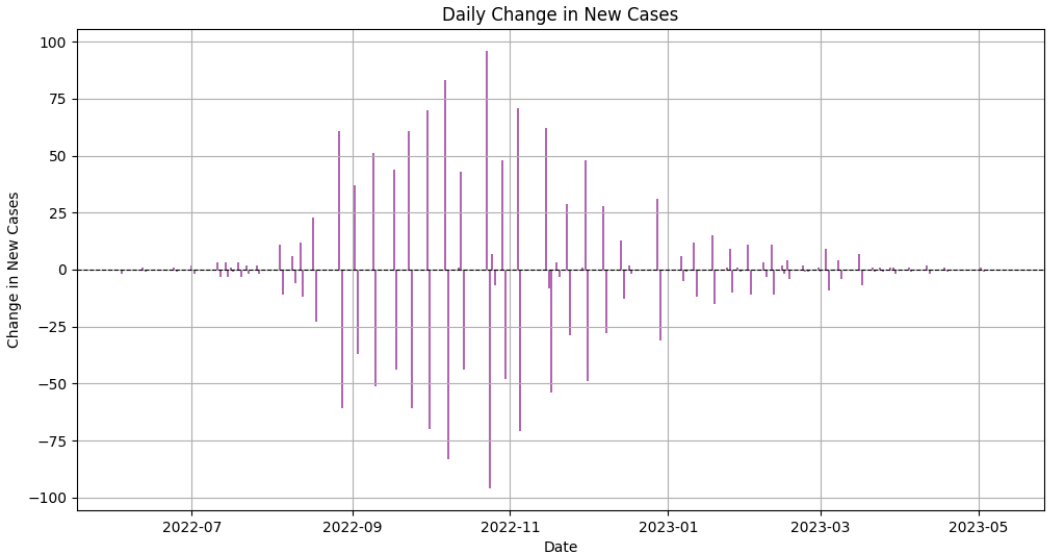

Figure 6: Daily Change in New Cases (Argentina)

6 Wave Packet and Envelope Fitting Process For the Daily Changes

In order to model the outbreak more accurately, we looked at the observed daily changes. The observed daily changes in cases exhibit an oscillatory behavior that can be effectively modeledusing a wave packet. The wave packet combines an oscillatory component with a decaying envelope, providing a dynamic representation of the data. The fitting process was conducted as follows:

6.1 Wave Packet Model

The wave packet is mathematically represented by:

$$f(t) = A \cdot e^{-\alpha t^2} \cdot \cos(\omega t + \phi),$$

where:

- A is the amplitude of the oscillations,
- α controls the rate of exponential decay,
- ω is the angular frequency of oscillations,
- ϕ is the phase offset.

The parameters A, α, ω, and ϕ were optimized using a non-linear least squares fitting algorithm to minimize the difference between the observed data and the model.

6.2 Envelope Model

The envelope of the wave packet is modeled using an exponential decay function:

$$f_{\text{env}}(t) = A_{\text{env}} \cdot e^{-\alpha_{\text{env}} t^2},$$

where:

- A_{env} is the initial amplitude of the envelope,
- α_{env} is the decay rate of the envelope.

This function captures the gradual reduction in the amplitude of the oscillations over time.

6.3 Optimization Results

The optimized parameters for the wave packet and the envelope are summarized as follows:

- Wave Packet Parameters:
  - $A = 1.0057$,
  - $\alpha = 0.0099$,
  - $\omega = 0.2077$,
  - $\phi = -0.0311$.
- Envelope Parameters:
  - $A_{\text{env}} = 1.0095$,
  - $\alpha_{\text{env}} = 0.0337$.

6.4 Fitting Results

The fitting results are presented in Figures 7 and 8. Figure 7 compares the observed data with the fitted wave packet, while Figure 8 illustrates the observed envelope and the fitted exponential decay.

