

A Bayesian Estimator of the Real-time Case Fatality Rate in Emerging Pandemic to Inform Public Health Policy-Making

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Abstract

Background: The case fatality rate (CFR) is a crucial metric for monitoring ongoing epidemics. However, existing CFR estimators often fail to account for the time lag between symptom onset and death, and cannot make real-time predictions. This limits their effectiveness in providing accurate and timely policy guidance during emerging epidemics, which motivates us to develop a more robust and accurate estimator.

Method: We present a novel Bayesian real-time adjusted CFR (BrtaCFR) estimator that operates in real-time and requires only basic epidemiological count data. The estimator is based on the Poisson model within a Bayesian framework, incorporating prior knowledge of fatality rates and a fused LASSO component for stability of posterior real-time estimation.

Results: Simulation studies showed that the BrtaCFR estimator accurately captured various patterns of true fatality rates, outperforming traditional estimators. The BrtaCFR estimator demonstrated high sensitivity to changes in disease severity over time and remained robust across different hyperparameter settings. When applied to the Japan COVID-19 dataset, the estimator effectively captured the impacts of both infection surges and implemented public health policies on the fatality rate across different pandemic waves.

Conclusions: The proposed BrtaCFR estimator offers a more accurate and responsive tool for assessing disease severity in real-time during emerging epidemics. By accounting for reporting delays and incorporating prior knowledge of mortality rates, it provides a more reliable basis for public health decision-making. This approach could significantly enhance our ability to monitor and respond to evolving epidemic situations, potentially improving the effectiveness of public health interventions and resource allocation during future outbreaks.

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1 Introduction

The global landscape of public health has been fundamentally reshaped by the increasing frequency of emerging and re-emerging infectious diseases [1]. Events such as the Severe Acute Respiratory Syndrome (SARS) epidemic in 2003, the Middle East Respiratory Syndrome (MERS) outbreak in 2012, and the recent COVID-19 pandemic have highlighted the profound challenges posed by novel pathogens [2, 3, 4, 5]. The rapid globalization of travel and trade accelerates the spread of such diseases, transforming regional outbreaks into global crises that can overwhelm healthcare systems and disrupt societal functions [6]. Even as the acute phase of the COVID-19 pandemic subsides, the emergence of new variants like JN.1 continues to test healthcare capacity, serving as a stark reminder of this persistent threat [7, 8, 9]. In this context, the capacity to accurately assess disease severity in real-time is a cornerstone of effective public health response [10, 11].

A key metric for this purpose is the fatality rate, a term that encompasses two distinct concepts: the Infection Fatality Rate (IFR) and the Case Fatality Rate (CFR) [12]. The IFR is defined as the proportion of all infected individuals, including asymptomatic and undiagnosed cases—who ultimately die from the disease. It is considered a more stable measure of a pathogen’s intrinsic virulence, but its estimation is a complex undertaking, often requiring resource-intensive seroprevalence studies to ascertain the true number of infections. Sophisticated Bayesian hierarchical models have been developed for this purpose, leveraging serology data to produce robust IFR estimates, often stratified by demographic factors [13, 14]. While powerful, these methods are often not feasible for real-time operational monitoring during an epidemic’s early stages when such data are scarce.

In contrast, the CFR is the proportion of confirmed cases resulting in death. Although susceptible to biases from testing strategies and case ascertainment, the CFR is a vital operational metric that reflects the severity of outcomes among individuals identified by the healthcare system. Crucially, it can be estimated using standard surveillance data—daily counts of confirmed cases and deaths—which are among the first and most consistently available data streams during an outbreak. The simplest version, the crude CFR (cCFR), calculated as the ratio of cumulative deaths to cumulative cases, is nevertheless known to be biased. It fails to account for the time lag between disease onset and death, often leading to significant underestimation of the true fatality rate during an active epidemic [15, 12, 16].

To address this delay-induced bias, [15] proposed a seminal method to adjust the cCFR by incorporating the distribution of the time from onset to death. While this marked a significant improvement, many epidemics, including COVID-19, exhibit time-varying severity due to factors such as the emergence of new variants, shifts in healthcare capacity, and the rollout of interventions [17]. This has motivated the development of estimators for a real-time, time-varying CFR. Early work in this area employed competing risk models [18, 19].

More advanced techniques, such as nowcasting, aim to predict the final outcome of active cases [6], but these methods often demand detailed line-list data that are unavailable in the aggregated daily counts provided by most health agencies. More recently, [20] introduced a real-time adjusted CFR (rtaCFR) estimator using a fused LASSO penalty. While effective at tracking trends, this frequentist approach has practical limitations: its formulation complicates the calculation of confidence intervals, and it requires practitioners to manually select a smoothing parameter. Other related work has focused on hypothesis testing to compare fatality rates rather than on continuous estimation [21, 22].

This study proposes a Bayesian real-time adjusted CFR (BrtaCFR) estimator that directly addresses the limitations of previous methods. By situating the problem within a comprehensive Bayesian framework, our approach offers three key advantages. First, it provides a principled approach to uncertainty quantification, yielding full posterior distributions for the time-varying fatality rates based only on daily aggregate counts. This allows for the calculation of intuitive credible intervals, which are essential for risk assessment. Second, it achieves automatic smoothing by placing a hyperprior on the regularization parameter, which allows the optimal degree of smoothing to be learned from the data itself, thus obviating manual tuning. Third, the Bayesian framework provides a formal mechanism for the incorporation of prior knowledge, a feature especially valuable for stabilizing estimates when data are sparse at the beginning of an outbreak. We demonstrate through simulation that the proposed BrtaCFR accurately captures diverse fatality rate patterns and demonstrates its practical utility by applying it to COVID-19 data from Japan, illustrating how it can reveal the dynamic impact of public health policies on disease severity.

The remainder of this paper is organized as follows. Section 2 details the data structure, notations, and our estimation methods. Section 3 presents the results of our simulation studies. The real-data analysis is demonstrated in Section 4 using the Japan COVID-19 dataset. Finally, Section 5 concludes with a discussion of the findings and their implications.

2 Methods

Our estimation method will be established based on the regularly collected epidemiological surveillance data. Let the observation period be $(0, T]$ such that the numbers of deaths d_t and confirmed cases c_t are obtained for $t = 1, \dots, T$. Suppose that the outcome for each diagnosed case will either be death or recovery. Let F be the cumulative distribution function of the time from disease onset to death. We denote its probability mass function by $f_t = F(t) - F(t-1)$ for $t = 1, 2, \dots, T$, representing the probability of death occurring t days after onset. By leveraging prior knowledge, such as data from previous outbreaks or analysis of individual-level data from hospitalized cases, we can inform the parameters of the cumulative distribution function F , which is typically adopted as the Gamma distribution with the mean parameter δ and shape parameter γ [23, 20, 24]. The primary objective is to accurately estimate the real-time case fatality rate at each time stamp using the epidemiological data (c_t, d_t) over T time stamps.

