



Markov switching modeling of covid-19 case counts and associated clinical and epidemiological characteristics in Kermanshah province, western Iran

Maryam Mohammadian-Khoshnoud¹, Fatemeh Khosravi Shadmani², Zohreh Manoochehri^{3*}

1. Non-Communicable Diseases Research Center, Hamadan University of Medical Sciences, Hamadan, Iran
2. Department of Social Welfare, School of Social Health, University of Social Welfare and Rehabilitation Sciences, Tehran, Iran
3. Substance Abuse Prevention Research Center, Research Institute for Health, Kermanshah University of Medical Sciences, Kermanshah, Iran

Received: 9 September 2026

Revised: 25 September 2026

Accepted: 26 September 2026

Published: 27 September 2026

Keywords	Abstract
COVID-19 Coronavirus Markov switching Time series Modeling	Background and Objectives: To effectively combat the novel coronavirus (COVID-19), it is crucial to have an accurate understanding of its epidemiological patterns and how it spreads within the community. In this context, a thorough grasp of statistical and epidemiological methods is more important than ever for policymakers and decision-makers. This study utilized a two-state Markov Switching model to analyze daily confirmed COVID-19 case counts, identify periods of outbreak and non-outbreak, and examine the overall clinical and epidemiological characteristics associated with daily case counts during these different periods. Methods: This time-series study included individuals who presented to hospitals in Kermanshah province with COVID-19-related symptoms from January 31, 2020, to January 5, 2021. Data were extracted from the MCMC system, which is affiliated with the Ministry of Health's emergency services. We used a two-state Markov Switching model to model daily COVID-19 case counts and examine their temporal association with daily aggregate clinical and epidemiological characteristics. Results: We recorded 9,255 confirmed COVID-19 cases, including 4,912 males and 4,343 females. The mean age was 54.65 years (median: 55.27 years). Among patients, 14.6% had hypertension, 8.8% had diabetes, and 8% had cardiovascular disease. In the outbreak regime (State 2), the daily proportion of confirmed cases with asthma was positively associated with daily case counts, whereas chronic neurological disorders (State 2) and chronic liver disease (State 1) showed negative associations. In the non-outbreak regime (State 1), contact history with a patient with coronavirus was positively associated with daily case counts. Conclusion: The Markov Switching approach provides a complementary framework for characterizing temporal variation in COVID-19 case counts and identifying outbreak and non-outbreak regimes. Further studies are needed to evaluate its applicability to infectious disease surveillance.

Highlights • Asthma, chronic liver disease, and cancer are the most important factors associated with COVID-19 outbreaks. • Contact history with an infected individual and hypertension positively affected daily case counts. • The transition probability matrix revealed high stability in both outbreak and non-outbreak states. • The model provides a suitable tool for monitoring and predicting emerging infectious diseases.	
How to cite this article:	Mohammadian-Khoshnoud M., Khosravi Shadmani F., Manoochehri Z. Markov switching modeling of covid-19 case counts and associated clinical and epidemiological characteristics in Kermanshah province, western Iran. Environ Med Toxicol. 2026;1(1):22-30. doi: 10.22034/emt.2026.601765.1006

* Corresponding author: Zohreh Manoochehri (E-mail: zohreh.manoochehri@kums.ac.ir)



This Open Access article is made available under the Creative Commons Attribution (CC BY 4.0) International License (<https://creativecommons.org/licenses/by/4.0/>), which allows unrestricted use, distribution, and reproduction in any medium, including commercial use, as long as the original work is properly cited.

Introduction

Based on phylogenetic analysis, coronaviruses belong to the subfamily Coronavirinae, comprising four genera: Alphacoronavirus, Betacoronavirus, Gammacoronavirus, and Deltacoronavirus. Among these, Alphacoronaviruses and Betacoronaviruses are responsible for respiratory diseases in humans [1, 2]. Fatal coronavirus infections that have emerged over the past two decades include Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and Middle East Respiratory Syndrome Coronavirus (MERS-CoV) [3]. SARS-CoV caused the SARS outbreak in 2002–2003 in Guangdong Province, China [1, 4, 5], while MERS-CoV was reported as the causative agent of severe respiratory illness in the Middle East in 2012 [6].

In late December 2019, physicians in Wuhan, China, identified unusual cases of pneumonia. On February 11, 2020, the World Health Organization (WHO) officially named the causative agent of this pneumonia as Coronavirus Disease 2019 (COVID-19) [7]. The term "coronavirus" derives from the Latin word "corona," meaning crown, which refers to the virus's appearance under electron microscopy [8]. The COVID-19 virus rapidly escalated into a global pandemic, infecting over 38 million people and causing more than 1 million deaths worldwide by October 2020 [9]. In Iran, the first official death from COVID-19 was reported on February 19, 2020, and the country has since faced significant challenges in controlling the outbreak [10].

