

Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.

34

The significance of daily incidence and mortality cases due to COVID-19 in some African countries

Olusola Samuel Makinde¹, Bamidele Mustapha Oseni¹, Akinola Oladiran Adepetun¹, Olubukola Olayemi Olusola-Makinde², Gbenga Jacob Abiodun³

¹DEPARTMENT OF STATISTICS, FEDERAL UNIVERSITY OF TECHNOLOGY, AKURE, ONDO, NIGERIA; ²DEPARTMENT OF MICROBIOLOGY, FEDERAL UNIVERSITY OF TECHNOLOGY, AKURE, ONDO, NIGERIA; ³DEPARTMENT OF MATHEMATICS, SOUTHERN METHODIST UNIVERSITY, DALLAS, TX, UNITED STATES

1. Introduction

Coronaviruses are single-stranded positive-sense RNA viruses; they are about 32 kbp in length [1,2], and this size shows the viruses have some of the largest genomes. According to de Groot et al. [3], the International Committee on Taxonomy of Viruses stated that the family Coronaviridae presently comprises of four genera, and this is as a result of an upswing in its genome sequences' figure based on ecology studies of the wild. Of the four genera, species of Alphacoronavirus and Betacoronavirus can infect their mammalian hosts, while Gammacoronavirus and Deltacoronavirus species particularly infect the *avians* [4,5]. The viruses have olden ancestries and recently exhibit crossover happenings that may result in interspecies infection based on phylogeny research [6,7]. Majority of the virus strains are those that infect bats and birds. Therefore gene-level activities such as mutation and recombination occur in these reservoirs, which in turn propagates intraspecies transmission to other mammals including humans [1,4,8].

A novel coronavirus (severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2]) was first discovered in a cluster of patients with pneumonia [9] in Wuhan, China, on December 31, 2019. The rate of transmission has been causing serious destruction, generating intense publicity in media and public health concern worldwide [10]. Health systems of many African countries have experienced repeated outbreaks of other

preventable emerging and reemerging infectious diseases. The ill-preparedness of some countries played a significant role in the destructive 2014–16 Ebola virus epidemic [11] in West Africa to rapidly identify the infection and stop transmission [12–15]. Also, Aruna et al. [16] argued that response on the smouldering remains of the 2018–19 Ebola virus outbreak can be hindered in the Democratic Republic of Congo due to geography and sociopolitical instability.

With the current outbreak of coronavirus disease 2019 (COVID-19), African countries have intensified their efforts in detecting and isolating any imported cases of the disease. Many African countries have already introduced screening for the disease on arrivals at airports and some seaports. For example, the WHO [17] announced that Uganda quarantined more than 100 individuals who arrived at Entebbe International Airport, some at hospitals in Entebbe and Kampala, and others were confined in their homes. In Zambia, thermal body scanners have also been set up at all ports of entry to detect travelers showing symptoms of the virus. Kenya has introduced compulsory screening at all ports of entry and established isolation facilities and a rapid response team to handle suspected cases. South Africa has set up national and provincial response teams, designated 300 health officials to ports of entry and begun screening all travelers from China. The African Center for Disease Control (CDC), in collaboration with the US CDC, WHO, and the International Civil Aviation Authority, have trained many participants from across Africa on enhancing points-of-entry detection of COVID-19. Additional training and resources have been provided to Egypt and other at-risk countries for infection prevention and control in healthcare facilities, medical management of COVID-19, and risk communication and community engagement [17].

The index case of COVID-19 in Africa was announced on February 14, 2020, in Egypt with confirmation that a patient of foreign origin has been detected, and contact tracing subsequently identified 17 people who were quarantined in the homes. The African CDC, several other national CDCs, and public health institutes in collaboration with the WHO have increased preparedness efforts in adding countries to implement recommendations outlined by the WHO International Health Regulations (IHR) Emergency Committee. Some countries in Africa, including the Democratic Republic of Congo and Senegal, are also leveraging on the experience acquired in the containment of other epidemics.

