Science of the Total Environment 729 (2020) 138817

Contents lists available at ScienceDirect

Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

Estimation of COVID-19 prevalence in Italy, Spain, and France

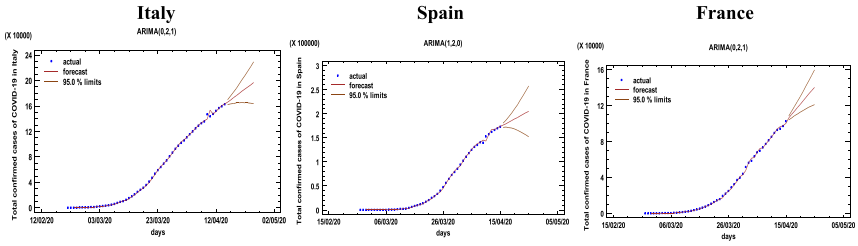
Zeynep Ceylan

Samsun University, Faculty of Engineering, Industrial Engineering Department, 55420 Samsun, Turkey

HIGHLIGHTS

- Europe has become the epicentre of the virus and hit the continent harder than China.
- The apparent mortality rate of COVID-19 is approximately 13% in Italy, 11% in Spain, and 15% in France.
- Time series models are significant in predicting the prevalence of the COVID-19 pandemic.
- ARIMA (0,2,1), ARIMA (1,2,0), and ARIMA (0,2,1) were chosen as the best models for Italy, Spain, and France, respectively.

GRAPHICAL ABSTRACT



ARTICLE INFO

Article history:
Received 10 April 2020
Received in revised form 17 April 2020
Accepted 17 April 2020
Available online 22 April 2020

Keywords:
COVID-19
Infection disease
Pandemic
Time series
ARIMA
Forecasting

ABSTRACT

At the end of December 2019, coronavirus disease 2019 (COVID-19) appeared in Wuhan city, China. As of April 15, 2020, >1.9 million COVID-19 cases were confirmed worldwide, including >120,000 deaths. There is an urgent need to monitor and predict COVID-19 prevalence to control this spread more effectively. Time series models are significant in predicting the impact of the COVID-19 outbreak and taking the necessary measures to respond to this crisis. In this study, Auto-Regressive Integrated Moving Average (ARIMA) models were developed to predict the epidemiological trend of COVID-19 prevalence of Italy, Spain, and France, the most affected countries of Europe. The prevalence data of COVID-19 from 21 February 2020 to 15 April 2020 were collected from the World Health Organization website. Several ARIMA models were formulated with different ARIMA parameters. ARIMA (0,2,1), ARIMA (1,2,0), and ARIMA (0,2,1) models with the lowest MAPE values (4.7520, 5.8486, and 5.6335) were selected as the best models for Italy, Spain, and France, respectively. This study shows that ARIMA models are suitable for predicting the prevalence of COVID-19 in the future. The results of the analysis can shed light on understanding the trends of the outbreak and give an idea of the epidemiological stage of these regions. Besides, the prediction of COVID-19 prevalence trends of Italy, Spain, and France can help take precautions and policy formulation for this epidemic in other countries.

1. Introduction

COVID-19 is defined as a new type of coronavirus that spreads rapidly from person to person and becomes a major epidemic that causes a great tragedy. COVID-19 has been identified from a family of zoonotic coronaviruses, such as the severe acute respiratory syndrome coronavirus (SARS-CoV) and the Middle East Respiratory Syndrome Coronavirus (MERS-CoV) seen in the past decade. The starting point of the virus is considered to be the Wuhan city of China, and the first fatal cases were reported in late 2019. At this point, this virus causes fatal effects, especially on the elderly and those with chronic diseases (Wang et al., 2020).

The disease has a very dynamic structure and spreads rapidly. Unfortunately, as of April 15, 2020, 123,010 deaths and approximately 2 million cases have been confirmed worldwide. The number of confirmed

E-mail address: zeynep.ceylan@samsun.edu.tr.

https://doi.org/10.1016/j.scitotenv.2020.138817
0048-9697/

cases varies due to differences in epidemiological surveillance and detection capacities between countries. However, it can be said that the disease has spread all over the world as of today. Since there is no treatment method determined for this type of virus yet, it requires the effective planning of the health infrastructure and services, where the rate of disease spread should be controlled. For this reason, the estimation of the total confirmed cases and possible new cases in the future is vital for managing and directing the demand to the health system. Mathematical and statistical modeling tools that can be used for making short and long-term case estimates to plan the number of additional materials and resources are needed to deal with the outbreak. Estimating the expected burden of disease is essential for public health officials to effectively and timely manage medical care and other resources needed to overcome the epidemic. Also, such estimates can direct the intensity and type of interventions needed to alleviate the outbreak (Zhang et al., 2020).

Recently, different statistical methods such as time series models (Kurbalija et al., 2014), multivariate linear regression (Thomson et al., 2006), grey forecasting models (Wang et al., 2018a; Zhang et al., 2017), backpropagation neural networks (Liu et al., 2019; Ren et al., 2013; Zhang et al., 2013), and simulation models (Nsoesie et al., 2013; Orbann et al., 2017) were used to predict epidemic cases. Epidemics are affected by many different factors. For this reason, the general spread of the outbreak is characterized by tendencies and randomness. Therefore, the mentioned statistical tools are insufficient to analyze the epidemic randomness, and the models are difficult to generalize.

The Automatic Regressive Integrated Moving Average (ARIMA) model has been successfully applied in the field of health as well as in different fields in the past due to its simple structure, fast applicability and ability to explain the data set (Cao et al., 2020). As seen in Table 1, ARIMA models have been successfully applied in the past to estimate the incidence and prevalence of influenza mortality, malaria incidence, hepatitis, and other infectious diseases. Besides, ARIMA models are widely used for time series prediction of epidemic diseases such as hemorrhagic fever with renal syndrome, dengue fever, and tuberculosis. ARIMA models are instrumental in modeling the temporal dependency structure of a time series, given the changing trends, periodic changes, and random distortions in the time series. It is relatively easy to explain to the end-user since ARIMA methods do not contain much mathematics or statistics. In this way, the end-user can have an idea of how the prediction model is developed and can rely more on the model during the decision-making process.