Two approaches are commonly employed for estimating the fatality rate during the epidemic. The first method is known as the crude case fatality rate (cCFR), providing a

straightforward computation by taking the ratio of the cumulative number of deaths to the confirmed cases up to a specified time point t . Specifically,

$$\text{cCFR}(t) = \frac{\sum_{i=1}^t d_i}{\sum_{i=1}^t c_i}. \quad (1)$$

Although cCFR offers a concise estimate, it fails to account for the delay between disease onset and death. This limitation results in an underestimation of the true fatality rate because deaths that may occur beyond the observation time point t are not considered in the calculation. For mitigating such a bias, [15] proposed an alternative estimator with the delay adjustment by incorporating the distribution of the time from disease onset to death, known as the modified case fatality rate (mCFR),

$$\text{mCFR}(t) = \frac{\sum_{i=1}^t d_i}{\sum_{i=1}^t \sum_{j=0}^{i-1} c_{i-j} f_{j+1}}. \quad (2)$$

However, it is important to acknowledge that both cCFR and mCFR assume a constant fatality rate over a given period and solely rely on cumulative information, disregarding the dynamic changes in the fatality rate over time. Another limitation of these estimators is their inability to incorporate prior knowledge, which renders them prone to instability and unreliability, especially in the initial stages of an epidemic when the number of available samples is limited. This lack of prior knowledge integration can result in inaccurate assessments of the severity and impact of the epidemic, impeding the effectiveness of early interventions.

In order to tackle these challenges, we propose a comprehensive Bayesian approach that incorporates the prior information and considers a time-delay adjustment to calculate the real-time fatality rate. We model the death count d_t using a Poisson distribution with mean μ_t , with probability mass function $P(d_t = d) = e^{-\mu_t} \mu_t^d / d!$, for $d = 0, 1, \dots$ and $t = 1, \dots, T$. The real-time fatality rate is estimated using the Poisson likelihood as follows:

$$\begin{aligned} \mu_t &= \sum_{j=0}^{t-1} p_{t-j} c_{t-j} f_{j+1}, \quad p_t = \frac{1}{1 + \exp(-\beta_t)}, \\ p(\mathbf{d}|\boldsymbol{\beta}) &= \prod_{t=1}^T e^{-\mu_t} \mu_t^{d_t} / d_t!, \quad \mathbf{d} = (d_1, \dots, d_T)^T, \quad \boldsymbol{\beta} = (\beta_1, \dots, \beta_T)^T, \end{aligned} \quad (3)$$

In this formulation, the quantity μ_t represents the daily expected number of deaths, calculated as the cumulative sum of the product of past fatality rates p_{t-j} , case counts c_{t-j} , and fatality reporting delays f_{j+1} up to time $t - 1$, as in [20]. The target is to estimate the fatality rate at time t , namely p_t . As p_t ranges from 0 to 1, we reparametrize p_t by a sigmoid function of $\beta_t \in (-\infty, \infty)$ and estimate β_t in the subsequent analysis. Given the estimate of $\boldsymbol{\beta}$, we can then obtain the estimates of p_1, \dots, p_T via backward transformation. The overall likelihood function $p(\mathbf{d}|\boldsymbol{\beta})$ is computed by combining the Poisson probabilities for each time point t .

We propose a joint prior distribution $\pi(\boldsymbol{\beta}|\tilde{\boldsymbol{\beta}}, \sigma, \lambda) = \pi_1(\boldsymbol{\beta}|\tilde{\boldsymbol{\beta}}, \sigma)\pi_2(\boldsymbol{\beta}|\lambda)$ for $\boldsymbol{\beta}$ where

$$\begin{aligned}\pi_1(\boldsymbol{\beta}|\tilde{\boldsymbol{\beta}}, \sigma) &= \frac{1}{(2\pi\sigma^2)^{T/2}} \exp \left[-\frac{1}{2\sigma^2} \sum_{t=1}^T (\beta_t - \tilde{\beta}_t)^2 \right], \quad \tilde{\boldsymbol{\beta}} = (\tilde{\beta}_1, \dots, \tilde{\beta}_T)^T, \\ \pi_2(\boldsymbol{\beta}|\lambda) &= \left(\frac{\lambda}{2} \right)^{T-1} \exp \left(-\lambda \sum_{t=2}^T |\beta_t - \beta_{t-1}| \right), \quad \lambda \sim C^+(0, 1),\end{aligned}\tag{4}$$

$(\tilde{\boldsymbol{\beta}}, \sigma)$ are hyperparameters, and λ is an auxiliary parameter with a prespecified prior distribution. The first component, $\pi_1(\boldsymbol{\beta}|\tilde{\boldsymbol{\beta}}, \sigma)$, is a normal prior that enhances the estimation of p_t and mitigates inflated estimates resulting from small values of c_t during the initial time stamps. The values of $\tilde{\beta}_t$ can be determined based on historical information or expert knowledge. As an empirical suggestion, we propose using the logarithmic cCFR as the initial values, $\tilde{\beta}_t = \log[\text{cCFR}(t)/(1 - \text{cCFR}(t))]$, for simplicity. For a vague normal prior, we set the variance parameter to be $\sigma^2 = 25$. On the logit scale, this represents a weakly informative prior that allows for a wide range of plausible fatality rates while regularizing against extreme values, especially during initial time points with sparse data. The second component, $\pi_2(\boldsymbol{\beta}|\lambda)$, is a fused LASSO prior that reduces variation among adjacent fatality rates, improving the stability of predictions, defined with a half-Cauchy hyper-prior $C^+(0, 1)$ for the shrinkage parameter λ . It is a standard choice for a weakly informative prior on a scale parameter, allowing the model to learn the appropriate degree of smoothing from the data itself [25].

The Bayesian inference for the model defined by equations (3) and (4) is performed using the PyMC probabilistic programming library in Python [26]. Given the need for rapid estimation in a real-time monitoring context, we employ Automatic Differentiation Variational Inference (ADVI) to approximate the posterior distribution based on the mean-field decomposition [27]. ADVI offers a significant speed advantage over traditional Markov chain Monte Carlo (MCMC) methods, making it well-suited for this application. The algorithm was run until the evidence lower bound (ELBO) converged with a maximum 10^5 iterations, indicating a stable posterior approximation. The complete estimation procedure is summarized in Algorithm 1. We obtain the Bayesian real-time adjusted fatality rate estimator, denoted as $\text{BrtaCFR}(t)$, by taking the posterior means of p_t 's with the Bayesian inference results. To quantify the uncertainty in our estimates, we construct a 95% credible interval for $\text{BrtaCFR}(t)$, which is determined by calculating the 2.5th and 97.5th percentiles of the approximated posterior distributions.

Compared with simple ratio estimators (1) and (2), the proposed estimation method offers several advantages for epidemiologists. First, it is a parsimonious statistic of Poisson likelihood for considering count data, effectively capturing the inherent variability of the observed case and death counts (c_t, d_t) . This likelihood enables a more accurate representation of the underlying epidemiological dynamics, leading to improved estimation quality [28]. Moreover, the reporting delay issue can be addressed easily through the modification of the means of the Poisson variables. Second, under the Bayesian framework, prior knowledge, such as some crude initial fatality rate estimates, can be incorporated into the estimation procedure, facilitating the robustness of the proposed estimator. Our modeling procedure

incorporates the fused LASSO for stabilizing the estimated fatality rates, and thus preventing excessive fluctuations in the final estimates. Finally, the hyper-prior assigned to the penalty λ allows the optimal value of λ to be estimated together with the real-time fatality rates through a data-adaptive approach, and prevents practitioners from tedious parameter tuning.