Since the first case in Egypt, 51 African countries have announced the incidence of COVID-19 as of April 25, 2020, with a total of 29,036 confirmed cases and 1334 reported deaths. Other measures have also been put in place to either halt or prevent community transmission. Nigeria, for example, has declared a total lockdown in some of its states with a huge potential of community transmission while partial lockdown was imposed in some other states.

Generalized estimating equation (GEE) [18] is utilized in estimating the parameters of generalized linear model with a possible unknown correlation between outcomes. GEE model is a marginal model for longitudinal data that estimates population-averaged parameters. GEE model is an extension of generalized linear models to longitudinal or

clustered data, where observations are no longer independent. The added advantage of GEE approach, which makes it suitable for the analysis, is its flexibility in analyzing correlated responses. The GEE approach does not require correct specification of the distribution of the data. Lee and Choi [19] applied a GEE model with an independent error component to model the Texas hospital data controlling for cluster error within hospitals. When observations are independent, the GEE model becomes an independent estimating equation model.

This study focuses on examining the daily counts of reported incidence and mortality due to COVID-19 in African countries. This is to determine if measures taken by the government of African countries should be relaxed or sustained. It also provides answers to some questions on whether there is a relationship between the daily incidence and the number of reported deaths and whether there is an increasing or decreasing trend of the incidence and reported death cases in African countries and also highlights the variables that affect the COVID-19 mortality rates in Africa.

2. Literature review

Severity of COVID-19 in African countries may differ from that of Europe, China, and other parts of the world due to diverse factors, which can be epidemiologic, demographical, socioeconomical, or environmental [20]. The evolution of the disease in three African countries with different range of age distributions was examined by Van Zandvoort et al. [20] using the Susceptible-Exposed-Infectious-Recovered model framework, stratified by age. The model predicted that self-isolation of people exhibiting the symptoms of the disease and practices of general physical distancing may be unable to obviate the expected large epidemics, except when stringent lockdown measures are employed. Further predictions carried out by Zhao et al. [21] utilized the Maximum-Hasting (MH) parameter estimation method and the modified Susceptible-Exposed-Infectious-Recovered model to examine the possibility of controlling the epidemics by imposing three intervention scenarios (suppression, mitigation, and mildness) in some African countries. The results indicated that countries strictly utilizing the first scenario (suppression) are likely to control the epidemic in late April, while those utilizing the second scenario (mitigation) are likely to have a further 10 days delay before controlling the epidemic. Utilization of the last scenario (mildness) resulted in the epidemic being controlled by late May.

Recent studies on COVID-19 have majorly focused on building mathematical models, formulating statistical models, and finding clinical solution. A number of mathematical models have been presented in the literature. These include the studies of Li et al., Liang, and Panovska-Griffiths [22–24]. Li et al. [22] formulated a mathematical model for the incidence rate of the susceptible population and estimated COVID-19 infection rate. Li et al. [22] also formulated a time series model based on linear regression with auto-correlated errors for COVID-19 cases in Wuhan, China, and found that autoregressive

integrated moving average model of order 0,1 and 0 (that is, autoregressive integrated moving average [ARIMA] (0,1,0)) was optimal for modeling autocorrelated errors in the formulated time series model in terms of Bayesian information criterion. Liang [23] presented the propagation growth models of COVID-19, SARS-CoV and Middle East respiratory syndrome coronavirus (MERS-CoV) by comparing the growth rate and inhibition constant of the infectious diseases. The study revealed that the growth rates of SARS-CoV and MERS-CoV are about half that of the COVID-19 virus. Panovska-Griffiths [24] argued that just one mathematical model cannot solve all current COVID-19 crisis and that more mathematical models can be employed to solve the current COVID-19 crisis and its spread.

