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A Study of Morbidity and Mortality from COVID-19 in India

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Abstract

The recent Human Coronavirus 2019 (hCoV-19) pandemic has devastated the whole world and impacted all aspects of human life. One of the most comprehensively recorded data for this outbreak is the daily morbidities and mortalities record. The analysis of this dataset would provide insight into the pattern and progression of this disease. The present study focused on the quantitative investigation and descriptive statistical examination of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) as part of a series of evaluations for this epidemic in the primarily affected geopolitical regions. The year 2021 is worse than 2020 in terms of the recorded daily newly emerging cases and deaths, and there are no signs that there would be an improvement in 2022, as could be estimated from early warning signs, even if there could be an apparent decline in the outbreak waves. India is one of the major countries that have been adversely affected by this global pandemic. The present study addressed this nation as a detailed record of COVID-19 cases and deaths extracted from a chronologically arranged dataset for the newly emerged cases and deaths on a daily basis. Cumulative counts were calculated and logarithmically transformed. Two significant peaks - embracing multiple waves - were observed with tailing for morbidity and mortality, which were highly correlated. There were no signs of a recession in the outbreak census. However, relative calm periods between waves might be detected. There were rising trends in morbidities and mortalities with a clustering tendency upon examination of the run charts. The Morgan-Mercer-Flodin (MMF) model was found to demonstrate the best-fitting non-linear curve for the transformed cumulative database. Derivatization of the model equation demonstrated a factor that could be used in the assessment of the outbreak effect numerically to show influence on the impacted population.

Keywords: Derivatization; HCoV-19; Morbidity; Mortality; Morgan-Mercer-Flodin.

1. Introduction

The coronavirus that causes COVID-19 (coronavirus disease 2019), the respiratory condition that is the source of the continuing COVID-19 pandemic, is known as the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) [1, 2]. The virus was previously known as the 2019 novel coronavirus (2019-nCoV) as well as the human coronavirus 2019 [3–6] (HCoV-19 or hCoV-19) [7–9]. The World Health Organization first recognized the epidemic in Wuhan, Hubei, China, and on January 30, 2020, it was deemed a public health emergency of international concern. On March 11, 2020, it was declared a pandemic [10, 11]. SARS-CoV2 is a human-contagious positive-sense single-stranded RNA virus [12, 13].

The COVID-19 pandemic has created many challenges for governments and authorities around the world [14]. One of the key challenges is to understand the spread of the disease and predict its future course [15]. To do this,

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epidemiological models are often used [16]. However, these models typically require a large amount of data, which can be difficult to obtain in the early stages of an outbreak. Epidemiologists, modelers, and decision-makers are at the centre of the global debate on how to stop the spread of coronavirus in light of the COVID-19 pandemic. Real-time estimates of changes in case numbers, hospitalizations, and fatalities, the effects of public health policy, and knowing how to apply various non-pharmaceutical interventions effectively are the key hurdles that modelling approaches must overcome [17]. Currently, only rough predictions can be made about the COVID-19 pandemic because of three challenging factors in particular. First, the scope of the protective immunity is still unknown [18]. Second, the level of transmission and immunity among those who have no or few symptoms (including children) is crucial for making forecasts; if there is very little asymptomatic infection, the epidemic peak is most likely still some time off [19]. Third, despite physical distance restrictions and numerous reopening scenarios, it is still very difficult to detect and model contact rates between susceptible and infectious individuals [20]. Models must make assumptions about how people interact with one another, and they frequently base these assumptions on daily studies carried out in various nations at various times.

The outbreak of 2019-nCoV, caused by the novel coronavirus hCoV-19, has resulted in significant challenges for public health worldwide and stimulated extensive data collection of morbidity and mortality reports [21]. Comprehensive and multiple research works have been published internationally, expressing attempts to understand the dissemination and spreading of this disease within communities [22]. There are many simulators that are based on theoretical models that were considered for disease modelling [23]. Particularly more recent models should only be taken into consideration with greater scientific care due to the large amount of pre-print research that the COVID-19 pandemic has generated and driven [24]. The projection of mathematical infectious disease models for the coronavirus disease outbreak is called COVID-19 simulation models [25]. Most of these approaches have their own limitations.