While dozens of countries experienced increasing case numbers, the pattern of disease spread in China began to decline. Initially, some countries, including Iran and Italy, were disproportionately affected by the disease [11]. The virus represents an unprecedented global challenge due to its high transmissibility and lethality. In response to the rapid spread, thousands of deaths, and exponential growth projections, many countries implemented containment measures such as lockdowns and closures of public places [12, 13]. Effective measures to combat this novel virus must be based on a correct understanding of the epidemiological pattern and assessment of its spread in society. In these circumstances, the proper understanding and use of statistical and epidemiological indicators and methods are crucial for policymakers and decision-makers [14].

Various mathematical and statistical approaches have been developed to model and study the patterns of epidemics, including numerous forecasting models applied to the COVID-19 pandemic worldwide [15,

16]. One specific model used for predicting complex phenomena is time series models. In regression models where data have a time-series structure, parameter instability over time is common [17]. Markov Switching models are among the most popular non-linear time series models in this field [18]. These models are also referred to as regime-switching models and belong to the state-space model family. They consist of two types of equations: measurement equations and transition equations. The measurement equation defines how hidden states affect observed random variables, while the transition equation describes how state variables evolve over time [19].

Unlike conventional time-series models that generally assume a single underlying temporal structure, Markov Switching models allow the temporal process to change between unobserved regimes. This feature is particularly relevant to COVID-19 case-count series, in which temporal patterns may vary across different phases of the epidemic. Thus, Markov Switching models provide a useful complementary framework for representing temporal heterogeneity in COVID-19 case-count series. Accordingly, this study aimed to characterize temporal variation in daily confirmed COVID-19 case counts, identify outbreak and non-outbreak regimes using a two-state Markov Switching model, and examine their associations with daily aggregate clinical and epidemiological characteristics. Such information can assist public health organizations in making informed decisions to combat this disease [20].

Materials and Methods

Study population and Data Collection

This time-series study included all individuals who presented to hospitals in Kermanshah province with COVID-19-related symptoms from January 31, 2020 to January 5, 2021. Data were extracted from the MCMC system, which is affiliated with the Ministry of Health's emergency services in Iran. This system records clinical information for patients who presented to hospitals in Kermanshah province with symptoms suggestive of COVID-19, with diagnoses confirmed by CT scan and/or PCR testing. The outcome variable was the daily number of confirmed COVID-19 cases in Kermanshah province. Because a population denominator was not available, incidence rates were not calculated. Predictor variables included mean age, and proportions of cardiovascular disease, chronic blood disorders, chronic kidney disease, asthma, other

pulmonary diseases, chronic neurological disorders, history of hypertension, contact history with an infected individual, smoking, substance abuse, cancer, sex, chronic liver disease, and diabetes on a daily basis. Thus, the predictors used in the Markov Switching model represent daily aggregate characteristics of the confirmed case series, rather than individual-level predictors. They were included to assess whether the clinical and epidemiological composition of the observed daily cases was associated with differences in daily case-count patterns across the outbreak and non-outbreak regimes identified by the Markov Switching model. These associations were interpreted at the aggregate temporal level and were not intended to establish individual-level risk factors or causal relationships.

Statistical analysis

In this study a two-state autoregressive Markov Switching regression model was used to characterize temporal changes in daily COVID-19 case counts. The unobserved state variable represented two regimes: an outbreak state and a non-outbreak state. The Markov Switching framework allows the regression parameters to vary across these unobserved regimes, thereby accounting for potential changes in the temporal relationship between the response variable and the covariates. Markov Switching models, also known as regime-switching models, have a key feature: the switching mechanism is controlled by an unobserved state variable that follows a first-order Markov chain [21]. The Markov property assumes that the current state depends only on the immediately preceding state. In the present study, a two-state Markov Switching regression model was used to characterize temporal variation in daily confirmed COVID-19 case counts, with State 1 representing the non-outbreak regime and State 2 representing the outbreak regime. A Markov Switching regression model includes a time series Y_t ($t = 1, \dots, T$) and a sequence of covariates $x_1, \dots, x_T$, with the relationship between x_t and Y_t defined as follows:

$$Y_t = f^{(s_t)}(x_t) + \sigma_{s_t} \varepsilon_t \quad (1)$$

where ε_t represents the conditional error term, and s_t represents the unobserved state at time t , following an N-state Markov chain. In a two-state model, defining state 2 as the outbreak period and state 1 as the non-outbreak period, the long-run probability of being in the outbreak state at time $t+1$ can be calculated as [22]:

$$P[St+1 = 1] = (1 - P_{22})/(2 - P_{11} - P_{22}), \quad (2)$$

$$P[St+1 = 2] = (1 - P_{11})/(2 - P_{11} - P_{22}).$$

In the present analysis, the response variable Y_t represented the daily number of confirmed COVID-19 cases, while the covariates represented daily aggregate clinical and epidemiological characteristics of the confirmed case series.