Using a statistical approach, Zhang et al. [25] estimated the dynamics of the net reproduction number of COVID-19 at the provincial level in China using a Bayesian approach. Hirk et al. [26] presented the statistics of the number of COVID-19 deaths, hospitalized cases, intensive-care cases, confirmed infections, and tested individuals, as well as the percentage of confirmed cases in Austria, available as of April 01, 2020, in comparison with the similar scenario in Iceland. Also, the true number of infected cases in Austria was estimated using the deCODE genetics study. Benvenuto et al. [27] formulated an ARIMA model of order p, d, and q on the COVID-2019 epidemic dataset to predict the trend of COVID-19 prevalence and incidence. The study identified ARIMA (1,0,4) as the optimal ARIMA model for the COVID-19 prevalence cases and ARIMA (1,0,3) as the optimal ARIMA model for the COVID-19 incidence cases. However, prevalence and incidence cases are count data. Time series model for count data is expected to produce a better result because the prevalence and incidence cases are count data. Time series model for count data is of and may exhibit some characteristics such as conditional heteroscedasticity. Also, analysis of daily COVID-19 mortality cases for some countries, for example, Africa, forms a longitudinal study.

3. Materials and methods

3.1 Data

The dataset utilized in this work was obtained from the European Centre for Disease Prevention and Control (ECDC) and is publicly available in https://www.ecdc.europa.eu/en/covid-19-pandemic. The dataset includes the cases and deaths from COVID-19 collated daily from health authorities worldwide by ECDC and is subjected to scrutiny, which ensures accuracy and reliability of the data. Other components of the data are the countries and territories of incidence, the continent, and population of the countries. The population data included in the dataset were from the World Bank [28].

Only countries with confirmed index cases were considered except for Eritrea that was dropped because the population statistic was not included in the dataset. To ensure that the data is suitable for the model utilized, daily values recorded from the index cases for each of the countries and territories were utilized. The time of incidence was coded in increasing order, with the index case coded as the initial case. Fig. 34.1 presents the



FIGURE 34.1 Plot of coronavirus disease 2019 (COVID-19) total incidence and mortality count in some African countries as at April 25, 2020.

COVID-19 total incidence and mortality counts in some African countries as at April 25, 2020. It was observed from Fig. 34.1 that Algeria, Egypt, Morocco, and South Africa experienced more COVID-19 incidence than other African countries. It can also be observed that Algeria, Egypt, and Morocco experienced more COVID-19 mortality counts than other African countries. Fig. 34.2 presents a bar plot showing African countries' length of days from the first incidence to April 25, 2020. It is shown in Fig. 34.2 that COVID-19 incidence cases were first reported in Egypt, Algeria, and Nigeria. COVID-19 incidence was recently reported in Sao Tome and Principe, South Sudan, and Malawi.

The following variables were considered in the data: the daily reported incidence cases, the reported mortality cases, and the population of each country. Figs. 34.3 and 34.4 present the plots of reported incidence cases and the daily reported mortality cases, respectively, over the study periods of some selected countries in Africa. It can be inferred from the plots that there are upward trends in daily reported COVID-19 incidence cases and the daily COVID-19 mortality cases in some African countries.

3.2 Methods

Mann-Kendall test [29-31] can be employed to statistically check if there is a monotonic upward or downward trend of the daily COVID-19 incidence count and the daily number of COVID-19 deaths over time in some African countries. A monotonic upward trend of the daily COVID-19 incidence count implies that the count consistently increases through time. Similarly, a monotonic downward trend of the daily COVID-19 incidence count implies that the count consistently decreases through time. The Mann-Kendall test is a distribution-free test. The Mann-Kendall test rejects the null hypothesis that the data do not exhibit a monotonic trend if the *P*-value of the test is less than the chosen level of significance.

Liang and Zeger [18] introduced the notions of GEEs. GEE models are employed to analyze correlated data, either discrete or continuous [32]. An approach based on GEEs [18] is used to analyze the mortality rates due to COVID-19 in some African countries. Suppose y_{jt} denotes the daily COVID-19 mortality cases in some African countries and x_{jt} is a vector of time from the day of a country's first incidence, country's population, and daily reported COVID-19 cases observed at time $t = 1, 2, ..., n_j$ among African countries j = 1, 2, ..., J. First, the distribution of y_{jt} is assumed normal with an identity link. The GEE model accounts for the dependence of observations by specifying a working correlation matrix to improve the efficiency of the estimators of the parameters [33]. The choice of correlation structure in this study, such as independent, unstructured, user-defined, exchangeable, and AR(1), is based on the structure that minimizes the quasi-likelihood under the quasi-information criterion [34]. Parameters of GEE are estimated using an iterative quasi-scoring procedure.