3 Simulation Studies

We conduct simulation studies to evaluate the performance of the proposed BrtaCFR estimator. The primary goal is to verify that the model, under idealized conditions where the data-generating process matches the model assumptions, can successfully recover the true underlying fatality rate and provide accurate uncertainty quantification. This serves as a crucial sanity check for the estimation framework before its application to real-world data.

We perform a comparative analysis of our proposed estimator BrtaCFR with the conventional cCFR and the delay-adjusted mCFR over a pandemic period of $T = 200$ days. The number of confirmed cases, denoted by c_t , is deterministically generated using the formula $c_t = 3000 - 5|100 - t|$, $t = 1, \dots, T$. This process simulates a scenario in which there is an initial rapid surge of infections at the beginning of the epidemic, followed by a decline after the implementation of some control strategies. To model the real-time fatality rate denoted by p_t , we consider six different scenarios as summarized in Table 1 and visualized in Figure 1, encompassing both constant and time-varying patterns. Scenario (A) considers the constant fatality rate. Scenario (B) considers an exponentially increasing rate. Scenario (C) considers the situation with constant rates at two ends and an increasing pattern in the middle. Scenario (D) starts with a constant rate followed by a decreasing trend. Scenario (E) mimics the case with an underlying effective intervention, leading to a sharp decrease in the fatality rate. Scenario (F) pertains to the case with a turning point potentially caused by a new outbreak. The number of deaths d_t is then randomly generated based on c_t and p_t . Specifically, the confirmed cases c_t would eventually die with the number d'_t following a binomial distribution with a probability p_t , i.e., $d'_t \sim B(c_t, p_t)$. Consequently, we obtain the daily number of deaths $d_t = \sum_{i=0}^{t-1} d'_{t-i} f_{i+1}$ by accounting for the time from disease onset to death with a gamma distribution F of $\delta = 15.43$ and $\gamma = 2.03$ respectively, following the situation of COVID-19 mentioned in [23].

We evaluate the accuracy of the three estimators by comparing them to the true values using 1000 replications for each scenario, based on synthetic data (c_t, d_t) over T time stamps. Figure 1 presents the averaged estimates based on the three methods together with the true fatality rate p_t , to assess how well the estimators approximate the true value. Additionally, we generate 1000 posterior samples for $\text{BrtaCFR}(t)$ to evaluate uncertainty and visualize the plausible range of values for fatality rate estimation. The average credible interval has been generated as a shaded region using the 2.5% and 97.5% posterior quantiles for $\text{BrtaCFR}(t)$. This credible interval provides a measure of uncertainty and represents the plausible range of values for fatality rate estimation.

In Figure 1, it is evident that the cCFR estimator used in the simulation studies has limitations in accurately capturing the evolving fatality rate. This lack of real-time capa-

bility undermines its usefulness in monitoring disease severity and making informed policy decisions based on up-to-date information. In particular, the cCFR estimator demonstrates a diverging trend compared to the true fatality rate, especially when the fatality rate declines initially (see Scenario F). This discrepancy could lead to misleading conclusions, potentially impacting policy-making decisions. After incorporating time-delay adjustments, the mCFR estimator, while still unable to capture the time-varying trend of the real fatality rate, demonstrated higher sensitivity compared to the cCFR estimator when faced with dynamic changes in the fatality rate over time. In contrast to the cCFR and mCFR estimators, the BrtaCFR estimator provides a robust and stable estimation of the fatality rate that closely aligns with the actual trends observed during the simulation studies. This alignment is crucial for effectively monitoring disease severity and guiding informed decision-making. Notably, the BrtaCFR estimator successfully predicts the sharp decrease and increase in the real-time fatality rate under Scenarios E and F, highlighting the potential of our proposed method in practice. The credible interval associated with the BrtaCFR estimator offers a real-time measure of uncertainty around the estimated fatality rate. This allows policymakers and researchers to assess the reliability and statistical significance of the estimation.

In practice, the parameters in the distribution F are determined based on historical records from various regions, where misspecification of these parameters may introduce bias into subsequent analysis. Sensitivity analyses are conducted to assess the robustness of our approach against such misspecifications. In comparison to the true parameter values $(\delta, \gamma) = (15.43, 2.03)$, the first setting involves refitting BrtaCFR using a larger mean parameter $(\delta, \gamma) = (18.8, 2.03)$ following [29], while the second setting considers completely misspecified smaller parameters $(\delta, \gamma) = (10.1, 0.53)$ following [30] and [31]. The results, depicted in Figure 2, show the performance of BrtaCFR+ and BrtaCFR−, corresponding to the estimators from the first and second settings, respectively. We observed that both curves can eventually capture the general trend of the real-fatality rate with small deviation from that of BrtaCFR, indicating the practical stability of our method. Similar conclusions can be drawn for the credible intervals, which we have omitted in the visual representation for simplicity.

4 Application to COVID-19 Data in Japan

Figure 3 depicts the trend of daily confirmed COVID-19 cases and deaths during several major waves of the COVID-19 pandemic in Japan from 2020 to 2022, and the daily surveillance data can be downloaded from the WHO COVID dashboard. Japan confirmed its first COVID-19 case on January 16, 2020 [32], followed by a significant outbreak on the ‘Diamond Princess’ cruise ship in February. In response, the government introduced measures in March, including nationwide school closures and travel restrictions for arrivals from heavily affected areas. Despite these efforts, infections surged in Tokyo and Osaka, prompting the declaration of a state of emergency in Tokyo and several prefectures on April 7 [33]. On April 16, the government extended the state of emergency nationwide, implementing social distancing, business restrictions, and remote working policies [34]. As infection rates declined by May in Figure 3, the state of emergency was lifted in phases, concluding on May 25, a

success attributed to public compliance and swift government intervention [35]. However, the economic impact was significant, leading to financial aid packages for affected businesses and individuals.

To stimulate the economy, the Japanese government introduced the ‘Go To Travel’ campaign in the summer of 2020 to promote domestic tourism [36]. Although the campaign initially succeeded in boosting economic activity, the surge in travel and social interactions led to a resurgence in COVID-19 infections. By the end of 2020, the situation deteriorated further with the emergence of the more transmissible Alpha variant, resulting in a sharp increase in daily cases. Figure 3 shows that, by early 2021, daily confirmed cases exceeded 3,000, accompanied by a significant rise in deaths. In response, the government declared a state of emergency in early 2021, implementing restrictions on large gatherings, encouraging remote work, and tightening regulations on public transportation and mask-wearing [37]. While these measures led to a decline in cases in the following months, a gradual easing of restrictions in March resulted in another rise in infections by April.

On February 17, 2021, the government launched a vaccination campaign targeting health-care workers, later expanding in June 2021 to include individuals aged 65 and above [38]. Consequently, despite a significant surge in confirmed cases during the highly transmissible Delta wave in September 2021, the number of fatalities remained notably lower compared to previous waves, as shown in Figure 3. In October 2021, the campaign extended to a wider population. By late 2021, the emergence of the Omicron variant drove a sharp increase in infections, leading to adjustments in public health policies. The government responded by accelerating booster shot distribution starting in December 2021. By the end of 2021, vaccination rates for the first and second doses had reached 75.1% and 74.6%, respectively [39]. Figure 3 finally demonstrates that the death rate remained low during the Omicron wave, despite a surge in confirmed cases. This was largely due to Omicron’s milder symptoms and widespread vaccination, which increased population immunity and reduced severe cases.