Statistical analyses were performed using SPSS version 26 and R version 3.6.3. SPSS was used for data management and descriptive statistical analyses. The two-state Markov Switching model, including estimation of regime-specific coefficients and transition probabilities, was fitted in R. The “msmFit” function from the “MSwM” package in R was employed for fitting the Markov Switching model using the Expectation-Maximization (EM) algorithm.

Results

Descriptive Characteristics

From January 31, 2020 to January 5, 2021, a total of 9,255 confirmed COVID-19 cases were recorded in Kermanshah province, including 4,912 males (53.1%) and 4,343 females (46.9%). The maximum daily number of confirmed COVID-19 cases was 92, and the minimum was 1. The mean age of patients was 54.65 years (median: 55.27 years). Approximately 49% of patients reported a history of contact with a confirmed COVID-19 case. Among all patients, 14.6% had hypertension, 8.8% had diabetes, and 8% had cardiovascular disease. The monthly trend of COVID-19 cases in Kermanshah province is illustrated in Fig. 1.

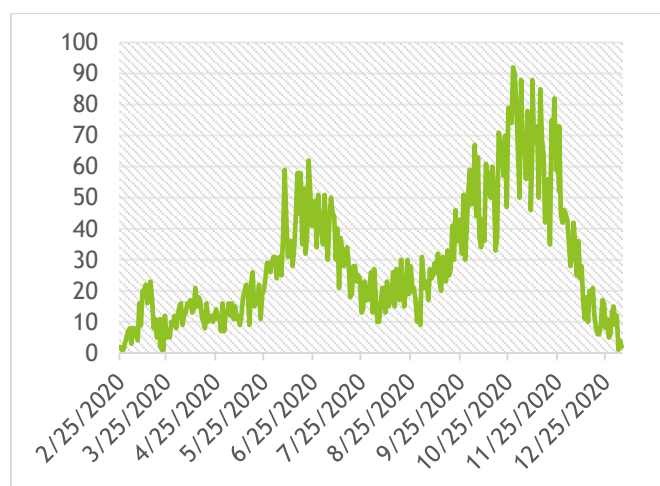


Fig. 1 Monthly trend chart of the number of COVID-19 cases 2020.

Markov Switching Model Results

A two-state Markov Switching model was fitted to the data. Daily aggregate clinical and epidemiological characteristics included mean age and proportions of cardiovascular disease, blood disorders, kidney disease, asthma, other pulmonary diseases, neurological disorders, hypertension, contact history with an infected individual, smoking, substance abuse, sex, liver disease, and diabetes. The response variable was the daily number of confirmed COVID-19 cases. The estimated coefficients for the two regimes are presented in Table 1. These variables therefore showed the greatest differences in their estimated associations between the outbreak and non-outbreak regimes.

In State 2, the daily proportion of confirmed cases with asthma showed a statistically significant positive association with daily case counts ($B = 3.066$, $SE = 1.359$, $p = 0.024$). Chronic neurological disorders showed a statistically significant negative association in State 2 ($B = -2.968$, $SE = 1.339$, $p = 0.027$). In State 1, contact history with a patient with coronavirus showed a statistically significant positive association with daily case counts ($B = 0.131$, $SE = 0.029$, $p < 0.001$). In State 1, chronic liver disease showed a statistically significant negative association with daily case counts ($B = -0.445$, $SE = 0.207$, $p = 0.031$). The other covariates did not show statistically significant associations in the corresponding regimes (Table 1). The smoothed and filtered state probabilities for regime 1 and regime 2 in the two-state model are shown in Figure 2. This figure illustrates the time-series trend of COVID-19 alongside the smoothed and filtered probabilities for regime 1. Smoothed probabilities were used to identify peaks and troughs, with a cut-off value of 0.5 for distinguishing between states 1 and 2. Filtered probabilities were computed using observations up to time t , while smoothed probabilities were computed using all observations.