FIGURE 34.2 Bar plot showing African countries' length of days under study.



FIGURE 34.3 Plot of the daily count of COVID-19 incidence in some selected countries in Africa from the first record of incidence to April 25, 2020.



FIGURE 34.4 Plot of the daily COVID-19 mortality cases in some selected countries in Africa from the first record of incidence to April 25, 2020.

4. Results and discussion

4.1 Analysis of daily reported COVID-19 incidence cases

The Kruskal-Wallis test is applied to test if daily reported COVID-19 cases across the countries in Africa, except Eritrea, are significantly different. The daily reported COVID-19 cases across the African countries are significantly different (*P*-value < 2.22e-16) over the study period. The incidence case patterns are different among African countries.

Incidence cases in some African countries such as Ghana, Egypt, Nigeria, and South Africa show upward trends. Similarly, there is upward trend in the reported death cases in Egypt, Nigeria, and South Africa, among other countries. Significance of the upward and downward trends of daily reported COVID-19 cases was examined in some of the countries using the Mann-Kendall test. The test checks if each upward (or downward) trend of daily reported COVID-19 cases is statistically significant. Using the Mann-Kendall test, the daily reported COVID-19 cases of Nigeria and South Africa show statistically significant increasing trends (*P*-value < 2.22e-16) over the study period from February 28, 2020, to April 25, 2020. The daily reported COVID-19 cases of Cote d'Ivoire show statistically significant increasing trends (P-value = 1e-07) from March 12, 2020, to April 25, 2020. The daily reported COVID-19 cases of Egypt show statistically significant increasing trends from March 2, 2020, to March 26, 2020 (P-value = .003) and March 27, 2020, to April 25, 2020 (P-value = 7e-04). The daily reported COVID-19 cases in Algeria show statistically significant increasing trends from February 26, 2020, to April 4, 2020 (P-value <2.2e-16); April 5, 2020, to April 20, 2020 (P-value = .10); and April 20, 2020, to April 25, 2020 (P-value = .10). Also, the daily reported COVID-19 cases of Cameroun show statistically significant increasing trends from March 7, 2020, to April 4, 2020 (P-value = .01) and nonsignificant decreasing trends from April 4, 2020, to April 25, 2020 (P-value = .30); Burkina Faso shows statistically significant increasing trends from March 11, 2020, to April 12, 2020 (P-value = .003) and nonsignificant decreasing trends from April 4, 2020, to April 25, 2020 (P-value = .10); and Djibouti shows statistically significant increasing trends from March 19, 2020, to April 20, 2020 (P-value = 1e-07) and nonsignificant decreasing trends from April 20, 2020, to April 25, 2020 (P-value = .50).

4.2 Analysis of daily reported COVID-19 mortality cases

The measure of correlation between the daily reported COVID-19 cases and the daily reported COVID-19 mortality cases in African countries is 0.454 (*P*-value < 2.22×10^{-16}), while the measure of correlation between the daily reported COVID-19 cases and the population of African countries is 0.0.252 (*P*-value < 2.22×10^{-16}). Similarly, the measure of correlation between the daily reported COVID-19 cases and the population of African countries is 0.259 (*P*-value < 2.22×10^{-16}). The Kruskal-Wallis test shows the daily reported COVID-19 cases across the countries are statistically significantly different (*P*-value < 2.22×10^{-16}) over the study period. The daily reported COVID-19 cases of Nigeria and South Africa show statistically significant increasing trends (*P*-value < 2.22×10^{-16}) over the study period from February 28, 2020, to April 25, 2020. The daily reported COVID-19 cases of Cote d'Ivoire show statistically significant increasing trends (*P*-value = 1.1921×10^{-7}) from March 12, 2020, to April 25, 2020. The daily reported COVID-19 cases of Egypt show statistically significant increasing trends from March 2, 2020, to April 25, 2020 (*P*-value < 2.22×10^{-16}). The daily reported COVID-19 cases of Egypt show statistically significant increasing trends (*P*-value = 1.921×10^{-7}) from March 12, 2020, to April 25, 2020. The daily reported COVID-19 cases of Egypt show statistically significant increasing trends from March 2, 2020, to April 25, 2020 (*P*-value < 2.22×10^{-16}). The daily reported COVID-19 cases in Algeria show statistically significant increasing trends from March 2, 2020, to April 25, 2020 (*P*-value < 2.22×10^{-16}). The daily reported COVID-19 mortality cases in Algeria show statistically significant increasing trends