Table 1
Various studies on disease prevalence/incidence prediction using the ARIMA model.

Reference	Disease	Method(s)
(Guan et al., 2004)	HAV	ARIMA, ANNs
(Earnest et al., 2005)	SARS	ARIMA
(Gaudart et al., 2009)	Malaria	ARIMA
(Liu et al., 2011)	HFRS	ARIMA
(Zhang et al., 2013)	Typhoid Fever	SARIMA, BPNN, RBFNN, and ERNN
(Ren et al., 2013)	HEV	ARIMA, BPNN
(Nsoesie et al., 2013)	HPS	ARIMA
(Zheng et al., 2015)	Tuberculosis	ARIMA
(Wu et al., 2015)	HFRS	ARIMA, GRNN, and NARNN
(Zeng et al., 2016)	Pertussis	ARIMA, ETS
(Wei et al., 2016)	Hepatitis	ARIMA, GRNN
(Sun et al., 2018)	SFTS	ARIMA, NBM, and GAM
(Wang et al., 2018a)	HBV	ARIMA, GM (1,1)
(Wang et al., 2018b)	Pertussis	SARIMA, NAR
(He and Tao, 2018)	Influenza	ARIMA
(Wu et al., 2019)	Human Brucellosis	ARIMA, ERNN, and JNN
(Liu et al., 2019)	Pulmonary Tuberculosis	ARIMA, BPNN
(Chen et al., 2020)	Influenza	SARIMA
(Fang et al., 2020)	Infectious Diarrhea	ARIMA/X models, RF
(Polwiang, 2020)	Dengue Fever	ARIMA, ANN, and MPR
(Cao et al., 2020)	Brucellosis	ARIMA

HAV: Hepatitis A Virus, HBV: Hepatitis B Virus, HEV: Hepatitis E Virus, SARS: Severe Acute Respiratory Syndrome, HFRS: Hemorrhagic Fever with Renal Syndrome, HPS: Hantavirus Pulmonary Syndrome, SFTS: Severe Fever with Thrombocytopenia Syndrome, ANN: Artificial Neural Networks, GM (1,1): Grey Model, SARIMA: Seasonal Autoregressive Integrated Moving Average, ETS: Exponential Smoothing, BPNN: Back Propagation Neural Networks, NARNN: Nonlinear Autoregressive Neural Network, RBFNN: Radial Basis Function Neural Networks, GRNN: Generalized Regression Neural Network, ERNN: Elman Recurrent Neural Networks, NBM: Negative Binomial Regression Model, GAM: Generalized Additive Model, NAR: Nonlinear Autoregressive Network, JNN: Jordan Neural Networks, RF: Random Forest, MPR: Multivariate Poisson Regression.

In recent studies different models have been used to predict COVID-19 incidence, prevalence, and mortality rate in China. For example, Li et al. (2020) developed a function to predict the ongoing trend with data-driven analysis and estimate the outbreak size of the COVID-19 in China (Li et al., 2020). Roosa et al. (2020) used validated phenomenological models during previous outbreaks to create and evaluate short-term forecasts of the cumulative number of confirmed cases in Hubei, China (Roosa et al., 2020). Fanelli and Piazza (2020) analyzed the temporal dynamics of the COVID-19 pandemic in mainland China, Italy, and France (Fanelli and Piazza, 2020). Roda et al. (2020) compared standard SIR and SEIR frameworks to model the COVID-19 in Wuhan Province, China (Roda et al., 2020). Wu et al. (2020) predicted the spread of COVID-19 for the national and global scale, to evaluate the effect of the metropolitan-wide quarantine of Wuhan and its neighbours (Wu et al., 2020). Al-qaness et al. (2020) improved the Adaptive Neuro-Fuzzy Inference System (ANFIS) by applying an Enhanced Flower Pollination Algorithm using the Salp Swarm Algorithm to estimate the number of confirmed COVID-19 cases in China (Al-qaness et al., 2020). Anastassopoulou et al. (2020) studied on the estimation of the critical epidemiological parameters as well as the modeling and predicting the spread of the COVID-19 epidemic in Hubei, China (Anastassopoulou et al., 2020). Wang et al. (2020) developed the Patient Information Based Algorithm for estimating the death rate of COVID-19 in real-time using publicly available data (Wang et al., 2020).

In summary, there are many studies in the literature to predict the spread of COVID-19 in China. However, Europe has become the epicenter of the virus and hit the continent harder than China. As of April 15, 2020, the apparent mortality rate of COVID-19 is 4% in China, 13% in Italy, 11% in Spain, and 15% in France. Therefore, it is significant to analyze the situation of the COVID-19 epidemic and predict the prevalence trend, especially in Italy and the two most affected countries, France and Spain.

The aim of this study is to estimate the prevalence of COVID-19 in Italy, Spain, and France, where the virus spreads fastest and causes tragic results. The data analyzed in this study correspond to the period between 21 February 2020 and 15 April 2020. The data set was used to perform and analyze a case estimation model by applying different ARIMA models. Thus, in addition to enlightening the characteristics of the spread of the epidemic, it was aimed to provide authorities with realistic estimates for the peak time and intensity of the epidemic using models based on simple quantitative models. These models can help predict the health infrastructure and material needs that patients will need in these countries in the near future.

2. Methods

2.1. Data collection

The prevalence data of COVID-19 was taken from the WHO website (https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports/), and MS Excel was used to build a time-series database. Descriptive statistics of the COVID-19 data of the mentioned countries between 21/02/2020–15/04/2020 are given in Table 2. To create a stable and effective ARIMA model, at least 30 observations are required (Box et al., 2015). Therefore, in this study, a time series containing at least 45 data was used to predict COVID-19 prevalence of Italy, Spain,

Table 2
Descriptive statistics on the prevalence and incidence of COVID-19 in Italy, Spain, and France.