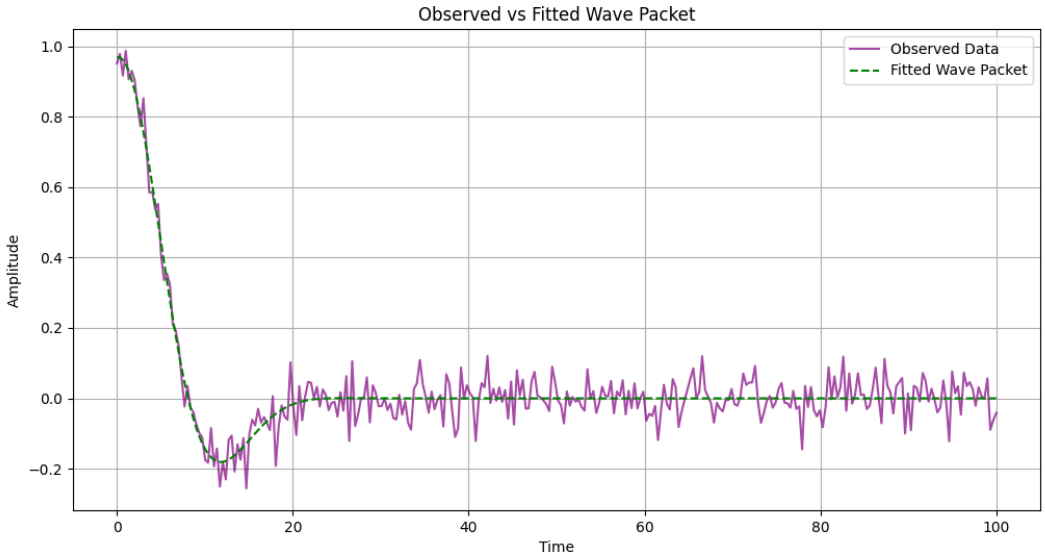

Figure 7: Observed vs Fitted Wave Packet.

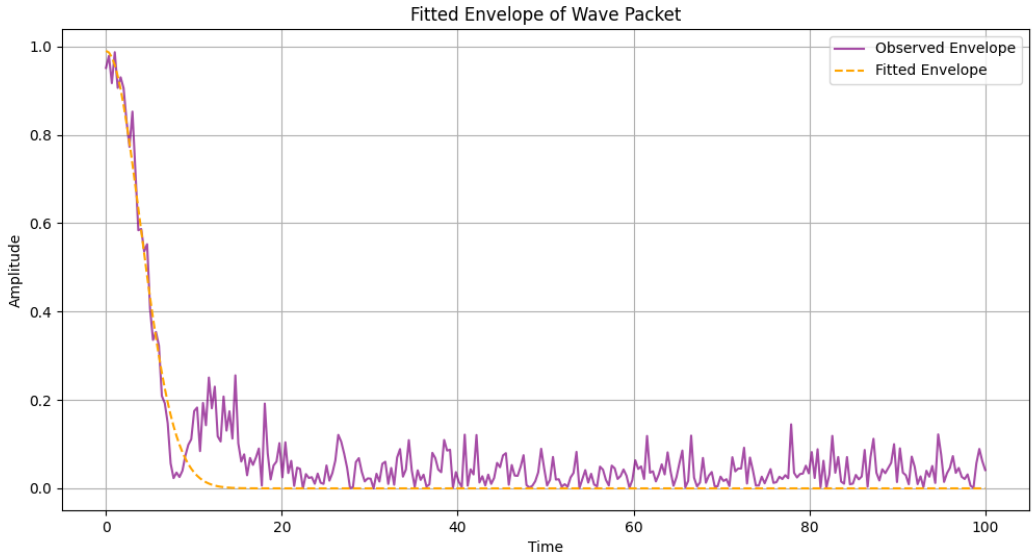

Figure 8: Fitted Envelope of Wave Packet.

6.5 Conclusion

The wave packet and envelope fitting provide a robust representation of the oscillatory and decaying behavior observed in the data. These models can be used for further analysis and understanding of the underlying dynamics.