The autocorrelation and partial autocorrelation plots of the residuals and squared residuals are presented in Fig. 3. The residual ACF and PACF plots were examined using their corresponding statistical confidence bounds. The diagnostic plots indicated evidence of residual serial correlation at several lags, particularly in State 2. Therefore, the residuals could not be considered completely independent. Q-Q plots were also examined to assess the normality of the residuals. The Q-Q plot in Fig. 4 shows that the normality assumption for the residuals was questionable. The transition probability matrix for the two-state Markov Switching model was:

$$\begin{bmatrix} P_{11} & P_{12} \\ P_{21} & P_{22} \end{bmatrix} = \begin{bmatrix} P_{11} & 1 - P_{11} \\ 1 - P_{22} & P_{22} \end{bmatrix} = \begin{bmatrix} 0.99 & 0.01 \\ 0.02 & 0.98 \end{bmatrix} \quad (3)$$

Thus, $P_{11} = 0.99$ (probability of staying in the non-outbreak state), $P_{22} = 0.98$ (probability of staying in the outbreak state), $P_{12} = 0.01$ (estimated long-run probability of transitioning from non-outbreak to outbreak), and $P_{21} = 0.02$ (estimated long-run probability of transitioning from outbreak to non-outbreak). The estimated long-run probability of an outbreak at time $t+1$ was:

$$P[S_{t+1} = 1] = \frac{1-0.98}{2-0.99-0.98} = 0.67 \quad (4)$$

$$P[S_{t+1} = 2] = 0.33 \quad (5)$$

The estimated long-run stationary probability of being in the outbreak regime (State 2) was 33.0%, compared with 67.0% for the non-outbreak regime (State 1). The expected duration of an outbreak was $1/(1 - P_{22}) = 50$ days, and the expected duration of a non-outbreak period was $1/(1 - P_{11}) = 100$ days. The fact that $P_{11} > P_{21}$ and $P_{22} > P_{12}$ indicates that both states (outbreak and non-outbreak) were persistent. Furthermore, $P_{21} > P_{12}$ suggests that prolonged non-outbreak periods may reduce the estimated long-run probability of subsequent outbreaks.

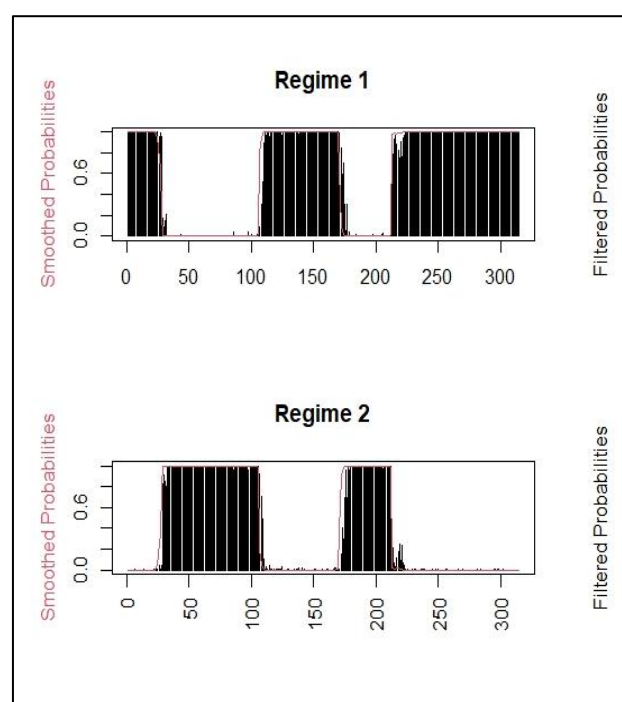


Fig. 2 Smoothed and filtered state probabilities for regimes one and two in the two-state model