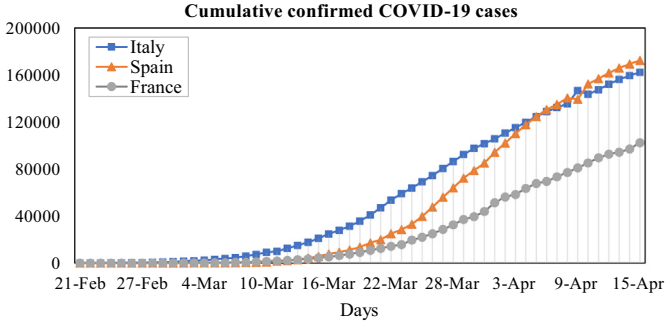
Case	Country	Mean	SE Mean	St. Dev	Minimum	Maximum	Skewness	Kurtosis
Prevalence	Italy	57,262	7664	56,840	3	162,488	0.53	−1.28
	Spain	54,075	8641	61,098	2	172,541	0.73	−1.06
	France	30,233	4822	34,097	12	102,533	0.82	−0.83
Incidence	Italy	3009	281	2065	6	6557	−0.15	−1.35
	Spain	3521	432	3026	7	9222	0.28	−1.35
	France	2092	269	1886	6	7500	0.69	−0.29

and France over the next ten days with 95% relative confidence intervals.

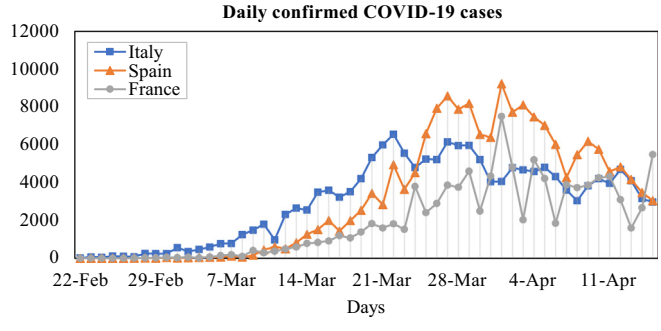
As seen from Fig. 1, the COVID-19 outbreak in Spain and France started later than Italy. Italy reported its first COVID-19 case on January 31, 2020. In Italy, the total number of confirmed cases of COVID-19 reported during the period is 162,488, with an average of 3009 new cases per day. The north of the country was most affected, and the region with the highest number of cases was Lombardy, which recorded 62,153 cases. The neighbouring regions of Emilia-Romagna and Piedmont recorded 21,029 and 18,229 cases, respectively. The overall prevalence of COVID-19 in Spain and France follow Italy, the hardest-hit country in Europe. Spain is the second country with the highest number of deaths in Europe. The first COVID-19 case in Spain was reported about a month after Italy, and since then the number of confirmed cases has jumped to about 172,541. In France, the other most affected European country, the first COVID-19 incident was reported on January 24, 2020, the number of deaths reached to 15,708, and the reported total confirmed cases hit to 102,533.

2.2. ARIMA models

A time series is simply expressed as a set of data points ordered in time (Fanoodi et al., 2019). Time series analysis aims to reveal reliable and meaningful statistics and use this knowledge to predict future values of the series (Liu et al., 2011; Elevli et al., 2016; He and Tao, 2018; Benvenuto et al., 2020). The ARIMA model was introduced by Box and Jenkins in the 1970s (Box et al., 2015). The ARIMA is one of the most used time series models as it takes into account changing trends, periodic changes and random disturbances in the time series. ARIMA is suitable for all kinds of data, including trend, seasonality,

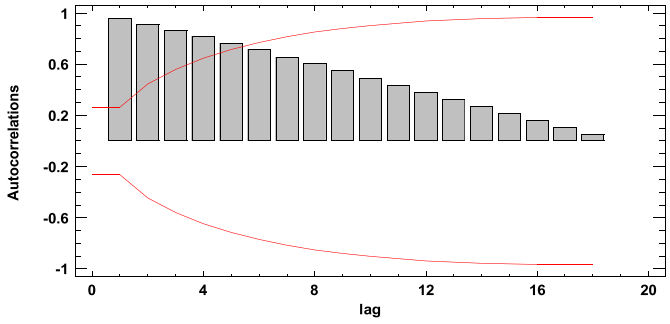


(a)

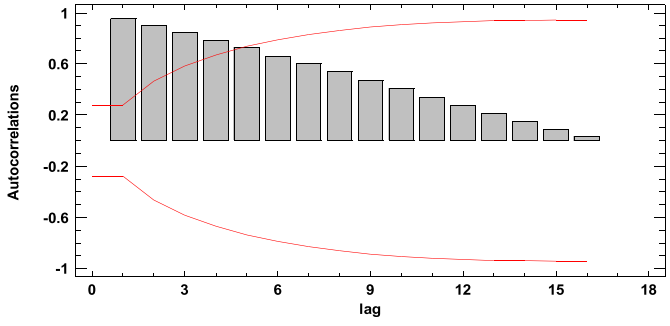


(b)

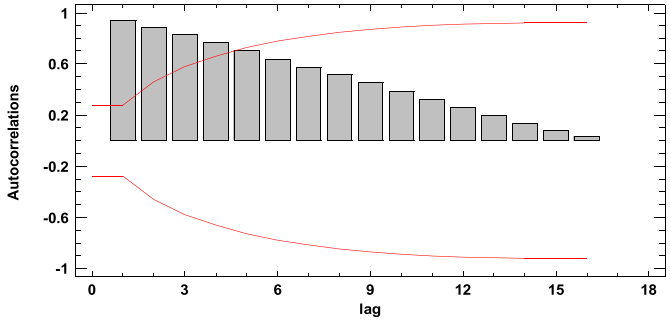
Fig. 1. The prevalence and incidence of the COVID-19 in Italy, Spain, and France.