We then leverage the proposed BrtaCFR estimator with the Japan COVID-19 pandemic dataset shown in Figure 3 to analyze the trend in disease fatality rates during the epidemic. The parameters $(\delta, \gamma) = (15.43, 2.03)$ for the distribution of disease onset to death are specified. To better visualize the underlying trend in the daily fatality rate estimates, the raw BrtaCFR point estimates are smoothed using a Gaussian kernel with a 21-day bandwidth. This bandwidth was chosen as it corresponds to a three-week moving average, a common choice in epidemiological time series analysis for smoothing out high-frequency noise (e.g., weekend reporting effects) while preserving meaningful medium-term trends in disease severity [40, 41, 42]. Additionally, we construct a 95% credible interval for the BrtaCFR estimator to quantify uncertainty and include the cCFR and mCFR estimators for comparative analysis. Figure 4 displays the results obtained from the three methods, along with a timeline of significant public health policies implemented by the government.

The following notable patterns can be observed. First, as established in the literature, the cCFR tends to underestimate the true underlying fatality rate during an active epidemic when the delay between case confirmation and death is substantial [15]. Our results align with this expectation, as the BrtaCFR estimates are positioned consistently above the cCFR curve at the beginning of the outbreak. Second, since both cCFR and mCFR estimators

are constructed based on cumulative statistics, they generally exhibit limited responsiveness to evolving trends in the fatality rate as data accumulates. As shown in Figure 4, both cCFR and mCFR display a delayed peak compared to BrtaCFR during the first wave of the epidemic around May 2020. As a result, cCFR and mCFR would have failed to suggest a timely assessment of the effectiveness of government policies, such as a declaration of a state of emergency in April 2020. Furthermore, as the number of infections increased, both cCFR and mCFR failed to capture the changes in disease fatality, exhibiting a flattened trend during both the Alpha and the Delta wave. This may provide misleading information to policymakers and lead to serious consequences. Thirdly, the BrtaCFR, on the other hand, is a smoother estimator that demonstrates a high responsiveness in capturing the fluctuation of case fatality rates across successive infection waves. Notably, the BrtaCFR exhibits three peaks of fatality rates at approximately 0.06, 0.04, and 0.01 during the initial wave, the Alpha wave in March 2021, and the Delta wave in October 2021, respectively. This is aligned with the number of deaths attributed to the Alpha and Delta waves as shown in Figure 3. Finally, the BrtaCFR converges to a low value together with cCFR and mCFR during the Omicron wave, owing to the effectiveness of vaccination and the reduced contagiousness of the variant.

5 Discussion

This study introduced the BrtaCFR, a Bayesian framework for estimating time-varying, delay-adjusted case fatality rates from standard epidemiological surveillance data. By leveraging a Poisson likelihood, a fused LASSO prior with a data-driven smoothing parameter, and efficient variational inference, the proposed method provides robust point estimates and principled uncertainty quantification. The application to Japan COVID-19 data demonstrated the estimator’s ability to capture dynamic changes in the fatality rate that coincided with major pandemic waves and the implementation of significant public health policies. The analysis provides a quantitative, retrospective assessment of how disease severity evolved over time, offering insights that can help evaluate the population-level impact of past interventions and pathogen evolution.

In future research work, the BrtaCFR estimator can be refined with enhanced model complexity to incorporate additional data sources. Motivated by previous works such as [16, 43, 44], we may extend the proposed method to incorporate demographic data into the estimation procedure. This can typically be accomplished by introducing the country- or region-specific covariates to the Poisson mean μ_t . These covariates can be time-independent or time-varying. Apart from demographic data, the integration of genomic data [45, 46, 47] and contact tracing information [48, 49] can contribute to a more comprehensive understanding of disease dynamics and allow for more precise fatality rate estimation. Genomic data can provide insights into the genetic variations of the virus, which may affect its virulence and transmissibility. This information, when combined with epidemiological data, can help identify specific viral strains that are associated with higher fatality rates or increased disease severity. Contact tracing information can provide valuable insights into the patterns of disease transmission and facilitate the identification of high-risk clusters or super-spreading events. By incorporating this information into the proposed CFR estimator, it would be

possible to capture the impact of specific transmission dynamics on the fatality rate.

As another research avenue, one can develop change point detection methods based on the BrtaCFR estimator, such as those described in Bayesian change point analysis [50] and sequential hypothesis testing methods [21, 51]. By detecting these change points, the CFR estimator can gain a more comprehensive understanding of the temporal dynamics of the fatality rate. It empowers practitioners and researchers to identify critical periods due to factors such as the introduction of new interventions, policy changes, or the emergence of new variants. Additionally, it assists experts in making informed decisions, evaluating the efficacy of interventions, and comprehending the influence of external factors on the fatality rate. By allowing a more complex model that incorporates change points or multiple relevant factors, this approach ultimately enhances the accuracy and effectiveness of CFR estimation, thereby facilitating the formulation of precise and targeted strategies to support public health efforts in managing emerging diseases.

6 Abbreviations

CFR: Case fatality rate

cCFR: Crude case fatality rate

mCFR: Modified case fatality rate

BrtaCFR: Bayesian real-time adjusted case fatality rate

7 Declarations

Ethics approval and consent to participate Not applicable.

Clinical Trial Not applicable.

Consent for publication Not applicable.

Availability of data and material The Japan COVID-19 surveillance data used in this study is publicly available from the World Health Organization COVID-19 dashboard at <https://srhdpeuwpubsa.blob.core.windows.net/whdh/COVID/WHO-COVID-19-global-daily-data.csv>. The codes used to implement the BrtaCFR estimator and reproduce the analysis in this manuscript can be accessed via <https://github.com/BobZhangHT/BrtaCFR/tree/main>.

Competing interests The authors declare that they have no competing interests.

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Authors’ contributions HZ, CYL, and YQ wrote the main manuscript text and HZ and YQ prepared Figures 1, 2, 3 and 4. HZ conducted all numerical studies. All authors reviewed the manuscript. All authors made a significant contribution to the work reported, whether in the conception, study design, analysis and interpretation, or in all these areas; participated in drafting, revising, or critically reviewing the article; and agreed to be accountable for all aspects of the work.