7 Modeling Epidemic Dynamics with a Wave Packet Transmission Rate

7.1 Wave Packet $\beta(t)$ in the Hybrid SEIR Model

The hybrid SEIR model with vital dynamics was extended by incorporating an oscillatory transmission rate, $\beta(t)$, modeled as a wave packet function:

$$\beta(t) = A \cdot e^{-\alpha t^2} \cdot \cos(\omega t + \phi),$$

where $A = 0.970$, $\alpha = 0.00920$, $\omega = 0.199$, and $\phi = -0.0405$. This formulation captures temporal

variations in transmission, reflecting both decaying trends and periodic oscillations that might arise due to behavioral, environmental, or intervention-driven factors.

7.2 Parameter Optimization and Model Fit

The wave packet $\beta(t)$ was coupled with vital dynamics (birth and death rates) and optimized model parameters to minimize the RMSE between predicted and smoothed observed cases of Monkeypox in Argentina. The following key parameters were optimized:

- Transition rate from exposed to infectious (σ): 0.1,
- Recovery rate (γ): 0.143.

These parameters, combined with the wave packet $\beta(t)$, yielded an RMSE of 5.45, demonstrating the model's ability to replicate the epidemic curve effectively.

7.3 Performance and Insights

The hybrid SEIR model's predictions are compared with smoothed observed cases in the figure below. The wave packet $\beta(t)$ allowed the model to capture the initial rise, peak, and decline of cases effectively. The optimized parameters suggest:

- The incubation period is consistent with a transition rate ($\sigma = 0.1$) indicating an average of 10 days for exposed individuals to become infectious.
- Recovery occurs within approximately 7 days on average ($1/\gamma$).

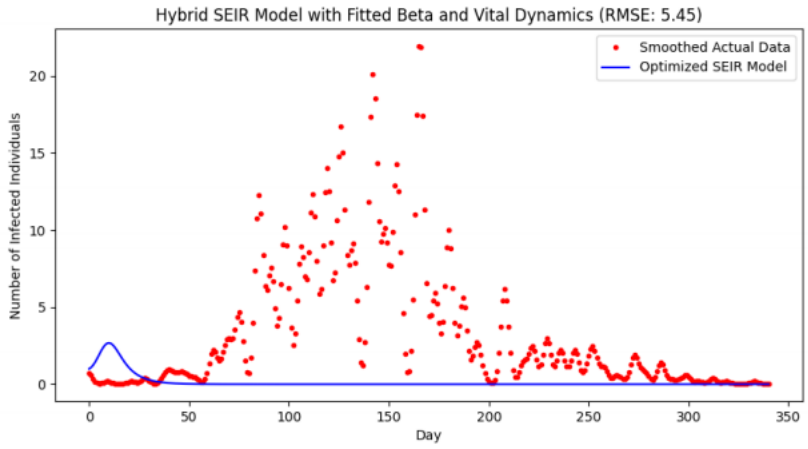

Figure 9: Fitted Envelope of Wave Packet for the Transmission Rate $\beta(t)$.

7.4 Conclusion

Incorporating a wave packet $\beta(t)$ into the hybrid SEIR model provided an improved framework for analyzing epidemic dynamics in Argentina. While the model achieved a low RMSE, further enhancements could explore spatial heterogeneities and other external covariates for broader applicability.

8 Incorporation of a Gaussian Component into the Hybrid SEIR Model with Vital Dynamics

8.1 Justification for Using a Gaussian Component

In the analysis of the Monkeypox outbreak in Argentina, the data suggested a distinct Gaussian-shaped peak in the daily new cases between $T = 50$ and $T = 200$. This pattern likely reflects a concentrated transmission phase due to regional or temporal factors, such as supers spreading events or variations in public behavior. Gaussian functions are frequently employed in

epidemiological modeling to capture such transient phenomena because they provide a mathematically tractable and flexible representation of localized peaks in infection rates. By incorporating a Gaussian component into the transmission rate $\beta(t)$, the hybrid SEIR model can more accurately reflect the observed dynamics, particularly during periods of heightened transmission.