(a)



(b)



(c)

Fig. 2. Estimated autocorrelations for (a) Italy, (b) Spain, and (c) France.

and cyclicity. It is also flexible and useful in modeling the temporal dependency structure of a time series.

ARIMA model is generally referred to as an ARIMA (p,d,q) where p is the order of autoregression, d is the degree of difference, and q is the order of moving average (Li et al., 2019). The ARIMA model can be modified to perform the function of an ARMA model as well as a simple AR, I or MA model. AR (p) model refers to the current value of the time series Y_t linearly in terms of its previous values Y_{t-1}, Y_{t-2},..,Y_{t-p} and the current residuals ε_t. MA (q) model refers to the current value of the time series Y_t linearly in terms of its current and previous residual series ε_{t-1},

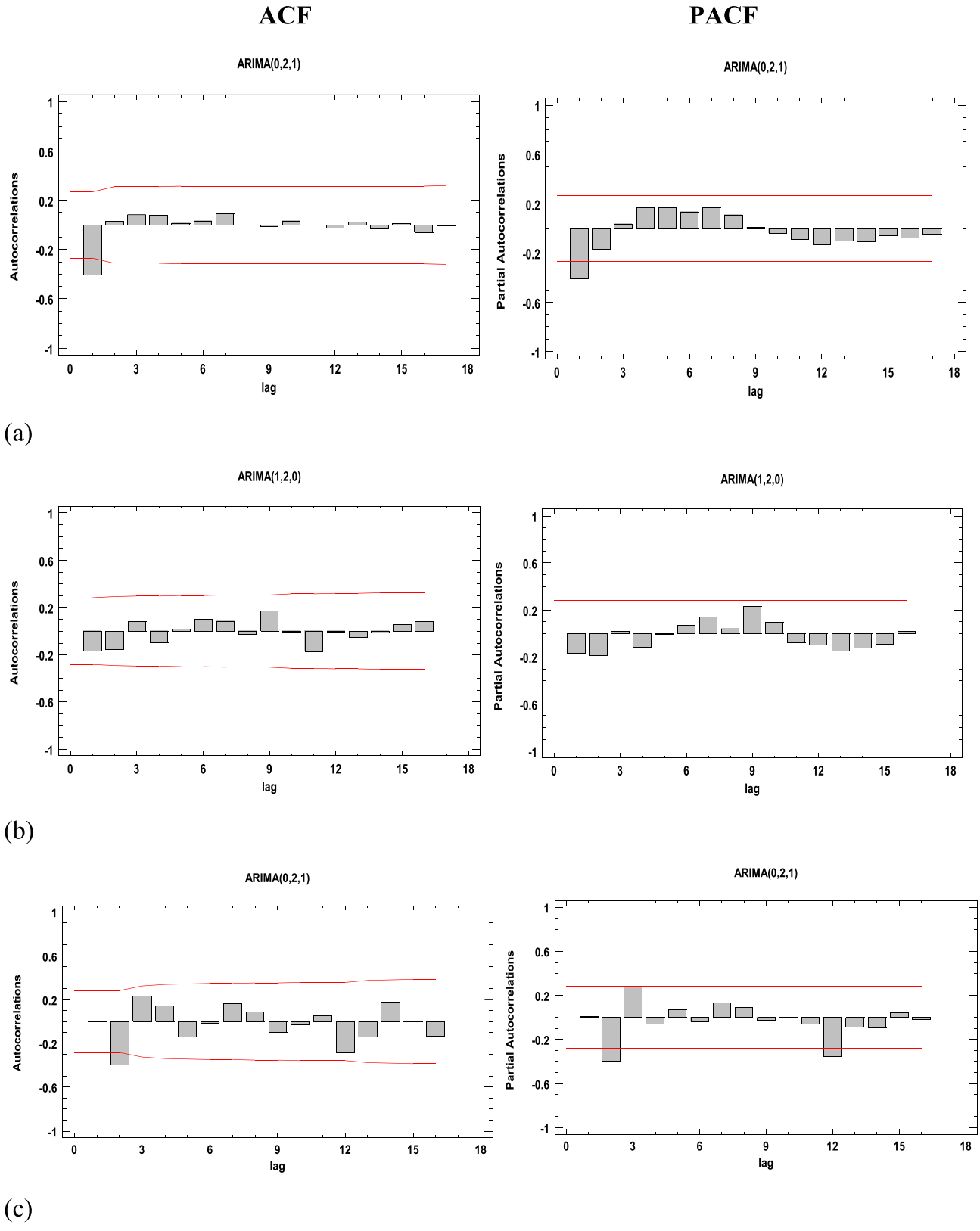


Fig. 3. The estimated ACF and PACF graphs to predict the epidemiological trend of COVID-19 prevalence for (a) Italy, (b) Spain, and (c) France.

Table 3
Comparison of tested ARIMA models.

Country	Model	RMSE	MAE	MAPE
Italy	ARIMA (0,2,1)	1821.1800	850.4290	4.7520
	ARIMA (1,2,0)	1939.5900	928.4860	4.8901
	ARIMA (2,2,0)	1729.4200	962.0600	5.1973
	ARIMA (1,2,1)	1687.1000	977.1580	5.2169
	ARIMA (3,2,1)	1654.6600	984.1700	5.4751
Spain	ARIMA (1,2,0)	2082.7000	1043.1400	5.8486
	ARIMA (2,2,0)	2037.0700	1123.8000	6.4824
	ARIMA (3,2,0)	2056.2100	1130.6600	6.5508
	ARIMA (1,2,2)	2054.1800	1150.7500	6.7158
	ARIMA (1,2,1)	2031.1200	1147.8900	6.6824
France	ARIMA (0,2,1)	1106.8900	660.2550	5.6335
	ARIMA (1,2,1)	1117.0700	664.5290	5.7458
	ARIMA (1,2,0)	1240.1300	733.2830	6.0335
	ARIMA (3,2,0)	972.5860	629.3750	6.2260
	ARIMA (2,2,1)	971.9250	635.8730	6.2467