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References

- [1] Kate E Jones, Nikkita G Patel, Marc A Levy, Adam Storeygard, Deborah Balk, John L Gittleman, and Peter Daszak. Global trends in emerging infectious diseases. *Nature*, 451(7181):990–993, 2008.
- [2] W K Lam, N S Zhong, and W C Tan. Overview on SARS in Asia and the world. *Respirology*, 8:S2–S5, 2003.
- [3] Alimuddin Zumla, David S Hui, and Stanley Perlman. Middle East respiratory syndrome. *The Lancet*, 386(9997):995–1007, 2015.
- [4] Gerardo Chowell and Hiroshi Nishiura. Transmission dynamics and control of Ebola virus disease (EVD): a review. *BMC Medicine*, 12:1–17, 2014.
- [5] Yi Shi, G Wang, X-p Cai, J-w Deng, L Zheng, H-h Zhu, M Zheng, B Yang, and Z Chen. An overview of COVID-19. *Journal of Zhejiang University. Science. B*, 21(5):343, 2020.
- [6] Joseph T Wu, Kathy Leung, and Gabriel M Leung. Nowcasting and forecasting the potential domestic and international spread of the 2019-nCov outbreak originating in Wuhan, China: a modelling study. *The Lancet*, 395(10225):689–697, 2020.
- [7] M Roney, A Huq, and M F F M Aluwi. Concerns regarding SARS-CoV-2 JN. 1 mutations should be raised. *Bulletin of the National Research Centre*, 48(1):1–5, 2024.
- [8] Guanhong Ou, Yuhan Yang, Shuting Zhang, Siyuan Niu, Qiaoxia Cai, Yalan Liu, and Hongzhou Lu. Evolving immune evasion and transmissibility of SARS-CoV-2: The emergence of JN. 1 variant and its global impact. *Drug Discoveries & Therapeutics*, 18(1):67–70, 2024.
- [9] Davidson Hamer. COVID-19 in 2025: ‘A Constant Threat, but a Manageable One’. Boston University School of Public Health News, 2025. Accessed: 2025-06-17.
- [10] Marc Lipsitch, Ted Cohen, Ben Cooper, James M Robins, Stefan Ma, Lyn James, Gopal Gopalakrishna, Suok Kai Chew, Chorh Chuan Tan, Matthew H Samore, et al. Transmission dynamics and control of severe acute respiratory syndrome. *Science*, 300(5627):1966–1970, 2003.

- [11] Neil M Ferguson, Derek AT Cummings, Christophe Fraser, J C Cajka, P C Cooley, and D S Burke. Strategies for mitigating an influenza pandemic. *Nature*, 442(7101):448–452, 2006.
- [12] Lucas Böttcher, Mingtao Xia, and Tom Chou. Why case fatality ratios can be misleading: individual-and population-based mortality estimates and factors influencing them. *Physical Biology*, 17(6):065003, 2020.
- [13] M V de Oliveira Peres, R P de Oliveira, J A Achcar, and A A Nunes. Case-fatality rate by COVID-19: a hierarchical Bayesian analysis of countries in different regions of the world. *Brazilian Journal of Biometrics*, 40(2), 2022.
- [14] Justin J Slater, Aiyush Bansal, Harlan Campbell, Jeffrey S Rosenthal, Paul Gustafson, and Patrick E Brown. A bayesian approach to estimating COVID-19 incidence and infection fatality rates. *Biostatistics*, 25(2):354–384, 2024.
- [15] Hiroshi Nishiura, Don Klinkenberg, Mick Roberts, and J A P Heesterbeek. Early epidemiological assessment of the virulence of emerging infectious diseases: a case study of an influenza pandemic. *PLoS ONE*, 4(8):e6852, 2009.
- [16] Robert Verity, Lucy C Okell, Ilaria Dorigatti, Peter Winskill, Charles Whittaker, Natsuko Imai, Gina Cuomo-Dannenburg, Hayley Thompson, Patrick GT Walker, Han Fu, et al. Estimates of the severity of coronavirus disease 2019: a model-based analysis. *The Lancet Infectious Diseases*, 20(6):669–677, 2020.
- [17] Gary McLean, Jeremy Kamil, Benhur Lee, Penny Moore, Thomas F Schulz, Alexander Muik, Ugur Sahin, Özlem Türeci, and Shanti Pather. The impact of evolving SARS-CoV-2 mutations and variants on COVID-19 vaccines. *MBio*, 13(2):e02979–21, 2022.
- [18] Paul SF Yip, K F Lam, Eric HY Lau, P H Chau, K W Tsang, and Anne Chao. A comparison study of realtime fatality rates: severe acute respiratory syndrome in Hong Kong, Singapore, Taiwan, Toronto and Beijing, China. *Journal of the Royal Statistical Society Series A: Statistics in Society*, 168(1):233–243, 2005.
- [19] Paul SF Yip, Eric HY Lau, K F Lam, and R M Huggins. A chain multinomial model for estimating the real-time fatality rate of a disease, with an application to severe acute respiratory syndrome. *American Journal of Epidemiology*, 161(7):700–706, 2005.
- [20] Yuanke Qu, Chun Yin Lee, and K F Lam. A novel method to monitor COVID-19 fatality rate in real-time, a key metric to guide public health policy. *Scientific Reports*, 12(1):18277, 2022.
- [21] Yuanke Qu, Chun Yin Lee, and K F Lam. A sequential test to compare the real-time fatality rates of a disease among multiple groups with an application to COVID-19 data. *Statistical Methods in Medical Research*, 31(2):348–360, 2022.

- [22] Chuanbo Zhou, Jiaohong Fang, and Mingzhi Mao. A new analysis of real-time fatality rate in the initial stage of COVID-19. *Entropy*, 25(7):1028, 2023.
- [23] H Diaz, G España, N Castañeda, L Rodriguez, and F De la Hoz-Restrepo. Dynamical characteristics of the COVID-19 epidemic: Estimation from cases in Colombia. *International Journal of Infectious Diseases*, 105:26–31, 2021.
- [24] Yuanke Qu and Chun Yin Lee. Estimation of standardized real-time fatality rate for ongoing epidemics. *PLoS ONE*, 19(5):e0303861, 2024.
- [25] Andrew Gelman. Prior distributions for variance parameters in hierarchical models (comment). *Bayesian Analysis*, 1(3):515–534, 2006.
- [26] Oriol Abril-Pla, Victor Andreani, Colin Carroll, Lin Dong, Chris Fonnesebeck, Maxim Kochurov, Ravin Kumar, Junpeng Lao, Christian Luhmann, Osvaldo A Martin, et al. PyMC: A modern and comprehensive probabilistic programming framework in Python. *PeerJ Computer Science*, 9:e1516, 2023.
- [27] Alp Kucukelbir, Dustin Tran, Rajesh Ranganath, Andrew Gelman, and David M Blei. Automatic differentiation variational inference. *Journal of Machine Learning Research*, 18(1):430–474, 2017.
- [28] Nicholas G Reich, Justin Lessler, Derek AT Cummings, and Ron Brookmeyer. Estimating absolute and relative case fatality ratios from infectious disease surveillance data. *Biometrics*, 68(2):598–606, 2012.
- [29] Ian C Marschner. Estimating age-specific COVID-19 fatality risk and time to death by comparing population diagnosis and death patterns: Australian data. *BMC Medical Research Methodology*, 21(1):126, 2021.
- [30] Eunha Shim, Kenji Mizumoto, W Choi, and Gerardo Chowell. Estimating the risk of COVID-19 death during the course of the outbreak in Korea, February-May 2020. *Journal of Clinical Medicine*, 9(6):1641, 2020.
- [31] Kenji Mizumoto, Katsuma Kagaya, and Gerardo Chowell. Early epidemiological assessment of the transmission potential and virulence of coronavirus disease 2019 (COVID-19) in Wuhan City, China, January-February, 2020. *BMC Medicine*, 18(1):1–9, 2020.
- [32] Walter Sim. Japan confirms first case of infection from Wuhan coronavirus; Vietnam quarantines two tourists. <https://www.straitstimes.com/asia/east-asia/japan-confirms-first-case-of-infection-with-new-china-coronavirus>, 2020. Accessed: 2024-09-19.
- [33] NHK. Abe declares state of emergency for 7 prefectures. https://web.archive.org/web/20200407111617/https://www3.nhk.or.jp/nhkworld/en/news/20200407_43/, 2020a. Accessed: 2024-09-19.