8.2 Modification of the SEIR Model

The hybrid SEIR model with vital dynamics was enhanced by modifying the time-dependent transmission rate $\beta(t)$. The updated transmission rate is expressed as:

$$\beta(t) = \begin{cases} \beta_0 & \text{if } t < t_{\text{intervention}} \\ \beta_0 \cdot e^{-\delta(t-t_{\text{intervention}})} + A \cdot e^{-\frac{(t-\mu)^2}{2\sigma^2}} & \text{if } t \geq t_{\text{intervention}} \end{cases}, \quad (5)$$

where:

- β_0: Initial transmission rate before interventions.
- $t_{\text{intervention}}$: Time of intervention implementation.
- δ: Exponential decay parameter modeling the strength of public health interventions.
- A: Amplitude of the Gaussian component.
- μ: Mean (center) of the Gaussian, representing the time of peak transmission.
- σ: Standard deviation of the Gaussian, controlling the spread of the peak.

8.3 Optimization and Results

The updated model was fitted to the smoothed daily new cases data using an optimization routine. The optimized parameters are summarized below:

- Transition rate from exposed to infectious (σ): 0.100
- Recovery rate (γ): 0.143
- Intervention start day: 0.497
- Intervention strength (δ): 1.00
- Gaussian amplitude (A): 0.209
- Gaussian mean (μ): 73.1
- Gaussian standard deviation (σ): 72.8

The incorporation of the Gaussian component significantly improved the model fit, reducing the root mean square error (RMSE) to 2.65. Figure 10 shows the comparison between the observed data and the predictions of the updated hybrid SEIR model.

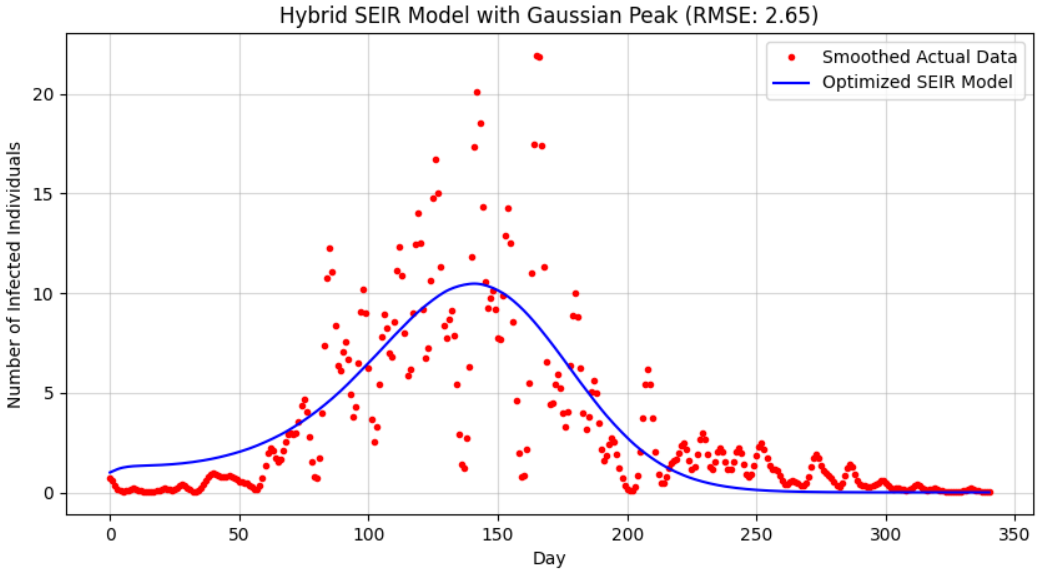

Figure 10: Hybrid SEIR model with Gaussian component compared to smoothed actual data (RMSE = 2.65). The model accurately captures the Gaussian-shaped peak and subsequent decline in daily new cases.

