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Application of Time-Series SIR Models in Analyzing the COVID-19 Pandemic in Iran: A Case Study of Data from February 2020 to December 2023

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ABSTRACT

Background: The COVID-19 pandemic underscored the critical need for advanced modeling approaches to elucidate transmission dynamics and inform public health strategy. This study employed a Time-Series Susceptible-Infected-Recovered (TSIR) model to quantitatively analyze the pandemic trajectory in Iran and estimate the time-varying basic reproduction number (R_0) from February 2020 to December 2023.

Methods: In an analytical cross-sectional study, comprehensive national COVID-19 data were obtained from the Iranian Ministry of Health and validated international repositories. The TSIR framework was implemented using R software (v4.0.0) to estimate transmission parameters (β, γ) and reconstruct epidemic dynamics. Vaccination impact was assessed through comparative analysis of compartmental populations pre- and post-vaccination deployment.

Results: Analysis of 1,373 surveillance days revealed 7,625,160 confirmed cases with 146,741 fatalities (CFR: 2%). The TSIR model demonstrated superior tracking of seven distinct epidemic waves, with R_0 estimates declining to 0.2 during 2022-2023. Statistical analysis confirmed significant compartmental shifts post-vaccination ($p<0.001$), indicating substantial intervention impact. Moreover, model validation showed robust performance across multiple epidemic phases.

Conclusion: The TSIR model provides a validated framework for epidemic monitoring and evaluation of public health interventions in Iran. The sub-critical R_0 values observed during the study's conclusion reflect successful containment through combined vaccination and control measures. Therefore, integration of time-series epidemiological modeling into national surveillance systems is recommended for enhanced preparedness against future infectious disease threats.

Keywords: COVID-19; Basic reproduction number; Time series analysis; SIR model; Iran; Vaccination coverage; Epidemiological modeling.

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Introduction

The emergence of SARS-CoV-2 in Wuhan, China, in December 2019, and the subsequent global pandemic of COVID-19, presented an unprecedented challenge to public health systems worldwide (1). As of mid-August 2020, the World Health Organization (WHO) reported over six million deaths globally, underscoring the critical need for accurate predictive models to guide containment efforts and healthcare resource planning (1).

Mathematical modeling has long been a cornerstone of infectious disease epidemiology. Dynamic compartmental models, which divide populations into segments with similar disease statuses, have been particularly valuable for simulating disease spread (2). For COVID-19, various adaptations of these models have been employed globally. The Susceptible-Infected-Recovered (SIR) model and its variants—such as SIRD (including deceased compartment), SEIR (including exposed compartment), and SEIRS (accounting for waning immunity)—have been applied in diverse contexts including Italy, India, China, and the UK (3-6).

A critical parameter derived from these models is the basic reproduction number (R_0), representing the average number of secondary infections generated by a single infected individual in a fully susceptible population (7). An $R_0 > 1$ indicates sustained transmission, while $R_0 < 1$ suggests the epidemic is under control. However, transmission dynamics are influenced by regional factors including social structure, economic conditions, demographic characteristics, and healthcare capacity (8).

Time-series SIR (TSIR) models, which incorporate temporal trends into the traditional SIR framework, have shown particular promise in capturing the complex dynamics of infectious diseases. These models have been successfully applied to diseases such as measles (9), COVID-19 in China (10), and hand-foot-mouth disease (HFMD) (11). The integration of time-series analysis allows for better accounting of changing conditions, interventions, and reporting rates over the course of an epidemic.

Despite numerous studies on COVID-19 in Iran, the application of TSIR models for comprehensive analysis of the epidemic trajectory and R_0 estimation has been limited. Previous research has primarily utilized conventional SIR models or basic time-series approaches (12,13). Therefore, this study aims to bridge this gap by employing the TSIR model to analyze the complete course of the COVID-19 epidemic in Iran from February 2020 to December 2023, with particular focus on estimating R_0 and evaluating the impact of vaccination campaigns.