$\varepsilon_{t-2},..,\varepsilon_{t-q}$.The general formula of AR (p) and MA (q) models can be expressed in Eqs. (1) and (2), respectively.

$$Y_t = \phi_1 Y_{t-1} + \phi_2 Y_{t-2} + \ldots + \phi_p Y_{t-p} + \varepsilon_t \quad (1)$$

$$Y_t = \theta_1 \varepsilon_{t-1} - \theta_2 \varepsilon_{t-2} - \ldots - \theta_q \varepsilon_{t-q} + \varepsilon_t \quad (2)$$

where ϕ and θ are the autoregressive and moving average parameters, respectively. Y_t is the observed value at time t and ε_t is the value of the random shock at time t. It is assumed to be independently and identically distributed with a mean of zero and a constant variance of σ^2. ARMA(p,q) model is composed of AR and MA models, in which the current value of the time series is defined linearly in terms of its previous values as well as current and previous residual series. The ARMA(p,q) model can be presented as given in the Eq. (3).

$$Y_t = \alpha + \phi_1 Y_{t-1} + \phi_2 Y_{t-2} + \ldots + \phi_p Y_{t-p} + \varepsilon_t - \theta_1 \varepsilon_{t-1} - \theta_2 \varepsilon_{t-2} - \ldots - \theta_q \varepsilon_{t-q} \quad (3)$$

where α is a constant, ε_{t-1} is the value of the previous random shock. The ARIMA model deals with non-stationary time series. The differenced stationary time series can be modelled as an ARMA model to perform the ARIMA model (He and Tao, 2018).

2.3. Model selection

The accuracy of a model can be tested by comparing the actual values with the predicted values. In this study, three performance criteria, namely Root Mean Square Error (RMSE), Mean Absolute Error (MAE) and Mean Absolute Percentage Error (MAPE) were applied to test the predictive accuracy of the developed ARIMA models. They are expressed mathematically in Eqs. (4) to (6).

$$RMSE = \sqrt{\frac{1}{n}\sum_{t=1}^{n} e_t^2} \quad (4)$$

$$MAE = \frac{1}{n}\sum_{t=1}^{n} |e_t| \quad (5)$$

$$MAPE = \frac{100\%}{n}\sum_{i=1}^{n}\left|\frac{e_t}{y_t}\right| \quad (6)$$

where y_t is the observed value at time point t, e_t is the difference between the observed and estimated values. Also, n is the number of time points. Lower RMSE, MAE, and MAPE values indicate a better fit of the data. All analyses were performed using STATGRAPHICS Centurion XVI. I software with a statistically significant level of $p < .05$.

3. Results and discussion

3.1. Forecasting the prevalence of COVID-19 pandemic using the ARIMA model

The ARIMA modeling procedure is composed of four iterative steps: assessment of the model, estimation of parameters, diagnostic checking, and prediction. The first step of the ARIMA model is to control whether the time series is stationary and seasonal. A time series is considered as stationary if its statistical properties such as mean, variance, autocorrelation are constant over time. The stationary of a time series observation is important as it will make it easier to get accurate estimates (Elevli et al., 2016). Time series plot, Autocorrelation Function (ACF), and Partial Autocorrelation Function (PACF) graphs were constructed to check the seasonality and stationarity. The ACF graph determines whether previous values in the series are related to the following values. The PACF graph finds out the degree of correlation between a variable and a lag of the said variable that is not explained by correlation at all low-order lags (He and Tao, 2018). Estimated autocorrelations for the time series of Italy, Spain, and France are shown in Fig. 2. Straight lines on the graph are two standard deviations limits and allow to detect non-zero correlations. Bars that extend beyond the lines show statistically significant autocorrelations for the COVID-19 data. Figs. 1 and 2 confirm that the overall prevalence of COVID-19 used in this study does not show seasonal patterns. However, the ACF plots in Fig. 2 shows that the prevalence of the COVID-19 is not stationary because autocorrelations reduce very slightly. Therefore, the first-order difference was taken to stabilize the mean of the COVID-19 prevalence. However, even after the first difference, it seems that the trends of all series not eliminated, so the second-order differences should be taken. All series became stationary after the second difference, and then parameters of ARIMA models were determined according to the ACF and PACF plots (see Appendix). In addition to the developed ARIMA models, different models were also created, and their performances were compared using various statistical tools. All statistical procedures were performed on the transformed COVID-19 data. ARIMA models with minimum MAPE values and statistically significant parameters were selected as the best models. Accordingly, the ARIMA (0,2,1), ARIMA (1,2,0), and ARIMA (0,2,1) models were chosen as the best models for Italy, Spain, and France, respectively. The models fitted the COVID-19 data reasonably well (Fig. 3, Table 3) with a minimum $MAPE_{Italy} = 4.752$, $MAPE_{Spain} = 5.849$, and $MAPE_{France} = 5.634$ values. Table 4 shows the parameter estimates for the best models. The p-values of the associated with the parameters are <0.05, so the terms are considerably different from zero at the 95.0% confidence level. The fitted and predicted values are presented in Fig. 4. As seen in Table 5, the next 10-day estimate of confirmed cases may be between 196,520–229,147 in Italy, 204,755–257,497 in Spain, and 140,320–159,619 in France.

Table 4
Parameters of ARIMA models.