(P-value $< 2.22 \times 10^{-16}$) from February 26, 2020, to April 4, 2020 and statistically significant decreasing trends (*P*-value = .10) from April 20, 2020, to April 25, 2020. Also, the daily reported COVID-19 cases of Cameroun show statistically nonsignificant increasing trends from March 7, 2020, to April 25, 2020 (*P*-value = .01); Burkina Faso show statistically nonsignificant increasing trends from March 11, 2020, to April 25, 2020 (*P*-value = .003); and Djibouti show statistically significant increasing trends from March 19, 2020, to April 25, 2020 (*P*-value = 1.9073 $\times 10^{-6}$), among others.

4.3 Analyzing COVID-19 death rate using generalized estimating equation

First, it is pertinent to ascertain whether the COVID-19 mortality cases are dependent or not. The Ljung-Box test, which examines the null hypothesis of independence in a given time series, is employed. The test rejects the null hypothesis and concludes that the COVID-19 mortality cases are correlated. GEE with unstructured correlation structure and user-defined correlation structure could not be implemented for COVID-19 mortality cases because there are not enough predictors for GEE with unstructured and user-defined correlation structures. Table 34.1 presents a comparison of three correlation structures: independence, exchangeable, and autoregressive of order one (AR(1)) using three selection criteria. These criteria are correlation information criterion (CIC), quasi-likelihood under independence model criterion (QIC) and corrected quasi-likelihood under independence model criterion (QIC). CIC and QIC are employed to choose between the three correlation structures, given a set of models terms while QICC can be employed in choosing between two sets of model terms, given a correlation structure. It is shown in Table 34.1 that the optimal correlation structure for this data is AR(1). Agresti [35] argued that choosing carefully a working correlation may improve the efficiency of the GEE estimates.

Table 34.2 presents estimates of coefficients of generalized estimating equation model for the daily COVID-19 mortality rate in Africa. The estimates of coefficients of time and country population are significant. Specifically, the daily COVID-19 mortality rate was expected to increase by 7.42×10^{-8} % when time increased by 100%. Similarly, the daily COVID-19 mortality rate was expected to decrease by 1.99×10^{-14} % when country population increased by 100%. It was also found that time from the first day of

Variance structure	OIC	CIC	
	QIC		QICC
Independence	48.7	24.3	48.7
Exchangeable	27.9	13.9	27.9
AR1	23.4	11.7	23.5

Table 34.1Comparison of selection criteria for choosing the
optimal variance structure.

QIC, Quasi-likelihood under independence model criterion; CIC, correlation information criterion; QICC, quasi-likelihood under independence model criterion.

Variables	Estimate	Std orr	Wald	
Variables		500. 611		
Intercept	7.53×10^{-7}	9.03×10^{-7}	0.7	.4043
Time	7.42×10^{-8}	3.34×10^{-8}	4.94	.0263*
Daily incidence count	7.79×10^{-8}	4.81×10^{-8}	2.63	.105
Country population	-1.99×10^{-14}	6.32×10^{-15}	9.91	.0016**
Daily incidence count * time	-5.61×10^{-10}	7.71×10^{-10}	0.53	.4668

 Table 34.2
 Estimates of coefficients of generalized estimating equation model for the daily COVID-19 mortality rate in Africa.

Signif. codes: "***" 0.001, "**" 0.01, "*" 0.05, "." 0.1, " " 1.

Correlation structure = ar1.

Link = identity.

incidence was positively associated with daily COVID-19 mortality rates while country population was negatively associated with the daily COVID-19 mortality cases. The estimate of coefficient of the daily COVID-19 incidence count was not significant at 5% level of significance. Similarly, the estimate of coefficient of the daily COVID-19 incidence count by time was not significant at 5% level of significance.