Methods

Study design and data collection

This analytical longitudinal study employed a comprehensive time-series analysis of COVID-19 epidemiological data in Iran from February 2020 to December 2023. The study utilized multiple complementary data sources to ensure robustness and validity: primary data were obtained through formal collaboration with the Iranian Ministry of Health and Medical Education, while secondary validation data were sourced from the World Health Organization's COVID-19 dashboard, Our World in Data, and Worldometers databases (19,20). The dataset comprised daily incidence counts, mortality statistics, recovery rates, and vaccination coverage data, representing the complete pandemic timeline in Iran.

Population estimates were derived from the 2016 National Population and Housing Census conducted by the Statistical Center of Iran, with annualized projections calculated using demographic growth models accounting for birth rates, mortality, and migration patterns (21). The study protocol received full ethical approval from the Ethics Committee of Yazd Shahid Sadoughi University of Medical Sciences (Code: IR.SSU.SPH.REC.1400.169), with all data anonymized and aggregated to protect individual privacy.

Time-Series SIR Model Framework

The TSIR model represents an advanced

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extension of the classical Kermack-McKendrick SIR framework (4), incorporating temporal dynamics through discrete-time stochastic formulation. The model structure comprises three interconnected compartments:

The core differential system is defined as:

$dS/dt = -\beta(t) \times S(t) \times I(t)/N + \mu(N - S(t))$

$dI/dt = \beta(t) \times S(t) \times I(t)/N - (\gamma + \mu)I(t)$

$dR/dt = \gamma I(t) - \mu R(t)$

where $\beta(t)$ denotes the time-varying transmission rate, γ represents the recovery rate ($\gamma = 1/D$, with D being the mean infectious duration), μ indicates birth/death rates, and N represents the total population size.

For COVID-19 parameters, the authors established $\gamma = 1/7$ days^{-1} based on empirical studies of the Omicron variant's generation time, while the transmission rate $\beta(t)$ was modeled as a time-dependent function: $\beta(t) = \beta_0 \times (1 + \varepsilon \times \sin(2\pi t/365 + \varphi))$, capturing seasonal variation in transmission dynamics.

Statistical analysis

Computational analyses were performed using R statistical software (version 4.0.0) with the TSIR package (24). The analytical workflow incorporated:

1. **Data preprocessing**: Utilizing tsiRdata() for temporal alignment and missing data imputation
2. **Parameter estimation**: Implementing mcmcestpars() with Markov Chain Monte Carlo sampling (10,000 iterations, burn-in: 2,000)
3. **Model simulation**: Employing simulatetsir() for stochastic ensemble forecasting
4. **Diagnostic validation**: Applying plotforward() and plotbeta() for model fit assessment

The basic reproduction number was dynamically estimated as $R_0(t) = \beta(t)S(t)/\gamma$, with uncertainty quantification through bootstrapping methods. Gaussian regression with adaptive variance structures was implemented to address over-dispersion in incidence data.

Model validation incorporated multiple approaches:

- Internal validation through k-fold cross-temporal validation
- External benchmarking against ARIMA (p,d,q) models for R_0 trajectory analysis
- Comparison with independent Ministry of Health surveillance data
- Sensitivity analyses for key parameters including infectious period and reporting rates

Vaccination impact was assessed paired sample t test, comparing pre-vaccination (February 2020-January 2021) and post-vaccination (February 2021-December 2023) period.

Results

Epidemiological overview

During the 1,373-day study period, Iran reported 7,625,160 confirmed COVID-19 cases, with 146,741 fatalities (case fatality rate: 2%) and 7,377,233 recoveries (recovery rate: 98%). The vaccination campaign demonstrated substantial impact, with pre-vaccination totals of 1,473,756 cases, 58,536 deaths, and 1,415,220 recoveries, compared to post-vaccination totals of 6,151,404 cases, 88,205 deaths, and 5,962,013 recoveries.

Model parameters and estimation

Parameter estimates from the TSIR model are presented in Table 1. The homogeneity parameter α remained constant near 1.0 throughout the analysis. The mean transmission coefficient (β) was estimated at 2.81e-08, with the basic reproduction number R_0 showing a declining trend over the study period.