Country	Best model	Parameters	Coefficient	Standart error	t-Statistic	p-Value
Italy	ARIMA (0,2,1)	MA (1)	0.6389	0.1340	4.7661	0.0000
Spain	ARIMA (1,2,0)	AR (1)	−0.6476	0.1112	−5.8229	0.0000
France	ARIMA (0,2,1)	MA (1)	0.6545	0.1083	6.0439	0.0000

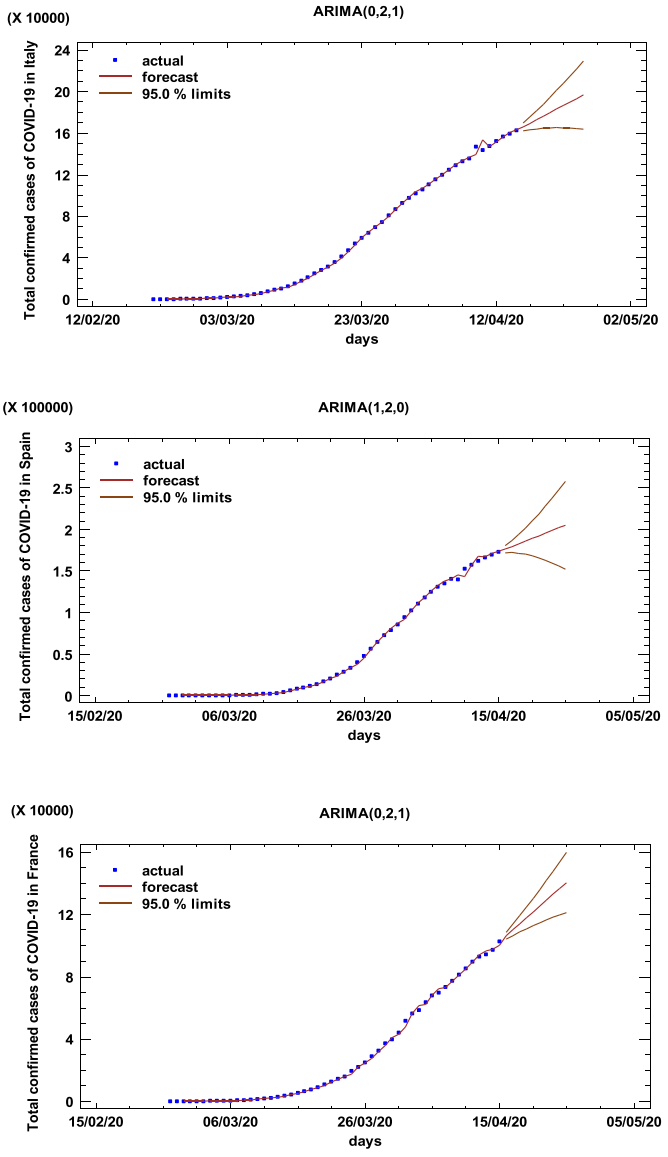


Fig. 4. Time-series plots for the best ARIMA models.

4. Discussion

Effective strategies are needed to prevent and control the spread of epidemics. Estimating the epidemiological trend of the prevalence of outbreaks is crucial for the allocation of medical resources, regulation of production activities, and even for the national economic development of countries. Thus, it is essential to create a reliable and suitable forecasting model that can help governments as a reference to decide on emergency macroeconomic strategies and medical resource allocation. Time series analysis is instrumental in developing hypotheses to understand the prevalence trend of various diseases and forecast the dynamics of observed phenomena, and then in the construction of a quality control system. ARIMA model is one of the most commonly used time series forecasting methods because of its simplicity and systematic structure and acceptable forecasting performance (Wang et al., 2018b). In this study, the current situation of the COVID-19 pandemic in Italy, Spain, and France was presented, and the ongoing trend and extent of the outbreak were estimated by the ARIMA model. To the best of our knowledge, this study is the first to implement ARIMA models to predict the prevalence of COVID-19 in Italy, Spain, and France.

There is great concern that European countries' health system capacity can effectively respond to the needs of infected patients who need intensive care for the COVID-19 pandemic. Especially in Italy, the number of patients infected since February 21 closely follows an exponential trend. Although the number of total confirmed cases of Italy is still increasing, the incidence of new confirmed cases is declining, and the government plans to return to normal life gradually. The daily new confirmed cases decreased to 2000–4500 over the last ten days. Meanwhile, Spain, Europe's second-worst-hit country with 18,056 deaths, has seen a drop in daily coronavirus deaths in the past five days. However, the total number of confirmed cases has overtaken Italy. On the other hand, there is no downward trend in new confirmed cases in France, and it seems that more days are needed to reach the plateau. This pattern will cause intensive care units to be at their maximum capacity. As a result, if the virus does not develop new mutations, the number of cases is expected to reach the plateau. Otherwise, clinical and social problems will be unmanageable, expected to result in disaster.

5. Conclusion

Forecasting the prevalence of the disease is important for health departments to strengthen surveillance systems and reallocate resources. Time series models play an important role in outbreak analysis and disease prediction. In this study, ARIMA time series models were applied to the overall prevalence of COVID-19 of three European countries most affected by COVID 19: Italy, Spain, and France. The results of the study can help politics and health authorities to plan and supply resources effectively, including staff, beds and intensive care facilities to manage the situation in these countries over the next few days and weeks. For more precise comparison and future perspectives, the data should be updated in real-time.

Table 5
Prediction of total confirmed cases of COVID-19 for the next ten days according to ARIMA models with 95% confidence interval.

Date	Italy			Spain			France		
	ARIMA (0,2,1)			ARIMA (1,2,0)			ARIMA (0,2,1)		
	Forecast	Lower limit	Upper limit	Forecast	Lower limit	Upper limit	Forecast	Lower limit	Upper limit
16/04/20	165,891	162,236	169,546	175,866	171,676	180,056	106,312	104,085	108,538
17/04/20	169,294	163,121	175,468	179,009	171,962	186,056	110,090	106,357	113,823
18/04/20	172,698	163,880	181,515	182,270	170,918	193,622	113,869	108,567	119,171
19/04/20	176,101	164,450	187,752	185,455	169,651	201,259	117,648	110,671	124,625
20/04/20	179,504	164,821	194,187	188,689	167,689	209,689	121,427	112,662	130,191
21/04/20	182,907	164,998	200,817	191,892	165,379	218,404	125,205	114,542	135,868
22/04/20	186,311	164,986	207,635	195,115	162,585	227,644	128,984	116,314	141,654
23/04/20	189,714	164,793	214,635	198,324	159,435	237,213	132,763	117,982	147,543
24/04/20	193,117	164,427	221,807	201,542	155,893	247,192	136,541	119,550	153,533
25/04/20	196,520	163,894	229,147	204,755	152,013	257,497	140,320	121,021	159,619

CRediT authorship contribution statement

Zeynep Ceylan: Writing - original draft, Writing - review & editing.