5. Conclusion

African countries have been on heightened alert to diagnose, quarantine, and isolate any case of COVID-19. This study investigates the dependence among daily COVID-19 incidence count, mortality count, and each of human population and duration of incidence from the first record. It also provides an insight into the effect of human population and the number of days from the first record on daily COVID-19 death rate. It was observed that each of the daily COVID-19 incidence and death counts among African countries may not be independent. Results of the Ljung-Box test showed that the daily COVID-19 incidence and death counts among African countries were not independent, rather both are time-dependent. Analyzing the daily COVID-19 incidence and death counts over time requires more specialized analytic tools. Trend analysis of daily counts of COVID-19 incidence and deaths is presented over time. Also, the GEE, a flexible tool for analyzing longitudinal data, is employed to analyze the daily COVID-19 death rates in African countries. Findings from this study show that patterns of incidence cases among African countries are statistically different. There are significant monotone trends in the daily COVID-19 incidence and death counts of many countries in Africa. There is a positive weak linear relationship between the daily reported COVID-19 cases and the population of African countries. However, the magnitude of the observed association was particularly small. It was further deduced that the farther the number of days from the day of first incidence if the pandemic is not properly managed, the more the daily COVID-19 death rate in Africa. The limitation of this study is that the same population value was used for each country over the days under study. It is observed that the number of COVID-19 cases becomes double in 2–3 days for some countries with increasing COVID-19 cases. This may be attributed to the fact that there are little human intervention and relaxation of lockdown policy in the countries, for example, Nigeria.

References

- J. Cui, F. Li, Z.L. Shi, Origin and evolution of pathogenic coronaviruses, Nat. Rev. Microbiol. 17 (2019) 181–192.
- [2] D. Schoeman, B.C. Fielding, Coronavirus envelope protein: current knowledge, Virol. J. 16 (2019) 69.
- [3] R.J. de Groot, S.C. Baker, R. Baric, L. Enjuanes, A.E. Gorbalenya, K.V. Holmes, Family Coronaviridae, in: A.M.Q. King, M.J. Adams, E.B. Carstens, E.J. Lefkowitz (Eds.), Virus Taxonomy. Ninth Report of the International Committee on Taxonomy of Viruses, Elsevier Academic Press, 2012, pp. 806–828.