Monitoring and assessing the influence of the epidemic in any geopolitical region is mandatory to track the progression of the disease [26]. With the implementation of suitable statistical tools and modelling, a quantitative evaluation of the incident could be measured to compare not only different political or geographical regions but also the effectiveness of the measures taken by authorities by contrasting the outcome before and after the actions taken within the population, such as herd immunization [27]. Public health measures could be assessed – provided the accuracy of the sample data collection – using factual recorded observations [28, 29]. Importantly, making policy during a pandemic might be quite difficult. Since COVID-19 is a new disease with enormous worldwide effects, decisions are made in a highly uncertain, complicated, and fast changing environment. It is contended that using concepts and ideas from contemporary decision theory, even informally, will make policymaking a more accountable and open process in such a setting, where people's lives and the economy are on the line [30]. Nevertheless, variation in responses from different geographical regions might be an issue of concern during epidemic periods [31]. Hence, attempts to understand the kinetics of the infectious disease by public health professionals should be mandatory.

Given the global nature of the outbreak, it is important to have a clear understanding of the disease in order to develop effective prevention and control strategies. To better grasp the key population health impact of the disease and its possible consequences, a novel statistical analysis was performed using data from the Humanitarian Data Exchange (HDX). This analysis used trending (control) charts to investigate the cumulative data and identify potential patterns that have stemmed from the reported cases and deaths database of COVID-19. Additionally, a curve-fitting program was used to model the transformed cumulative data. We aimed to use a user-friendly, cost-effective, and commercial software platform for the statistical examination and analysis of the datasets.

2. Materials and Methods

Using both mortalities and morbidities as quantifiable indicators of the severity of the pandemic and the time-limited extension of the disease, the current study offered a long-term investigation of the impact of COVID-19 on public health [32]. The records of the coronavirus disease were downloaded and processed from Humanitarian Data Exchange (HDX) (https://data.humdata.org/) [33]. Using the database, the dedicated country's dataset was extracted. The territorial classification was conducted according to the World Health Organization (WHO).

Indian data made sure that cases and deaths were organized chronologically, as well as the daily totals of morbidities and fatalities [33, 34]. The cumulative datasets underwent a logarithmic transformation (to the base ten) and a unity value was added to the raw data to account for zero values without changing the original record's integrity [35]. The previous procedure was carried out entirely within a Microsoft Excel sheet [36]. We used statistical tools to create run charts. Using a curve-fitting program, modelling of the modified cumulative data was studied [37, 38]. Global charts and tables were created using Tableau 2018.3 [39]. The scheme of the process is shown in Figure 1.