Acknowledgements

No funding to declare.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Appendix A. Supplementary material

Supplementary data to this article can be found online at https://doi.org/10.1016/j.scitotenv.2020.138817.

References

Al-qaness, M.A.A., Ewees, A.A., Fan, H., Aziz, Abd El, El, M.A., 2020. Optimization method for forecasting confirmed cases of COVID-19 in China. J. Clin. Med. 9, 674. https://doi.org/10.3390/jcm9030674.

Anastassopoulou, C., Russo, L., Tsakris, A., Siettos, C., 2020. Data-based analysis, modelling and forecasting of the COVID-19 outbreak. PLoS One 15, e0230405. https://doi.org/10.1371/journal.pone.0230405.

Benvenuto, D., Giovanetti, M., Vassallo, L., Angeletti, S., Ciccozzi, M., 2020. Data in brief application of the ARIMA model on the COVID- 2019 epidemic dataset. Data Br 29, 105340. https://doi.org/10.1016/j.dib.2020.105340.

Box, G.E., Jenkins, G.M., Reinsel, G.C., Ljung, G.M., 2015. Time Series Analysis: Forecasting and Control. John Wiley & Sons.

Cao, L. Ting, Liu, H. Hui, Li, J., Yin, X. Dong, Duan, Y., Wang, J., 2020. Relationship of meteorological factors and human brucellosis in Hebei province, China. Sci. Total Environ. 703, 135491. https://doi.org/10.1016/j.scitotenv.2019.135491.

Chen, Y., Leng, K., Lu, Y., Wen, L., Qi, Y., Gao, W., Chen, H., Bai, L., An, X., Sun, B., Wang, P., Dong, J., 2020. Epidemiological features and time-series analysis of influenza incidence in urban and rural areas of Shenyang, China, 2010-2018. Epidemiol. Infect. 148, e29. https://doi.org/10.1017/S0950268820000151.

Earnest, A., Chen, M.I., Ng, D., Leo, Y.S., 2005. Using autoregressive integrated moving average (ARIMA) models to predict and monitor the number of beds occupied during a SARS outbreak in a tertiary hospital in Singapore. BMC Health Serv. Res. 5, 1–8. https://doi.org/10.1186/1472-6963-5-36.

Elevli, S., Uzgören, N., Bingöl, D., Elevli, B., 2016. Drinking water quality control: control charts for turbidity and pH. Journal of Water, Sanitation and Hygiene for Development 6 (4), 511–518.

Fanelli, D., Piazza, F., 2020. Analysis and forecast of COVID-19 spreading in China, Italy and France. Chaos, Solitons and Fractals 134, 1–12. https://doi.org/10.1016/j.chaos.2020.109761.

Fang, X., Liu, W., Ai, J., He, M., Wu, Y., Shi, Y., Shen, W., Bao, C., 2020. Forecasting incidence of infectious diarrhea using random forest in Jiangsu Province, China. BMC Infect. Dis. 20, 1–8. https://doi.org/10.1186/s12879-020-4930-2.

Fanoodi, B., Malmir, B., Firouzi, F., 2019. Reducing demand uncertainty in the platelet supply chain through artificial neural networks and ARIMA models. Comput. Biol. Med. 113, 103415. https://doi.org/10.1016/j.compbiomed.2019.103415.

Gaudart, J., Touré, O., Dessay, N., Dicko, A.L., Ranque, S., Forest, L., Demongeot, J., Doumbo, O.K., 2009. Modelling malaria incidence with environmental dependency in a locality of Sudanese savannah area, Mali. Malar. J. 8. https://doi.org/10.1186/1475-2875-8-61.

Guan, P., Huang, D.S., Zhou, B. Sen, 2004. Forecasting model for the incidence of hepatitis a based on artificial neural network. World J. Gastroenterol. 10, 3579–3582. https://doi.org/10.3748/wjg.v10.i24.3579.

He, Z., Tao, H., 2018. International Journal of Infectious Diseases Epidemiology and ARIMA model of positive-rate of in fl uenza viruses among children in Wuhan, China: a nine-year retrospective study. Int. J. Infect. Dis. 74, 61–70. https://doi.org/10.1016/j.ijid.2018.07.003.

Kurbalija, V., Ivanovi, M., Schmidt, D., Lindemann, G., Trzebiatowski, V., Burkhard, H., Hinrichs, C., 2014. Time-series analysis in the medical domain: a study of Tacrolimus administration and influence on kidney graft function. Comput. Biol. Med. 50, 19–31. https://doi.org/10.1016/j.compbiomed.2014.04.007.

Li, X., Zhang, C., Zhang, B., Liu, K., 2019. A comparative time series analysis and modeling of aerosols in the contiguous United States and China. Sci. Total Environ. 690, 799–811. https://doi.org/10.1016/j.scitotenv.2019.07.072.

Li, Q., Feng, W., Quan, Y.H., 2020. Trend and forecasting of the COVID-19 outbreak in China. J. Inf. Secur. 80, 469–496. https://doi.org/10.1016/j.jinf.2020.02.014.

Liu, Q., Liu, X., Jiang, B., Yang, W., 2011. Forecasting incidence of hemorrhagic fever with renal syndrome in China using ARIMA model. BMC Infect. Dis. 11. https://doi.org/10.1186/1471-2334-11-218.

Liu, Q., Li, Z., Ji, Y., Martinez, L., Zia, U.H., Javaid, A., Lu, W., Wang, J., 2019. Forecasting the seasonality and trend of pulmonary tuberculosis in Jiangsu Province of China using advanced statistical time-series analyses. Infect. Drug Resist. 12, 2311–2322. https://doi.org/10.2147/IDR.S207809.