- [34] NHK. Japan’s state of emergency extended nationwide. https://web.archive.org/web/20200417044037/https://www3.nhk.or.jp/nhkworld/en/news/20200417_01/, 2020b. Accessed: 2024-09-19.
- [35] NHK. PM Abe to lift state of emergency across Japan. https://web.archive.org/web/20200604041659/https://www3.nhk.or.jp/nhkworld/en/news/20200525_31/, 2020c. Accessed: 2024-09-19.
- [36] K Wortley. Japan injects US\$12.5 billion to restart domestic tourism. <https://www.ttgasia.com/2020/05/26/japan-injects-us12-5-billion-to-restart-domestic-tourism/>, 2020. Accessed: 2024-09-19.
- [37] Motoko Rich and Makiko Inoue. Japan Declares State of Emergency in Tokyo Area After Days of Hesitation. <https://www.nytimes.com/2021/01/07/world/asia/japan-tokyo-state-of-emergency.html>, 2021. Accessed: 2024-09-19.
- [38] VOA News. Japan begins COVID-19 vaccination efforts for citizens 65 and older. https://www.voanews.com/a/covid-19-pandemic_japan-begins-covid-19-vaccination-efforts-citizens-65-and-older/6204462.html, 2021. Accessed: 2024-09-19.
- [39] Statista. Japan: COVID-19 vaccination rate 2023. <https://www.statista.com/statistics/1239927/japan-covid-19-vaccination-rate/>, 2023. Accessed: 2024-09-19.
- [40] Kristin J Marks. Hospitalization of infants and children aged 0–4 years with laboratory-confirmed COVID-19—COVID-NET, 14 states, March 2020–February 2022. *MMWR. Morbidity and Mortality Weekly Report*, 71, 2022.
- [41] Butros M Dahu, Solaiman Khan, Wei Syuan Li, Xin Shu, Henok Woldu, Mihail Popescu, Lincoln R Sheets, and Grant J Scott. Demographic and time trend analysis of COVID-19 test results of Boone County, Missouri. *AMIA Summits on Translational Science Proceedings*, 2023:91, 2023.
- [42] Sumit Bhardwaj, Manohar Lal Choudhary, Mandeep S Chadha, Aarti Kinikar, Ashish Bavdekar, Nilesh Gujar, Pradeep Dcosta, Rajesh Kulkarni, Sanjay Bafna, Sonali Salvi, et al. Resurgence of respiratory syncytial virus infection during COVID-19 pandemic in Pune, India. *BMC Infectious Diseases*, 24(1):586, 2024.
- [43] Daji Xiong, L Zhang, G L Watson, P Sundin, T Bufford, J A Zoller, J Shamshoian, M A Suchard, and C M Ramirez. Pseudo-likelihood based logistic regression for estimating COVID-19 infection and case fatality rates by gender, race, and age in California. *Epidemics*, 33:100418, 2020.

- [44] N F Brazeau, R Verity, S Jenks, H Fu, C Whittaker, P Winskill, I Dorigatti, P G Walker, S Riley, R P Schnekenberg, et al. Estimating the COVID-19 infection fatality ratio accounting for seroreversion using statistical modelling. *Communications Medicine*, 2(1):54, 2022.
- [45] Yuki Toyoshima, Kouji Nemoto, Shinya Matsumoto, Yusuke Nakamura, and Kazuma Kiyotani. SARS-CoV-2 genomic variations associated with mortality rate of COVID-19. *Journal of Human Genetics*, 65(12):1075–1082, 2020.
- [46] V B Franceschi, G D Caldana, A de Menezes Mayer, G B Cybis, C A M Neves, P A G Ferrareze, M Demoliner, P R de Almeida, J S Gualarte, A W Hansen, et al. Genomic epidemiology of SARS-CoV-2 in Esteio, Rio Grande do Sul, Brazil. *BMC Genomics*, 22(1):371, 2021.
- [47] Babak Bakhshandeh, Zohreh Jahanafrooz, Alireza Abbasi, Morteza B Goli, M Sadeghi, Mohammad S Mottaqi, and M Zamani. Mutations in SARS-CoV-2; Consequences in structure, function, and pathogenicity of the virus. *Microbial Pathogenesis*, 154:104831, 2021.
- [48] Olushayo O Olu, Mary Lamunu, Miriam Nanyunja, Foday Dafee, Tete Samba, Noah Sempira, Fatu Kuti-George, F Z Abebe, B Sensasi, A Chimbaru, et al. Contact tracing during an outbreak of Ebola virus disease in the western area districts of Sierra Leone: lessons for future Ebola outbreak response. *Frontiers in Public Health*, 4:130, 2016.
- [49] Krzysztof Gogolewski, Błażej Miasojedow, Małgorzata Sadkowska-Todys, Michał Stepień, Urszula Demkow, Adam Lech, Ewa Szczurek, Daniel Rabaczynski, Magdalena Rosińska, and Anna Gambin. Data-driven case fatality rate estimation for the primary lineage of SARS-CoV-2 in Poland. *Methods*, 203:584–593, 2022.
- [50] Daniel Barry and J A Hartigan. A Bayesian analysis for change point problems. *Journal of the American Statistical Association*, 88(421):309–319, 1993.
- [51] K F Lam and Yuanke Qu. A sequential test for assessing the effectiveness of response strategies during an emerging epidemic. *Biometrical Journal*, 65(1):2100293, 2023.

Algorithm 1 Estimation procedure for BrtaCFR

Input: Surveillance data $\{c_t, d_t\}_{t=1}^T$, Probability mass of time onset to death $\{f_t\}_{t=1}^T$, Hyperparameters $(\tilde{\beta}, \sigma^2)$, Posterior sample size N .

Output: Point estimates and 95% credible intervals (CrI) for the real-time fatality rate p_t .

Initialize

Set prior mean $\tilde{\beta}_t \leftarrow \log[\text{cCFR}(t)/(1 - \text{cCFR}(t))]$.

Model Specification (in a probabilistic programming framework PyMC)

Define unconstrained parameters $\beta = (\beta_1, \dots, \beta_T)^\top$.

Specify priors for β :

Normal prior: $\beta_t \sim N(\tilde{\beta}_t, \sigma^2)$.

Fused LASSO prior: $|\beta_t - \beta_{t-1}| \sim \text{Laplace}(0, 1/\lambda)$.

Hyperprior: $\lambda \sim C^+(0, 1)$.

Take logit-transformation of fatality rate: $p_t \leftarrow 1/(1 + \exp(-\beta_t))$.

Calculate expected daily deaths: $\mu_t \leftarrow \sum_{j=0}^{t-1} p_{t-j} c_{t-j} f_{j+1}$.