Table 1 Results of fitting the two-state Markov switching model

Variables (state)	MSM with two states		
	B	SE	p-value
Intercept (1)	14.941	4.193	< 0.001*
Intercept (2)	34.597	44.943	0.441
Age (1)	-0.107	0.067	0.111
Age (2)	-0.109	0.494	0.826
Chronic blood disorders (1)	-0.106	0.353	0.764
Chronic blood disorders (2)	-1.244	1.923	0.518
Cardiovascular disease (1)	0.035	0.059	0.551
Cardiovascular disease (2)	-0.021	0.901	0.981
Chronic kidney disease (1)	0.051	0.203	0.803
Chronic kidney disease (2)	0.280	1.946	0.886
Asthma (1)	-0.093	0.173	0.592
Asthma (2)	3.066	1.359	0.024*
other pulmonary diseases except asthma (1)	0.190	0.167	0.255
other pulmonary diseases except asthma (2)	-0.093	2.075	0.964
Chronic neurological disorders (1)	0.039	0.346	0.910
Chronic neurological disorders (2)	-2.968	1.339	0.027*
History of hypertension (1)	0.095	0.057	0.093
History of hypertension (2)	0.002	0.030	0.956
Contact history with an infected individual (1)	0.131	0.029	< 0.001*
Contact history with an infected individual (2)	0.326	0.206	0.113
Cigarette smoking history (1)	0.147	0.164	0.370
Cigarette smoking history (2)	0.037	0.023	0.112
History of Drug Abuse (Opium) (1)	-0.136	0.197	0.490
History of Drug Abuse (Opium) (2)	1.398	1.017	0.169
Cancer (1)	-0.013	0.142	0.930
Cancer (2)	-1.279	0.673	0.057
Chronic liver disease (1)	-0.445	0.207	0.031*
Chronic liver disease (2)	1.332	6.063	0.826
Diabetes (1)	-0.075	0.049	0.137
Diabetes (2)	0.037	0.333	0.911
Gender ratio (1)	3.268	3.084	0.289
Gender ratio (2)	5.979	32.315	0.853

Note: (1) State 1: Non-outbreak; (2) State 2: Outbreak. * Indicates statistical significance at the 0.05 level ($p < 0.05$).

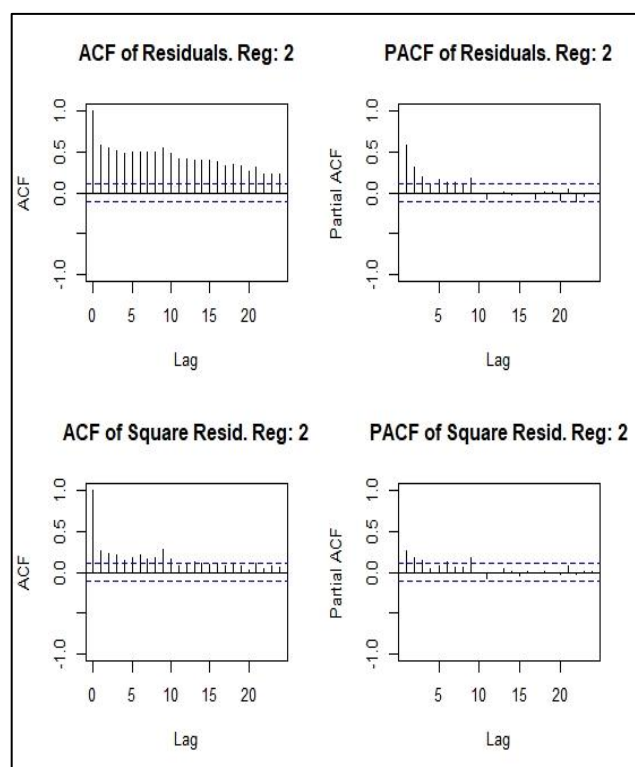


Fig. 1 Autocorrelation and partial autocorrelation plots of residuals and squared residuals for the two-state model

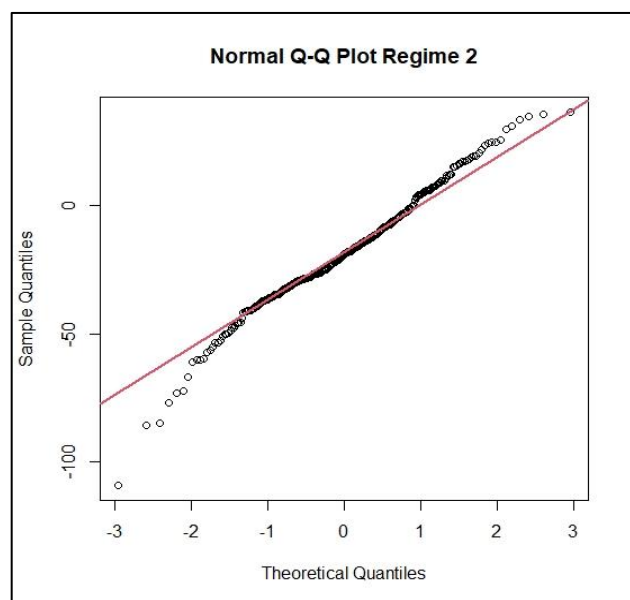


Fig. 4 Normal probability plot of model residuals in the two-state model

Discussion

This study employed a two-state Markov Switching model to decompose the temporal pattern of daily COVID-19 case counts in Kermanshah province into two distinct regimes—"outbreak" and "non-outbreak"—and to examine aggregate clinical and epidemiological characteristics associated with daily case counts within these regimes. The model identified