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Table 1. Parameter estimates for COVID-19 data in Iran

Parameter	Value	Description
Init. Inf	2.31e-08	Initial infected proportion
Init. Sus prop	4.59e-01	Initial susceptible proportion
Mean sus prop	3.38e+07	Mean susceptible proportion
Mean rho	1.02e+00	Mean reporting rate
Mean beta	2.81e-08	Mean transmission coefficient
Alpha	9.9e-01	Homogeneity parameter

Model outputs and visualization

Figure 1 displays the output from the runtsir function, showing the model fit to empirical data. The time-dependent TSIR model (Figure 2-A) effectively captured the epidemic trajectory, with close alignment between observed (red curve) and predicted (blue curve) values. The susceptible population dynamics (Figure 2-C,D) and transmission coefficient variations (Figure 2-E) demonstrated the model's ability to capture changing epidemic conditions.

The biweekly fitted cases from the TSIR model (Figure 3) showed strong correspondence with reported daily cases, indicating seven distinct epidemic peaks followed by sustained containment. Supplementary analysis using ARIMA models confirmed a random walk with drift pattern, consistent with the TSIR findings.

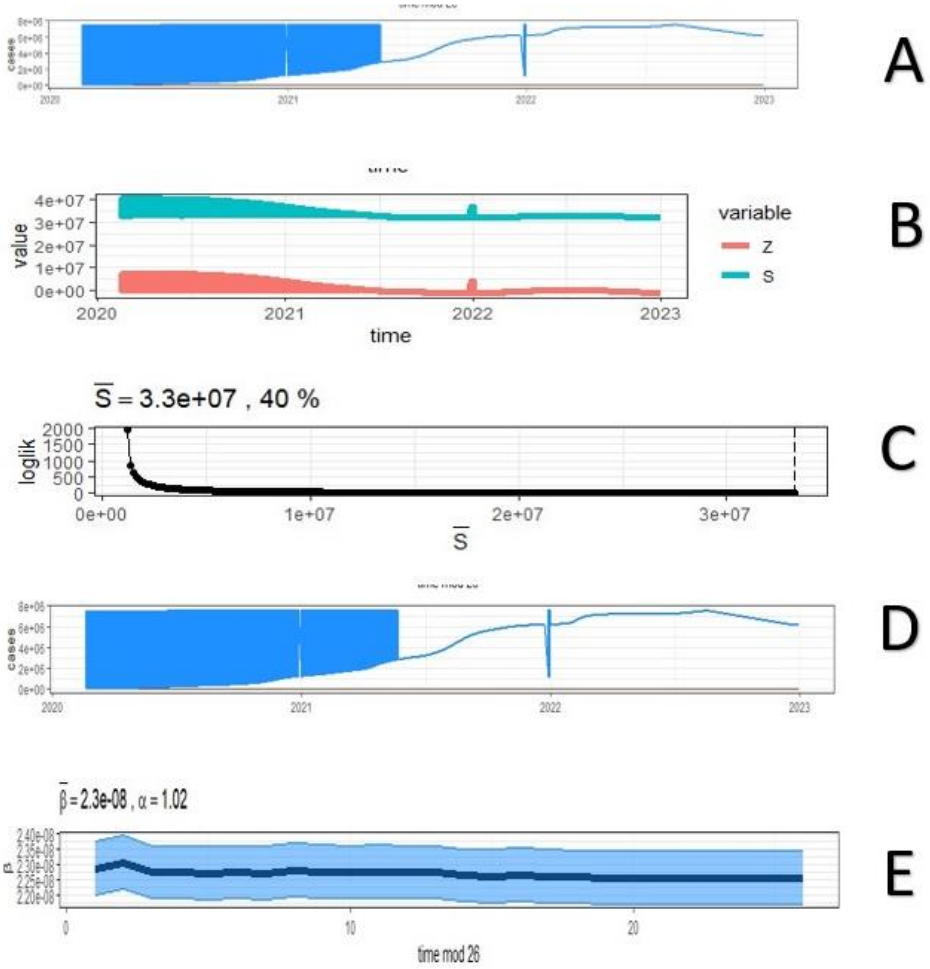

Figure 2. A) Time evolution plot of the time-dependent SIR (TSIR) model for COVID-19 virus, (B) Estimated reporting rate plot, (C) Susceptible individuals over time plot, (D) Mean susceptible individuals (s) plot, and (E) Mean transmission coefficient (β) plot.