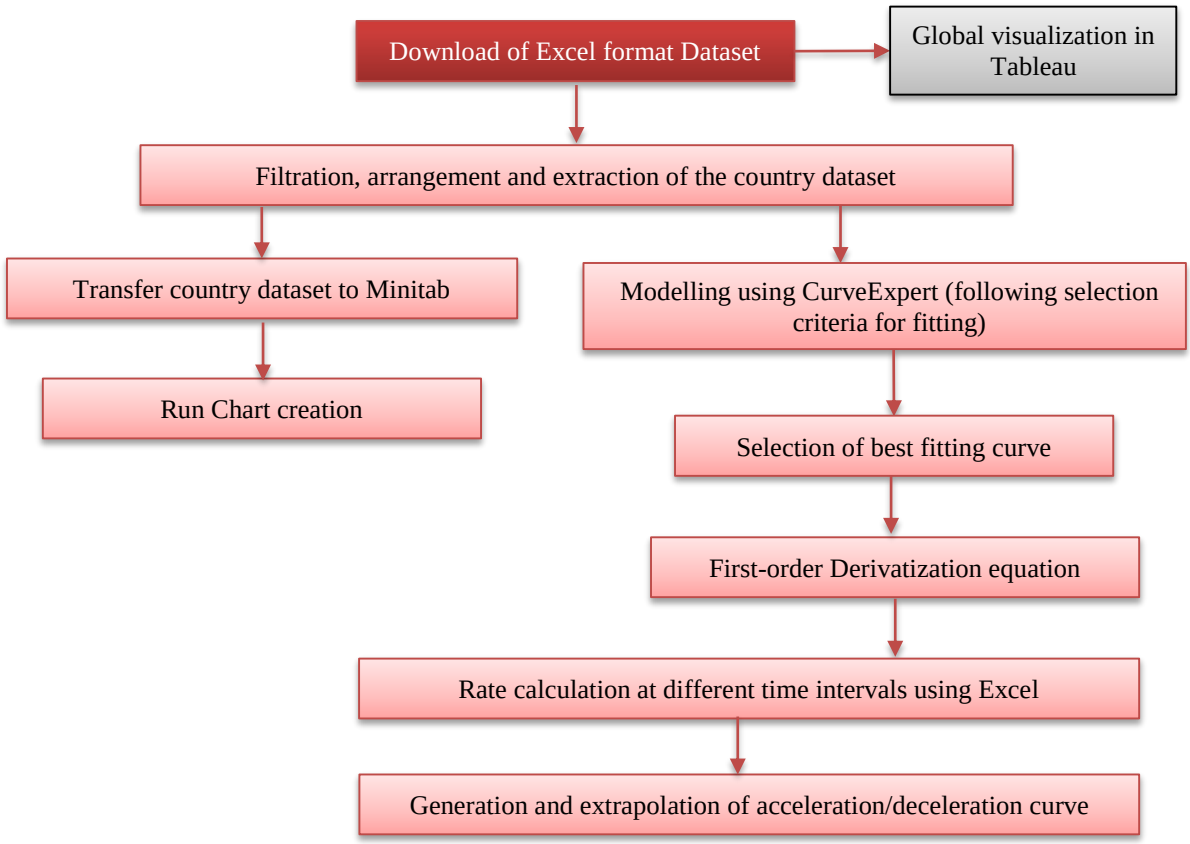


Figure 1. Flowchart diagram showing the process of data extraction, analysis and modelling of COVID-19 morbidity and mortality

3. Results and Discussion

Segregation of the political geographical areas into WHO regions would demonstrate the most devastated territories by the Coronavirus pandemic. The Regional Office of the Americas (AMRO) and European Regional Office (EURO) showed more than three-fourths of the global mortalities with 44.3% and 31.1% contributions, respectively [34]. The remaining countries were from the South-East Asian Regional Office (SEARO), Eastern Mediterranean Regional Office (EMRO), Western Pacific Regional Office (WPRO), and African Regional Office (AFRO), with a fractional share of the total emerging new daily deaths of 0.3107, 0.0568, 0.0293, and 0.0290, respectively. The epidemic markers for each WHO region are shown in Table 1 which demonstrates an overview of yearly collective cases and deaths [40]. These data were transformed into two-dimensional Table 2 which simplifies the illustration of time and region contribution characteristics for each territory. The second year of the pandemic is worse than the previous year when the outbreak starts to spread since each country was subjected to an initial lag phase before the disease spread [41, 42]. This is accompanied by the shift of the disease maximum census from the American WHO region to the European nations [43]. The unspecified area is different being relatively easy to contain and control such as incidents in the navigating cruise ships which were subjected to quarantine due to infection of the individuals onboard.

Table 1. Total number of cases and deaths of WHO regions from 03 January 2020 till 14 January 2022

WHO Region*	Epidemic Indicator	Year of Date Reported		
		2020	2021	2022**
Unidentified Political Regions	New Cases	745	19	0
	New Deaths	13	0	0
AFRO	New Cases	1,895,471	5,351,087	515,110
	New Deaths	42,211	113,863	3,895
WPRO	New Cases	1,087,675	10,176,953	1,567,414
	New Deaths	20,044	135,628	5,859
EMRO	New Cases	4,758,194	11,938,470	434,201
	New Deaths	119,380	191,544	1,963

SEARO	New Cases	11,973,259	33,001,946	1,890,064
	New Deaths	184,188	536,984	4,842
AMRO	New Cases	35,733,850	67,875,475	13,116,215
	New Deaths	951,036	1,459,645	29,351
EURO	New Cases	27,139,238	74,247,060	15,472,154
	New Deaths	583,397	1,086,666	42,829

* African Regional Office (AFRO), Western Pacific Regional Office (WPRO), Eastern Mediterranean Regional Office (EMRO), South-East Asian Regional Office (SEARO), Regional Office of the Americas (AMRO) and European Regional Office (EURO).

** The end period of this screening period covers only two weeks from this year.

Table 2. Two-dimensional analysis of contributors in COVID-19 morbidity and mortality within WHO political regions based on time (in years) and geopolitical areas

WHO* Region	Epidemic Indicator	Contribution Percentage by Time (Year)			Contribution Percentage by Political Area		
		2020	2021	2022**	2020	2021	2022**
Unidentified Political Regions	Cases	97.51%	2.49%	0.00%	0.00%	0.00%	0.00%
	Deaths	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%
AFRO	Cases	24.42%	68.94%	6.64%	2.30%	2.64%	1.56%
	Deaths	26.39%	71.18%	2.43%	2.22%	3.23%	4.39%
WPRO	Cases	8.48%	79.31%	12.21%	1.32%	5.02%	4.75%
	Deaths	12.41%	83.96%	3.63%	1.05%	3.85%	6.60%
EMRO	Cases	27.78%	69.69%	2.53%	5.76%	5.89%	1.32%
	Deaths	38.15%	61.22%	0.63%	6.28%	5.43%	2.21%
SEARO	Cases	25.55%	70.42%	4.03%	14.50%	16.29%	5.73%
	Deaths	25.37%	73.96%	0.67%	9.69%	15.24%	5.46%
AMRO	Cases	30.61%	58.15%	11.24%	43.27%	33.50%	39.75%
	Deaths	38.98%	59.82%	1.20%	50.05%	41.42%	33.08%
EURO	Cases	23.22%	63.54%	13.24%	32.86%	36.65%	46.89%
	Deaths	34.06%	63.44%	2.50%	30.70%	30.83%	48.26%

* African Regional Office (AFRO), Western Pacific Regional Office (WPRO), Eastern Mediterranean Regional Office (EMRO), South-East Asian Regional Office (SEARO), Regional Office of the Americas (AMRO) and European Regional Office (EURO).