- [4] J.O. Wertheim, D.K.W. Chu, J.S.M. Peiris, S.L.K. Pond, L.L.M. Poon, A case for the ancient origin of coronaviruses, J. Virol. 87 (2013) 7039–7045.
- [5] H.K.H. Luk, X. Li, J. Fung, S.K.P. Lau, P.C.Y. Woo, Molecular epidemiology, evolution and phylogeny of SARS coronavirus, Infect. Genet. Evol. 71 (2019) 21–30.
- [6] S.K. Lau, K.S. Li, A.K. Tsang, C.T. Shek, M. Wang, G.K. Choi, R. Guo, B.H. Wong, R.W. Poon, C.S. Lam, S.Y. Wang, R.Y. Fan, K.H. Chan, B.J. Zheng, P.C. Woo, K.Y. Yuen, Recent transmission of a novel alphacoronavirus, bat coronavirus HKU10, from Leschenault's rousettes to pomona leaf-nosed bats: first evidence of interspecies transmission of coronavirus between bats of different suborders, J. Virol. 86 (21) (2012) 11906–11918.
- [7] R. Lu, X. Zhao, J. Li, P. Niu, B. Yang, H. Wu, W. Wang, H. Song, B. Huang, N. Zhu, Y. Bi, X. Ma, F. Zhan, L. Wang, T. Hu, H. Zhou, Z. Hu, W. Zhou, L. Zhao, J. Chen, Y. Meng, J. Wang, Y. Lin, J. Yuan, Z. Xie, J. Ma, W.J. Liu, D. Wang, W. Xu, E.C. Holmes, G.F. Gao, G. Wu, W. Chen, W. Shi, W. Tan, Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding, Lancet 395 (2020) 565–574.
- [8] D. Vijaykrishna, G.J.D. Smith, J.X. Zhang, J.S.M. Peiris, H. Chen, Y. Guan, Evolutionary insights into the ecology of coronaviruses, J. Virol. 81 (2007) 4012–4020.
- [9] Q. Li, X. Guan, P. Wu, X. Wang, L. Zhou, Y. Tong, R. Ren, K.S.M. Leung, E.H.Y. Lau, J.Y. Wong, X. Xing, N. Xiang, Y. Wu, C. Li, Q. Chen, D. Li, T. Liu, J. Zhao, M. Liu, W. Tu, C. Chen, L. Jin, R. Yang, Q. Wang, S. Zhou, R. Wang, H. Liu, Y. Luo, Y. Liu, G. Shao, H. Li, Z. Tao, Y. Yang, Z. Deng, B. Liu, Z. Ma, Y. Zhang, G. Guoqing Shi, T.T.Y. Lam, J.T. Wu, G.F. Gao, B.J. Cowling, B. Yang, G.M. Leung, Z. Feng, Early transmission dynamics in Wuhan, China, of novel coronavirus-infected pneumonia, N. Engl. J. Med. 382 (2020) 1199–1207.
- [10] G. Ippolito, D.S. Hui, F. Ntoumi, M. Maeurer, A. Zumla, Toning down the 2019-nCoV hype and restoring hope, Lancet Respir. Med. 8 (3) (2020) 230–231. https://doi.org/10.1016/S2213-2600(20) 30070-9.
- [11] WHO, Ebola Outbreak 2014–2016, 2020. Available from: www.who.int/csr/disease/ebola/en/ (Retrieved on 26 April 2020).
- [12] WHO, Ebola Virus Disease, 2020. https://www.afro.who.int/health-topics/ebola- virus-disease (Retrieved on 26 April 2020).
- [13] E.A. Largent, EBOLA and FDA: reviewing the response to the 2014 outbreak, to find lessons for the future, J. Law Biosci. 3 (3) (2016) 489–537. https://doi.org/10.1093/jlb/lsw046.
- [14] S.J. Hoffman, S.L. Silverberg, Delays in global disease outbreak responses: lessons from H1N1, Ebola, and Zika, Am. J. Publ. Health 108 (3) (2018) 329–333. https://doi.org/10.2105/AJPH.2017. 304245.