periods with different temporal patterns in the observed case-count series, reflecting the wave-like nature of the COVID-19 pandemic described in previous studies [23, 24]. However, these regimes were identified in-sample using the same data used for model estimation and were not independently validated. Therefore, the identified outbreak and non-outbreak periods should be interpreted as model-derived temporal regimes rather than externally validated epidemic phases. The application of Markov Switching models to time-series data, particularly in the presence of structural changes, was pioneered by Hamilton [25]. These models can identify hidden regime changes in time series—a capability often overlooked in classical linear models such as random-walk or fixed-parameter models [26]. In the context of COVID-19 modeling, studies have shown that dynamic and non-linear models can provide more accurate predictions than simple linear models, especially when transmission intensity varies over time [27].

Among the factors examined, the daily proportion of confirmed cases with asthma showed a positive association with daily case counts during the outbreak regime. This finding should be interpreted cautiously, as the present analysis does not estimate an individual-level association between asthma and COVID-19 infection or establish a causal relationship. Rather, it indicates that days with a higher proportion of confirmed cases reporting asthma were temporally associated with higher daily case counts within the outbreak regime. This finding aligns with studies indicating that underlying respiratory conditions can increase susceptibility to infection or severity of COVID-19 outcomes [28]. Contact history with an infected individual also showed a positive association with daily case counts in the non-outbreak regime, which is epidemiologically expected, as close contact is a primary transmission route for SARS-CoV-2 [29]. Conversely, some chronic conditions, including neurological disorders, and chronic liver disease, showed negative associations in certain regimes. This finding may be attributable to more protective behaviors adopted by these patients or stricter restrictions imposed on these vulnerable groups [30]. However, these findings should not be interpreted as protective effects. Several factors may potentially contribute to such temporal patterns, including differences in healthcare-seeking behavior, case ascertainment, clinical presentation, behavioral

responses, public-health restrictions, and other contextual factors. However, these factors were not directly measured or included in the present study. Therefore, these explanations should be considered hypothesis-generating rather than direct explanations supported by the study data.

From a statistical perspective, the residual diagnostics indicated serial correlation at several lags, particularly in State 2, as well as departures from normality. These findings indicate that some of the underlying assumptions of the Gaussian Markov Switching model were not fully satisfied. In addition, the discrete and potentially over dispersed nature of the daily COVID-19 case counts should be considered when interpreting the model estimates. In such settings, generalized models with alternative distributions, such as Poisson or negative binomial models, may provide alternative approaches [31]. The findings of this study have important practical applications. Early identification of entry into an outbreak regime can assist public health officials in implementing non-pharmaceutical interventions more rapidly. Epidemiological modeling studies have demonstrated that timely interventions can significantly reduce mortality burden and healthcare system strain [32].

Recent evidence further supports the value of regime-based approaches for COVID-19 surveillance, while highlighting their role as complementary rather than stand-alone approaches. Regime-switching models can capture shifts between different phases of COVID-19 case-count patterns and to provide an interpretable representation of changing epidemic states [33]. Other modeling approaches have also emphasized the importance of incorporating time-varying parameters, external data sources, and epidemiological information when characterizing changing transmission dynamics [34, 35]. Importantly, comparative evaluations of COVID-19 modeling approaches further indicate that no single modeling framework consistently outperforms all others across different epidemic waves and settings [36]. Taken together, these findings support the use of the Markov Switching framework as a complementary approach for characterizing temporal variation in daily COVID-19 case counts and identifying outbreak and non-outbreak regimes in a regional setting. Future studies could extend this approach by incorporating directly measured behavioral, public-health, healthcare-seeking, and virological information to better

characterize the contextual factors underlying temporal changes in COVID-19 case counts.

Limitations

This study has several limitations. First, the analysis was based on hospital-ascertained confirmed cases and lacked a population denominator; therefore, the findings represent daily case counts rather than population-based incidence. Changes in testing, case ascertainment, and reporting over time may also have influenced the observed patterns. Second, the clinical and epidemiological predictors were aggregated as daily proportions among confirmed cases, which may introduce ecological bias and limits individual-level or causal interpretation. Third, the Gaussian error specification does not explicitly account for the discrete and potentially over dispersed nature of the outcome. Finally, no formal out-of-sample forecasting evaluation or external validation was performed. Therefore, the findings should be considered primarily as an exploratory characterization of temporal regimes, and independent validation would be needed before broader monitoring or predictive applications.