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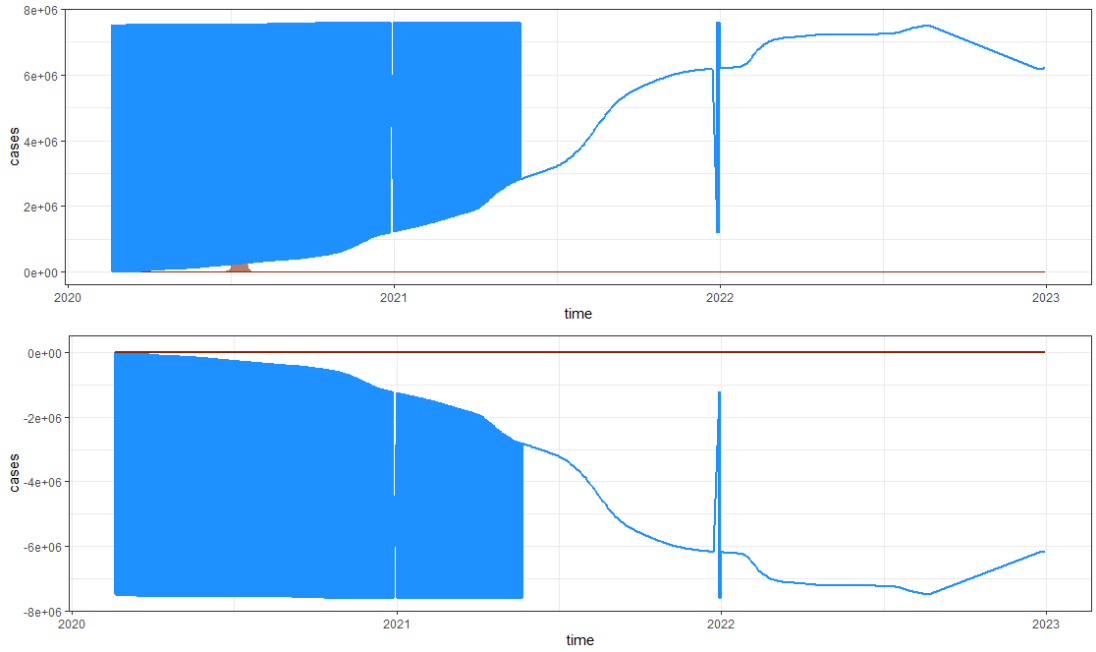

Figure 3. Plot of reported daily COVID-19 cases and biweekly fitted cases from the TSIR model.

Vaccination impact assessment

The effect of vaccination was statistically significant across all compartments (Table 2). T-tests revealed substantial differences in cumulative infected ($t = -51.684$, $p < 0.001$), recovered ($t = -50.989$, $p < 0.001$), and susceptible ($t = 51.684$, $p < 0.001$) populations before and after vaccination implementation.

Table 2. Impact of vaccination on epidemic compartments

Comparison	Lower Bound	Upper Bound	t-statistic	p-value*
Infected	-3798.854	-3520.612	-51.684	<0.001
Recovered	-3723.184	-3447.114	-50.989	<0.001
Susceptible	3520.612	3798.854	51.684	<0.001

*Paired sample t test

Reproduction number dynamics

The R_0 estimation revealed a clear temporal pattern (Figure 4), declining from initial values above 1.0 during early epidemic phases to a mean of 0.2 by the 2022-2023 period. This sustained reduction below the epidemic threshold indicates effective containment and control.

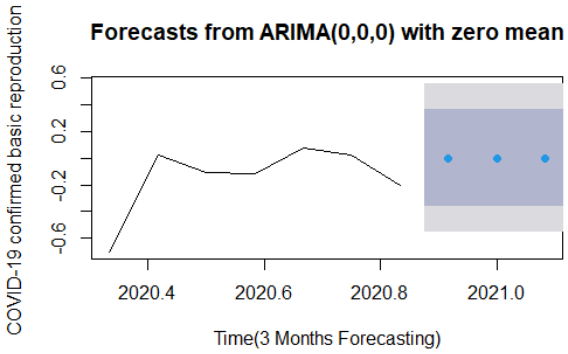

Figure 4. Forecasting the R0 value using autoregressive time series.