Define likelihood for observed deaths: $d_t \sim \text{Poisson}(\mu_t)$.

Posterior Inference

Use ADVI to find an approximation $q(\beta)$ for the posterior $p(\beta|\mathbf{d}, \mathbf{c})$.

while the ELBO has not converged under 10^5 iterations **do**

Update variational parameters to maximize the ELBO.

end while

Draw N samples from the approximate posterior: $\beta^{(i)} \sim q(\beta)$ for $i = 1, \dots, N$.

Output Generation

for $i \in \{1, \dots, N\}$ **do**

Calculate the fatality rate vector $\mathbf{p}^{(i)} \leftarrow 1/(1 + \exp(-\beta^{(i)}))$.

end for

Set point estimate: $\text{BrtaCFR}(t) \leftarrow \frac{1}{N} \sum_{i=1}^N p_t^{(i)}$.

Set 95% CrI from 2.5th and 97.5th percentiles of $\{p_t^{(i)}\}_{i=1}^N$.

return $\text{BrtaCFR}(t)$ and 95% CrI.

Table 1: Six scenarios for the real-time fatality rate p_t with descriptions of their patterns.

Scenario	p_t	Pattern
A	0.034	Constant rate
B	$0.01 \cdot e^{0.012t}$	Exponentially increasing rate
C	$0.04 \cdot e^{0.016 \cdot I(t>60) \cdot \min(40, t-60)}$	Linearly increasing rate sandwiched with constant ends
D	$0.1 \cdot e^{-0.009 \cdot (t-70) \cdot I(t>70)}$	Constant rate followed by an exponential decline
E	$0.1 \cdot e^{-0.015 \cdot t-80 }$	Exponentially increasing rate followed by an exponential decline
F	$0.015 \cdot e^{0.018 \cdot t-120 }$	Exponentially decreasing rate followed by an exponential growth

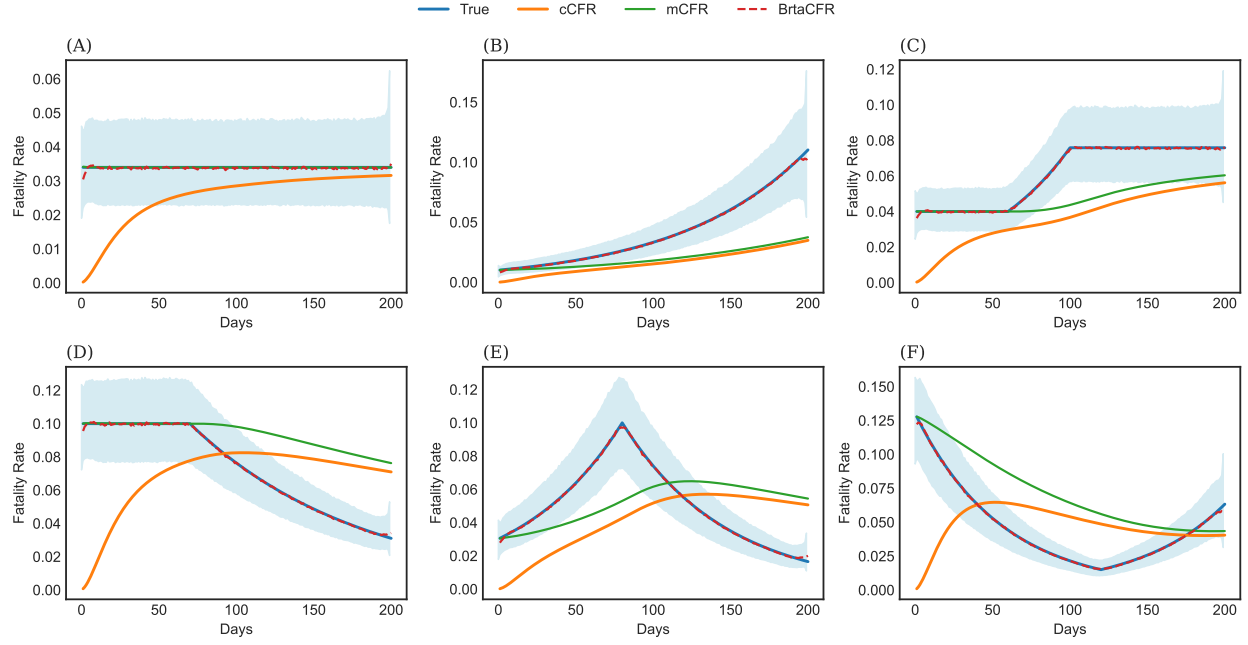


Figure 1: Simulation results of the three fatality rate estimators under Scenarios A–F. cCFR refers to the crude case fatality rate, and mCFR stands for the time-delay modified alternative, whereas BrtaCFR is the Bayesian real-time adjusted fatality rate estimator. The line for each estimator corresponds to the average estimated rate of over 1000 replications. The blue-shaded region refers to the averaged 95% credible interval of BrtaCFR constructed by the 2.5th and 97.5th percentiles of the approximated posterior distributions.

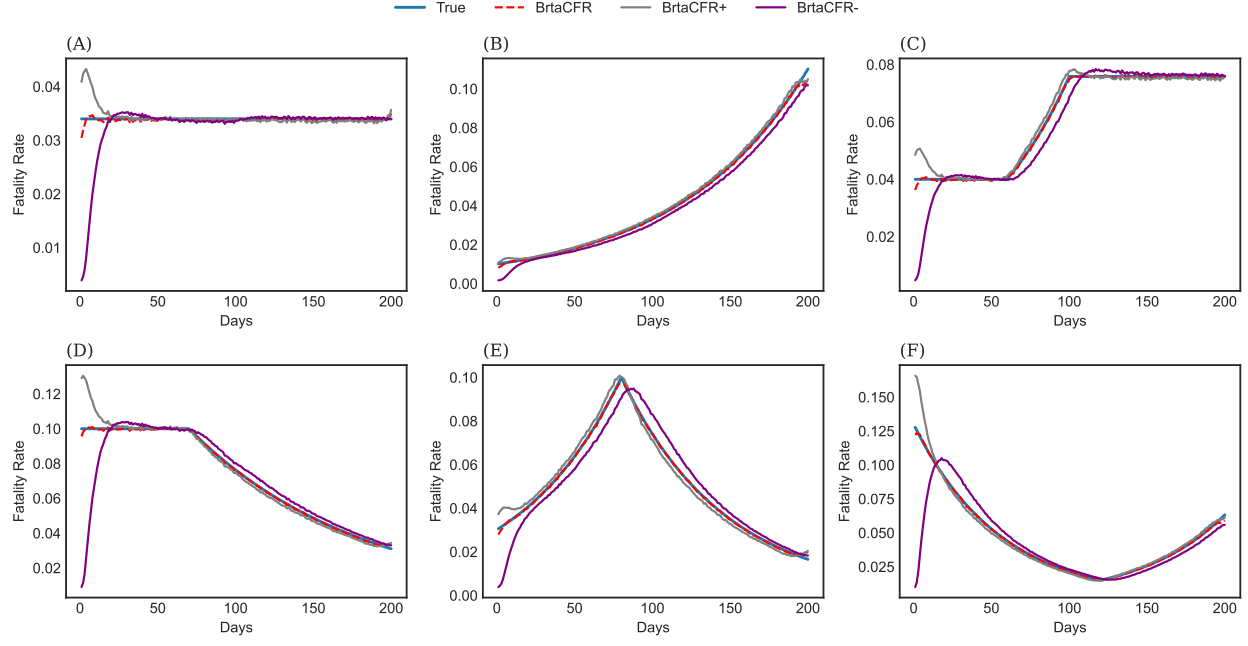


Figure 2: The simulation results depict the performance of the BrtaCFR under Scenarios A–F, with possibly misspecified mean δ and shape parameter γ in distribution F . The default setting for BrtaCFR is denoted by $(\delta, \gamma) = (15.43, 2.03)$. We further examine the performance of BrtaCFR+ and BrtaCFR–, for the settings $(\delta, \gamma) = (18.8, 2.03)$ and $(\delta, \gamma) = (10.1, 0.53)$, respectively.