Conclusion

In summary, the two-state Markov Switching model identified distinct outbreak and non-outbreak regimes in the temporal pattern of daily confirmed COVID-19 case counts in Kermanshah province. Several aggregate clinical and epidemiological characteristics showed statistically significant temporal associations with daily case counts within specific regimes, including asthma, chronic neurological disorders, chronic liver disease, and contact history. These associations should be interpreted at the aggregate temporal level and should not be considered individual-level risk factors, protective effects, or causal relationships.

Acknowledgements

The authors would like to express their gratitude to the staff of the MCMC system and the Ministry of Health for providing the data used in this study. We also thank the Clinical Research Development Center of Imam Khomeini and Mohammad Kermanshahi Hospitals for their administrative support.

Authors' Contributions

MMK contributed to the study concept and design, statistical analysis, and drafted the initial manuscript.

FKS contributed to data collection, investigation, and critical revision of the manuscript. ZM conceptualized the study, supervised the entire project, performed formal analysis, and critically revised the manuscript. All authors read and approved the final manuscript.

Data availability

The datasets used and/or analyzed during the current study available from the corresponding author on reasonable request.

Conflicts of interest

The authors declare that they have no competing or conflicting interests in conducting this study.

Funding

This study was funded by Vice-chancellor for Research and Technology, Kermanshah University of Medical Sciences (No. 4000541).

Ethics approval and consent to participate

The study's protocols were reviewed and approved by Kermanshah University of Medical Sciences' Ethics Committee (Ethics code: IR.KUMS.MED.REC.1404....). Also, each participating woman reviewed the study protocol and signed a consent form prior to being enrolled in the study.

References

- [1] Zhong N, Zheng B, Li Y, Poon L, Xie Z, Chan K, et al. Epidemiology and cause of severe acute respiratory syndrome (SARS) in Guangdong, People's Republic of China, in February, 2003. *Lancet*. 2003;362(9393):1353-1358.
- [2] Fouchier RA, Kuiken T, Schutten M, Van Amerongen G, Van Doornum GJ, Van Den Hoogen BG, et al. Koch's postulates fulfilled for SARS virus. *Nature*. 2003;423(6937):240.
- [3] Huang C, Wang Y, Li X, Ren L, Zhao J, Hu Y, et al. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. *Lancet*. 2020;395(10223):497-506.
- [4] Ksiazek TG, Erdman D, Goldsmith CS, Zaki SR, Peret T, Emery S, et al. A novel coronavirus associated with severe acute respiratory syndrome. *N Engl J Med*. 2003;348(20):1953-1966.
- [5] Drosten C, Günther S, Preiser W, Van Der Werf S, Brodt H-R, Becker S, et al. Identification of a novel coronavirus in patients with severe acute respiratory syndrome. *N Engl J Med*. 2003;348(20):1967-1976.
- [6] Zaki AM, Van Boheemen S, Bestebroer TM, Osterhaus AD, Fouchier RA. Isolation of a novel coronavirus from a man with pneumonia in Saudi Arabia. *N Engl J Med*. 2012;367(19):1814-1820.
- [7] Chang L, Yan Y, Wang L. Coronavirus disease 2019: coronaviruses and blood safety. *Transfus Med Rev*. 2020.
- [8] Hindson J. COVID-19: faecal-oral transmission? *Nat Rev Gastroenterol Hepatol*. 2020;17(5):259.
- [9] World Health Organization. COVID-19 Dashboard. Geneva: WHO; 2020. Available from: <https://covid19.who.int/>
- [10] Takian A, Raoofi A, Kazempour-Ardebili S. COVID-19 battle during the toughest sanctions against Iran. *Lancet*. 2020;395(10229):1035.
- [11] Tuite A, Bogoch I, Sherbo R, Watts A, Fisman D, Khan K. Estimation of COVID-2019 burden and potential for international dissemination of infection from Iran. *medRxiv*. 2020.
- [12] Sibley CG, Greaves LM, Satherley N, Wilson MS, Overall NC, Lee CH, et al. Effects of the COVID-19 pandemic and nationwide lockdown on trust, attitudes toward government, and well-being. *Am Psychol*. 2020.
- [13] Yoosefi Lebni J, Abbas J, Moradi F, Salahshoor MR, Chaboksavar F, Irandoost SF, et al. How the COVID-19 pandemic effected economic, social, political, and cultural factors: A lesson from Iran. *Int J Soc Psychiatry*. 2020;0020764020939984.
- [14] Mirmohammadkhani M, Paknazar F, Rashidy-pour A. Evaluation of the epidemiological pattern of COVID-19 applying basic reproduction number: An educational review article. *Koomesh*. 2020;22(3):373-379.
- [15] Gilbert M, Pullano G, Pinotti F, Valdano E, Poletto C, Boëlle P-Y, et al. Preparedness and vulnerability of African countries against importations of COVID-19: a modelling study. *Lancet*. 2020;395(10227):871-877.
- [16] Peng L, Yang W, Zhang D, Zhuge C, Hong L. Epidemic analysis of COVID-19 in China by dynamical modeling. *arXiv preprint arXiv:200206563*. 2020.
- [17] Kim C, Piger J, Startz R. Estimation of Markov regime-switching regression models with endogenous switching. *J Econom*. 2008;143(2):263-273.
- [18] Hamilton JD. A new approach to the economic analysis of nonstationary time series and the business cycle. *Econometrica*. 1989;57(2):357-384.
- [19] Lu M, Zeng D, Chen H. Prospective infectious disease outbreak detection using Markov switching models. *IEEE Trans Knowl Data Eng*. 2010;22(4).
- [20] Roda WC, Varughese MB, Han D, Li MY. Why is it difficult to accurately predict the COVID-19 epidemic? *Infect Dis Model*. 2020.
- [21] Goldfeld S, Quandt R. A Markov model for switching regressions. *J Econom*. 1973;1(1):3-15.
- [22] Langrock R, Kneib T, Glennie R, Michelot T. Markov-switching generalized additive models. *Stat Comput*. 2017;27(1):259-270.