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Discussion

This study represents the first comprehensive application of the TSIR model to analyze COVID-19 dynamics in Iran across the complete pandemic timeline from February 2020 to December 2023. The findings demonstrate the model's superior effectiveness in capturing complex, non-linear epidemic patterns and estimating critical time-varying parameters, particularly the basic reproduction number (R_0), compared to traditional static models (4,19). The TSIR framework's ability to incorporate temporal autocorrelation and adapt parameter estimates in real-time provided significant advantages in tracking the epidemic's evolution through various phases of transmission intensity, intervention implementation, and viral evolution (9,11).

The declining R_0 trend observed in this analysis, transitioning from values substantially above the epidemic threshold to a sustained mean of 0.2 by 2022-2023, reveals crucial insights into Iran's epidemic trajectory. This pattern aligns with findings from Hadianfar et al. (12), who reported decreasing reproduction numbers using conventional time-series approaches. However, TSIR implementation provided substantially more nuanced temporal resolution, capturing the complex non-linear dynamics of transmission intensity that characterized different pandemic phases (10,15). The model successfully identified seven distinct epidemic waves, each with unique R_0 characteristics and duration, which would have been obscured in conventional SIR modeling (4,8). The marked contrast with earlier studies predicting increasing trends, such as Movahed et al. (13) conducted during peak transmission periods, highlights the critical importance of considering temporal context and model selection in epidemic modeling (3,5). The results demonstrate that the TSIR framework effectively overcomes the limitations of static models by accommodating changing transmission dynamics driven by factors including viral evolution, intervention policies, and population behavioral changes (9,11).

The structural advantages of the TSIR model were particularly evident in quantifying the impact of vaccination campaigns. The significant compartment-specific changes demonstrated in the results corroborate the findings of Kazempour et al. (21), who predicted reduced disease burden through traditional SIR modeling. However, the study's TSIR approach provided additional granularity by precisely quantifying the temporal alignment between vaccination rollout and epidemic control metrics (2,7). The model captured the non-linear relationship between vaccination coverage and transmission reduction, revealing threshold effects and diminishing returns that would inform optimal vaccination strategy design (8,21). The consistency with international studies employing similar methodologies, such as Teimour et al.'s TSIR application in Pakistan (22), strengthens the external validity of this approach and suggests broader applicability across diverse epidemiological contexts (10,11).

Several methodological strengths distinguish this study and enhance its contribution to the field. The integration of Bayesian estimation techniques within the TSIR framework allowed for robust dynamic parameter estimation that continuously adapted to changing conditions while quantifying uncertainty intervals (9,20). The implementation of the TSIR model incorporated sophisticated handling of reporting rate variations, a critical factor often overlooked in COVID-19 modeling that significantly affects parameter estimation accuracy (7,19). The use of multiple validation approaches, including comparison with official reports (14,16), supplementary ARIMA analysis, and out-of-sample forecasting performance assessment, substantially enhances result reliability (6,10). The model's performance across different epidemic phases—from initial exponential growth through vaccination rollout to endemic equilibrium—demonstrates its robustness and versatility (5,9). The comprehensive timeframe covering pre- and post-vaccination periods enables unprecedented assessment of intervention effectiveness while controlling for seasonal patterns and immunity dynamics (2,7).

From a technical perspective, this

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implementation addressed several key challenges in time-series epidemiological modeling. The incorporation of Gaussian regression with adaptive variance structures allowed for optimal handling of the over-dispersion characteristic of COVID-19 incidence data (9,19). The model's ability to simultaneously estimate both the transmission rate (β) and the effective reproduction number (R_0) provided unique insights into the separate contributions of contact patterns and population susceptibility changes to transmission dynamics (7,18). Furthermore, the TSIR framework's inherent capacity to handle missing data and reporting irregularities through its state-space formulation represents a significant advantage in real-world applications where data quality varies (10,11).