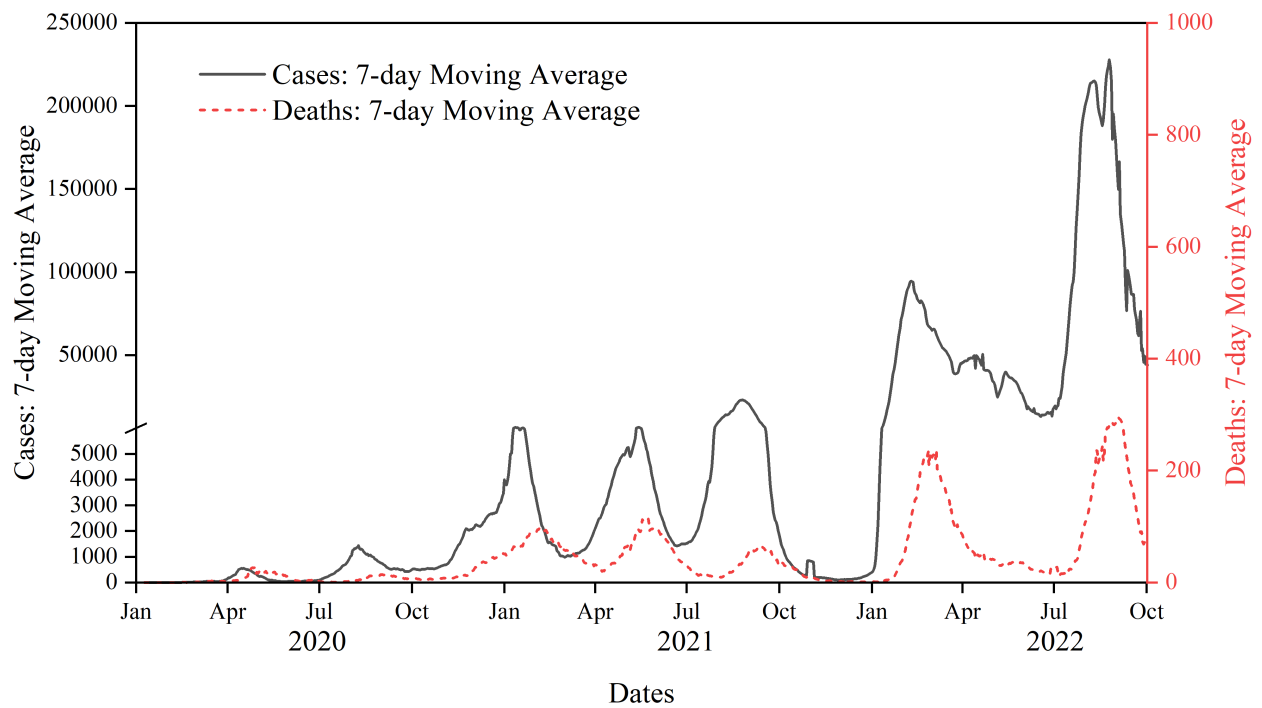


Figure 3: Seven-day moving average of daily numbers of confirmed cases and deaths in Japan from 3rd January 2020 to 31st October 2022.

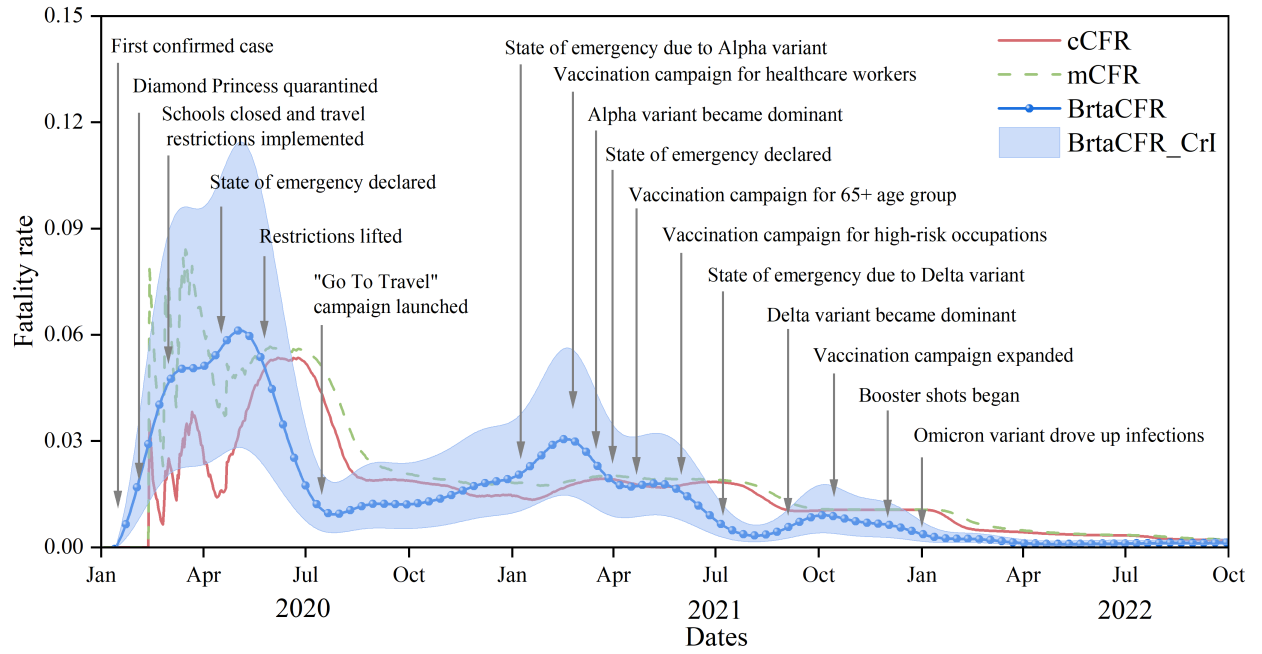


Figure 4: Different estimators of the case fatality rate (CFR) for COVID-19 data in Japan. cCFR refers to the crude case fatality rate, and mCFR stands for the time-delay modified alternative, whereas BrtaCFR is the Gaussian-kernel-smoothed Bayesian real-time adjusted fatality rate estimator.