- [23] World Health Organization. WHO Director-General's opening remarks at the media briefing on COVID-19 – 11 March 2020. Geneva: WHO; 2020.
- [24] World Health Organization. Coronavirus disease (COVID-19) Weekly Epidemiological Update. Geneva: WHO; 2020.
- [25] Hamilton JD. A new approach to the economic analysis of nonstationary time series and the business cycle. *Econometrica*. 1989;57(2):357-384.
- [26] Nelson CR, Plosser CI. Trends and random walks in macroeconomic time series. *J Monet Econ*. 1982;10(2):139-162.
- [27] Sanche S, Lin YT, Xu C, Romero-Severson E, Hengartner N, Ke R. High contagiousness and rapid spread of severe acute respiratory syndrome coronavirus 2. *Emerg Infect Dis*. 2020;26(7):1470-1477.
- [28] Guan WJ, Liang WH, Zhao Y, Liang HR, Chen ZS, Li YM, et al. Comorbidity and its impact on 1590 patients with COVID-19 in China: A nationwide analysis. *Eur Respir J*. 2020;55(5):2000547.
- [29] Centers for Disease Control and Prevention. Scientific Brief: SARS-CoV-2 Transmission. Atlanta: CDC; 2020.
- [30] Clark A, Jit M, Warren-Gash C, Guthrie B, Wang HH, Mercer SW, et al. Global, regional, and national estimates of the population at increased risk of severe COVID-19 due to underlying health conditions in 2020: a modelling study. *Lancet Glob Health*. 2020;8(8):e1003-e1017.
- [31] Bolker BM, Brooks ME, Clark CJ, Geange SW, Poulsen JR, Stevens MH, et al. Generalized linear mixed models: a practical guide for ecology and evolution. *Trends Ecol Evol*. 2009;24(3):127-135.
- [32] Ferguson NM, Laydon D, Nedjati-Gilani G, Imai N, Ainslie K, Baguelin M, et al. Impact of non-pharmaceutical interventions (NPIs) to reduce COVID-19 mortality and healthcare demand. London: Imperial College London; 2020.
- [33] Haimeri P, Hartl T. Modeling COVID-19 infection rates by regime-switching unobserved components models. *Econometrics*. 2023;11(2):10. doi:10.3390/econometrics11020010.
- [34] Rodríguez A, Kamarthi H, Agarwal P, Ho J, Patel M, Sapre S, et al. Machine learning for data-centric epidemic forecasting. *Nat Mach Intell*. 2024;6:1122–1131. doi:10.1038/s42256-024-00895-7.
- [35] Baccega D, Castagno P, Fernández Anta A, Sereno M, et al. Enhancing COVID-19 forecasting precision through the integration of compartmental models, machine learning and variants. *Sci Rep*. 2024;14:19220. doi:10.1038/s41598-024-69660-5.
- [36] Ayodeji IO. Forecasts of the mortality risk of COVID-19 using the Markov-switching autoregressive model: a case study of Nigeria (2020–2022). *Statistics in Transition New Series*. 2024;25(3):123–140. doi:10.59170/stattrans-2024-031.