- [15] S.A. Omoleke, I. Mohammed, Y. Saidu, Ebola viral disease in West Africa: a threat to global health, economy and political stability, J. Publ. Health Afr. 7 (1) (2016) 534. https://doi.org/10.4081/jphia. 2016.534.
- [16] A. Aruna, P. Mbala, L. Minikulu, D. Mukadi, D. Bulemfu, F. Edidi, J. Bulabula, G. Tshapenda, J. Nsio, R. Kitenge, G. Mbuyi, C. Mwanzembe, J. Kombe, L. Lubula, J.C. Shako, M. Mossoko, F. Mulangu, A. Mutombo, E. Sana, Y. Tutu, L. Kabange, J. Makengo, F. Tshibinkufua, S. Ahuka-Mundeke, J. Muyembe, Ebola virus disease outbreak – Democratic Republic of the Congo, August 2018-November 2019, MMWR (Morb. Mortal. Wkly. Rep.) 68 (50) (2019) 1162–1165.
- [17] WHO, Management of Ill Travellers at Points of Entry–International Airports, Seaports and Ground Crossings–In The Context of COVID-19 Outbreak, 2020. Available from: https://www.who.int/ publications-detail/management-of-ill-travellers-at-points-of-entry-international-airports-seaportsand-ground-crossings-in-the-context-of-covid–19-outbreak (Retrieved on 26 April 2020).
- [18] K.-Y. Liang, S. Zeger, Longitudinal data analysis using generalized linear models, Biometrika 73 (1) (1986) 13–22. https://doi.org/10.1093/biomet/73.1.13.
- [19] J. Lee, J.-Y. Choi, Texas hospitals with higher health information technology expenditures have higher revenue: a longitudinal data analysis using a generalized estimating equation model, BMC Health Serv. Res. 16 (2016) 117. https://doi.org/10.1186/s12913-016-1367-9.
- [20] K. Van Zandvoort, C.I. Jarvis, C.A.B. Pearson, G.D. Nicholas, COMMID COVID-19 Working group, T.W. Russell, A.J. Kucharski, M. Jit, S. Flasche, R.M. Eggo, F. Checchi, Response Strategies for COVID-19 Epidemics in African Settings: A Mathematical Modelling Study, MedRxiv Preprint, 2020, pp. 1–39. https://doi.org/10.1101/2020.04.27.20081711.
- [21] Z. Zhao, X. Li, F. Liu, G. Zhu, C. Ma, L. Wang, Prediction of the COVID-19 spread in African countries and implications for prevention and control: a case study in South Africa, Egypt, Algeria, Nigeria, Senegal and Kenya, Sci. Total Environ. 729 (2020) 1–10.
- [22] Y. Li, B. Wang, R. Peng, C. Zhou, Y. Zhan, Z. Liu, X. Jiang, B. Zhao, Mathematical modeling and epidemic prediction of COVID-19 and its significance to epidemic prevention and control measures, Ann. Infect. Dis. Epidemiol. 5 (1) (2020) 1052.
- [23] K. Liang, Mathematical model of infection kinetics and its analysis for COVID-19, SARS and MERS, Infect. Genet. Evol. 82 (2020) 104306. https://doi.org/10.1016/j.meegid.2020.104306.
- [24] J. Panovska-Griffiths, Can mathematical modelling solve the current Covid-19 crisis? BMC Publ. Health 20 (2020) 551. https://doi.org/10.1186/s12889-020-08671-z.
- [25] J. Zhang, M. Litvinova, W. Wang, Y. Wang, X. Deng, X. Chen, M. Li, W. Zheng, L. Yi, X. Chen, Q. Wu, Y. Liang, X. Wang, J. Yang, K. Sun, I.M. Longini, M.E. Halloran, P. Wu, B.J. Cowling, S. Merler, C. Viboud, A. Vespignani, M. Ajelli, H. Yu, Evolving epidemiology and transmission dynamics of coronavirus disease 2019 outside Hubei province, China: a descriptive and modelling study, Lancet Infect. Dis (2020). https://doi.org/10.1016/S1473-3099(20)30230-9.
- [26] R. Hirk, G. Kastner, L. Vana, Investigating the dark figure of COVID-19 cases in Austria: borrowing from the deCODE genetics study in Iceland, Austrian J. Stat. 49 (2020) 1–17.
- [27] D. Benvenuto, M. Giovanetti, L. Vassallo, S. Angeletti, M. Ciccozzi, Application of the ARIMA model on the COVID-2019 epidemic dataset, Data Br. 29 (2020) 105340.
- [28] ECDC, European Centre for Disease Control, 2020. https://www.ecdc.europa.eu/en/covid-19pandemic (Retrieved on 26 April 2020).
- [29] H.B. Mann, Non-parametric tests against trend, Econometrica 13 (1945) 163-171.
- [30] M.G. Kendall, Rank Correlation Methods, fourth ed., Charles Griffin, London, 1975.
- [31] R.O. Gilbert, Statistical Methods for Environmental Pollution Monitoring, Wiley, NY, 1987.
- [32] S.L. Zeger, K.Y. Liang, P.S. Albert, Models for longitudinal data: a generalized estimating equation Approach, Biometrics 44 (4) (1988) 1049–1060.

- [33] A. Salazar, B. Ojeda, M. Dueñas, F. Fernández, I. Failde, Simple generalized estimating equations (GEEs) and weighted generalized estimating equations (WGEEs) in longitudinal studies with dropouts: guidelines and implementation in R, Stat. Med. 35 (19) (2016) 3424–3448. https://doi. org/10.1002/sim.6947.
- [34] J. Cui, QIC program and model selection in GEE analyses, Stata J. 7 (7) (2007) 209-220.
- [35] A. Agresti, Categorical Data Analysis, third ed., John Wiley and Sons, Inc., Hoboken, New Jersey, 2013.