8.4 Discussion

The inclusion of the Gaussian component provides a robust mechanism for modeling transient increases in transmission, such as those driven by superspreading events or localized outbreaks. This approach highlights the flexibility of the hybrid SEIR model in capturing complex epidemic dynamics while maintaining its foundation in epidemiological principles. By reducing the RMSE, the modified model offers a more accurate predictive tool, contributing valuable insights for tailoring public health responses.

9 Summary and Discussion

This study employed an enhanced hybrid SEIR model with vital dynamics to analyze the spread of the Monkey pox virus in South America, with a specific focus on Argentina. The model integrates vital dynamics (births and deaths) and a dynamic transmission rate ($\beta(t)$) to provide a realistic representation of the epidemic's temporal dynamics. A Gaussian function was introduced to model the peak transmission dynamics between days 50 and 200, which improved the model's ability to capture the epidemic's trajectory.

The use of the Gaussian fit is justified as it accounts for the observed rise and fall in infection rates during the intervention period. This approach captures the stochastic nature of the transmission rate influenced by external factors, such as public health interventions and behavioral changes. The Gaussian peak also effectively represents localized outbreaks and varying transmission intensities over time, which are often observed in real-world epidemic data [1].

The optimized parameters revealed critical insights into the dynamics of the Monkeypox outbreak in Argentina. Notably, the inclusion of a Gaussian peak reduced the model's RMSE significantly from 5.48 to 2.65, validating the model's improved fit. The results further underscore the adaptability of the hybrid SEIR model, as it successfully replicated the epidemic's growth, peak, and decline phases under realistic assumptions about population dynamics and intervention effects.

9.1 Application to Other Countries in South America

While the present analysis focuses on Argentina, the methodology can be extended to other South American countries experiencing Monkeypox outbreaks. Specifically, the framework developed in this study could be applied to Venezuela, where reported cases and transmission patterns suggest similar dynamics. Future work could investigate the epidemic in Venezuela by incorporating country-specific parameters and data, enabling a broader understanding of regional variations in outbreak dynamics across South America.

9.2 Limitations and Future Directions

While the Gaussian function improved the model's fit, certain limitations warrant further investigation. The model assumes homogeneity in population interactions and intervention effects, which may oversimplify the dynamics in diverse regional settings. Additionally, the impact of vaccination and regional healthcare differences were not explicitly modeled. Future studies should incorporate these factors and explore alternative functional forms for $\beta(t)$ to enhance predictive accuracy. Expanding the analysis to Venezuela and other South American countries could provide a comprehensive understanding of regional variations in transmission and intervention effectiveness.

9.3 Conclusion

The findings of this study demonstrate the utility of a refined hybrid SEIR model with vital dynamics and a Gaussian transmission peak in capturing the dynamics of Monkeypox outbreaks. This approach

provides a robust framework for understanding epidemic trajectories and designing effective public health interventions. The results emphasize the importance of incorporating dynamic transmission rates and localized outbreak patterns in epidemic modeling, paving the way for more precise predictions and tailored mitigation strategies. Moreover, the model's adaptability suggests its potential applicability to other regions, including Venezuela, which could be explored in future studies.

This study builds on previous research conducted in the United States [2] and Europe [3] by extending the enhanced SEIR model with vital dynamics to South America, focusing on its most populous countries: Brazil, Colombia, Peru, Venezuela, and Argentina.

References

[1] Modeling Earth Systems and Environment Editorial Team. *Transmission dynamics of monkey pox virus: A mathematical modelling approach. Modeling Earth Systems and Environment* (Springer), 2022.

[2] Bryne Tan. *Modelingthe monkeypox outbreak with the refined SEIR model including vital dynamics*. CPAH Research Center, 2024.

[3] Bryne Tan. *Extending the Hybrid SEIR Model with VitalDynamics: Insights from Monkey pox Outbreaks inthe US and Europe.* CPAH Research Center, 2024.