Nsoesie, E.O., Beckman, R.J., Shashaani, S., Nagaraj, K.S., Marathe, M.V., 2013. A simulation optimization approach to epidemic forecasting. PLoS One 8. https://doi.org/10.1371/journal.pone.0067164.

Orbann, C., Sattenspiel, L., Miller, E., Dimka, J., 2017. Defining epidemics in computer simulation models: how do definitions influence conclusions? Epidemics 19, 24–32. https://doi.org/10.1016/j.epidem.2016.12.001.

Polwiang, S., 2020. The time series seasonal patterns of dengue fever and associated weather variables in Bangkok (2003-2017). BMC Infect. Dis. 20, 208. https://doi.org/10.1186/s12879-020-4902-6.

Ren, H., Li, J., Yuan, Z.A., Hu, J.Y., Yu, Y., Lu, Y.H., 2013. The development of a combined mathematical model to forecast the incidence of hepatitis E in Shanghai, China. BMC Infect. Dis. 13, 1–6. https://doi.org/10.1186/1471-2334-13-421.

Roda, W.C., Varughese, M.B., Han, D., Li, M.Y., 2020. Why is it difficult to accurately predict the COVID-19 epidemic? Infect. Dis. Model. 5, 271–281.

Roosa, K., Lee, Y., Luo, R., Kirpich, A., Rothenberg, R., Hyman, J.M., Yan, P., Chowell, G., 2020. Real-time forecasts of the COVID-19 epidemic in China from February 5th to February 24th, 2020. Infect. Dis. Model. 5, 256–263. https://doi.org/10.1016/j.idm.2020.02.002.

Sun, J.M., Lu, L., Liu, K.K., Yang, J., Wu, H.X., Liu, Q.Y., 2018. Forecast of severe fever with thrombocytopenia syndrome incidence with meteorological factors. Sci. Total Environ. 626, 1188–1192. https://doi.org/10.1016/j.scitotenv.2018.01.196.

Thomson, M.C., Molesworth, A.M., Djingarey, M.H., Yameogo, K.R., Belanger, F., Cuevas, L.E., 2006. Potential of environmental models to predict meningitis epidemics in Africa. Trop. Med. Int. Heal. 11, 781–788. https://doi.org/10.1111/j.1365-3156.2006.01630.x.

Wang, Y. wen, Shen, Z. zhou, Jiang, Y., 2018a. Comparison of ARIMA and GM(1,1) models for prediction of hepatitis B in China. PLoS One 13, 1–11. https://doi.org/10.1371/journal.pone.0201987.

Wang, Y., Xu, C., Wang, Z., Zhang, S., Zhu, Y., Yuan, J., 2018b. Time series modeling of pertussis incidence in China from 2004 to 2018 with a novel wavelet based SARIMA-NAR hybrid model. PLoS One 13, 1–23. https://doi.org/10.1371/journal.pone.0208404.

Wang, L., Li, J., Guo, S., Xie, N., Yao, L., Day, S.W., Howard, S.C., Graff, J.C., Gu, T., 2020. J. ur of. Sci. Total Environ., 138394 https://doi.org/10.1016/j.scitotenv.2020.138394.

Wei, W., Jiang, J., Liang, H., Gao, L., Liang, B., Huang, J., Zang, N., Liao, Y., Yu, J., Lai, J., Qin, F., Su, J., Ye, L., Chen, H., 2016. Application of a combined model with autoregressive integrated moving average (ARIMA) and generalized regression neural network (GRNN) in forecasting hepatitis incidence in Heng County, China. PLoS One 11, e0156768. https://doi.org/10.1371/journal.pone.0156768.

Wu, W., Guo, J., An, S., Guan, P., Ren, Y., Xia, L., Zhou, B., 2015. Comparison of two hybrid models for forecasting the incidence of hemorrhagic fever with renal syndrome in Jiangsu Province, China. PLoS One 10, 1–13. https://doi.org/10.1371/journal.pone.0135492.

Wu, W., An, S.Y., Guan, P., Huang, D.S., Zhou, B. Sen, 2019. Time series analysis of human brucellosis in mainland China by using Elman and Jordan recurrent neural networks. BMC Infect. Dis. 19, 1–11. https://doi.org/10.1186/s12879-019-4028-x.

Wu, J.T., Leung, K., Leung, G.M., 2020. Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. Lancet 395, 689–697. https://doi.org/10.1016/S0140-6736(20)30260-9.

Zeng, Q., Li, D., Huang, G., Xia, J., Wang, X., Zhang, Y., Tang, W., Zhou, H., 2016. Time series analysis of temporal trends in the pertussis incidence in Mainland China from 2005 to 2016. Sci. Rep. 6, 1–8. https://doi.org/10.1038/srep32367.

Zhang, X., Liu, Y., Yang, M., Zhang, T., Young, A.A., Li, X., 2013. Comparative study of four time series methods in forecasting typhoid fever incidence in China. PLoS One 8. https://doi.org/10.1371/journal.pone.0063116.

Zhang, L., Wang, L., Zheng, Yanling, Wang, K., Zhang, X., Zheng, Yujian, 2017. Time prediction models for echinococcosis based on gray system theory and epidemic dynamics. Int. J. Environ. Res. Public Health 14. https://doi.org/10.3390/ijerph14030262.

Zhang, S., Diao, M., Yu, W., Pei, L., Lin, Z., Chen, D., 2020. International Journal of Infectious Diseases Estimation of the reproductive number of novel coronavirus (COVID-19) and the probable outbreak size on the Diamond Princess cruise ship: a data-driven analysis. Int. J. Infect. Dis. 93, 201–204. https://doi.org/10.1016/j.ijid.2020.02.033.

Zheng, Y.L., Zhang, L.P., Zhang, X.L., Wang, K., Zheng, Y.J., 2015. Forecast model analysis for the morbidity of tuberculosis in Xinjiang, China. PLoS One 10, 1–13. https://doi.org/10.1371/journal.pone.0116832.