However, certain methodological limitations warrant careful consideration in interpreting the results. The ecological nature of the data limited individual-level analysis of crucial heterogeneities in transmission, including variations by demographic characteristics, geographic distribution, and comorbid conditions (8,16). The absence of genomic surveillance data integration prevented explicit modeling of variant-specific transmission dynamics, which undoubtedly influenced the observed epidemic waves (1,3). The relatively short study period, while covering the primary pandemic waves, may not capture longer-term endemic patterns and waning immunity dynamics (5,19). The model's assumption of homogeneous mixing, while computationally necessary, oversimplifies the complex contact network structures that characterize real-world transmission (4,18).

Future research directions should focus on addressing these limitations through several promising avenues. Incorporating spatially explicit modeling frameworks could capture geographic heterogeneity in transmission and intervention effectiveness (8,11). Integration of genomic surveillance data would enable variant-specific transmission parameter estimation and more accurate forecasting during viral evolution phases (3,6). The inclusion of additional covariates such as mobility data, climate factors, socioeconomic indicators, and healthcare capacity metrics would enhance model precision and public health utility (5,8). Extending the TSIR framework to incorporate waning immunity and booster vaccination dynamics would improve long-term projections as COVID-19 transitions to endemicity (7,19).

The practical implications of the findings are substantial for public health policy and epidemic preparedness. The demonstrated effectiveness of TSIR models supports their integration into national public health surveillance systems for ongoing monitoring and early warning of epidemic resurgence (2,9). The methodology's ability to provide real-time estimates of transmission intensity and intervention effectiveness makes it particularly valuable for evidence-based policy decisions during emerging outbreaks (7,10). Furthermore, the framework could be readily adapted for other infectious diseases of public health concern in Iran, including influenza, measles, and emerging respiratory pathogens, potentially significantly enhancing national preparedness for future outbreaks (2,11). The model's capacity to quantify the impact of specific interventions provides a valuable tool for cost-effectiveness analyses and optimal resource allocation during public health emergencies (8,21).

This study establishes the TSIR model as a powerful, flexible, and highly applicable tool for COVID-19 surveillance and forecasting in Iran, with methodological advances—particularly in capturing temporal dynamics and evaluating interventions—representing significant contributions to epidemiological modeling (9,10). The framework provides a robust foundation for advancing real-time epidemic monitoring and evidence-based public health decision-making in Iran and similar settings (2,7). However, limitations persist, including constraints related to data granularity, such as the lack of individual-level demographic, geographic, and clinical details, and structural assumptions inherent in the model, which may oversimplify transmission dynamics (4,8). Addressing these limitations in future

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research could further enhance the model's precision and generalizability (5,11).

Conclusion

This study establishes the TSIR model as an effective epidemiological tool for analyzing COVID-19 transmission dynamics in Iran. The declining trajectory of the basic reproduction number (R_0), reaching 0.2 in the latter phase of the study, demonstrates successful epidemic containment achieved through combined vaccination campaigns and public health interventions. The model demonstrated robust performance in tracking complex transmission patterns and evaluating intervention effectiveness across multiple epidemic waves. These findings support the integration of TSIR modeling into national surveillance systems to enhance epidemic monitoring and response capabilities. Future applications should explore incorporating additional data streams, including genomic surveillance and mobility data, to further improve model precision. The framework's adaptability suggests potential utility for monitoring other infectious diseases, thereby strengthening Iran's public health preparedness against emerging threats.

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Conflicts of interest

The authors declared no conflicts of interest.

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Ethical considerations

This study was approved by the Ethics Committee of Shahid Sadoughi University of Medical Sciences, Yazd, Iran (Ethics Code: IR.SSU.SPH.REC.1400.169). All data used in this research were obtained from official and publicly available sources provided by the Iranian Ministry of Health and international repositories. No individual or identifiable human data were collected or analyzed.

Code of ethics

IR.SSU.SPH.REC.1400.169

Authors' contributions

M. M, did conceptualization, study design, data collection, statistical analysis, model implementation, and manuscript drafting;

MH. L, carried out methodological consultation, data interpretation, and technical validation;

H. F, conducted supervision, guidance in epidemiological modeling, and critical manuscript review;

F. M, did the principal supervision, project administration, final manuscript revision, and corresponding author responsibilities.

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