** The end period of this screening period covers only two weeks from this year.

X% Grey shaded numbers are the top contributors in the two-dimensional analysis table.

The overall picture of the reported emerging cases and deaths could be visualized in Figure 2 which shows the major affected countries by the SARS-CoV-2 global manifestation. The pandemic indices in the geopolitical map showed the major devastated countries by this coronavirus disease, including the USA, Brazil, Mexico, India and Russia [34]. The globalized view by WHO regions could be extracted from Figure 3 time series plot illustrates the outbreak waves showing major peaks with time. It could be deduced that the west pacific and African followed by East Mediterranean regions were much less in magnitude compared with American, European and Southeast Asian countries [34, 44]. This observation confirms the previous finding of the major focus group for the main contributing nations in the Coronavirus morbidities and mortalities [43]. There are signs of multiple waves that might exceed three interfering peaks together in the examined political regions

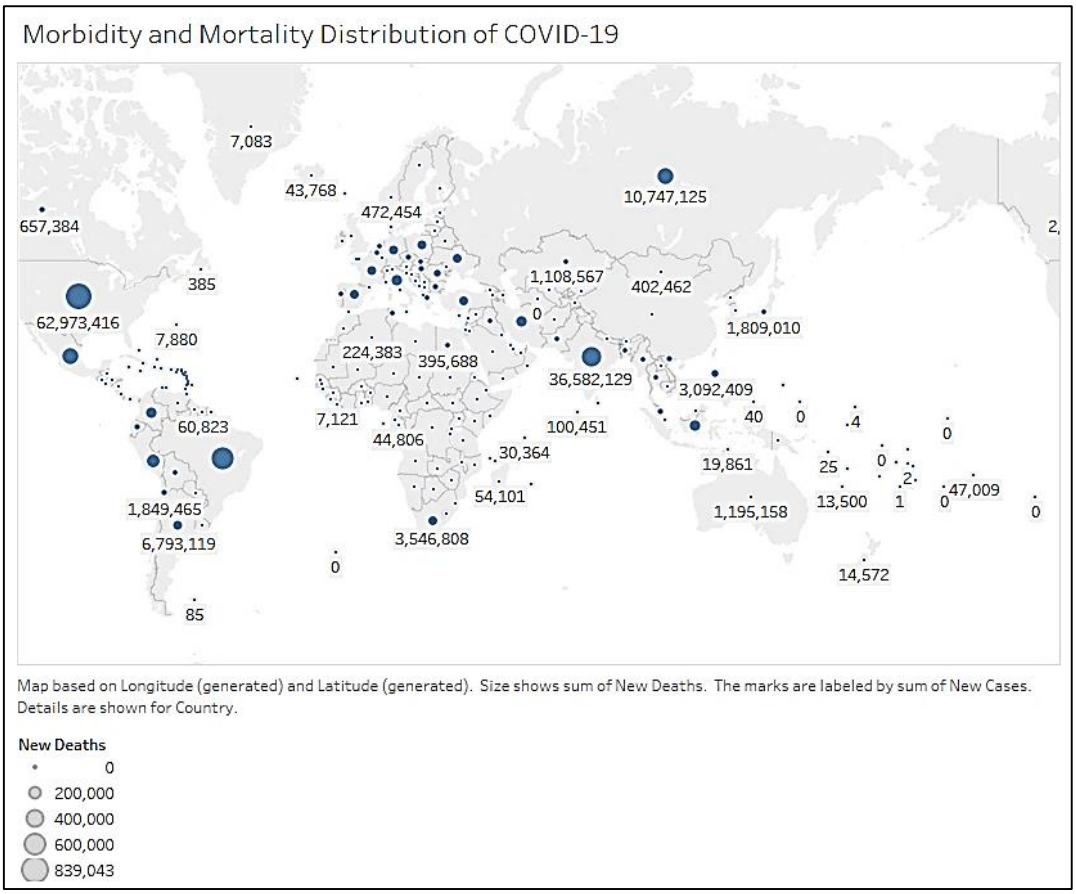
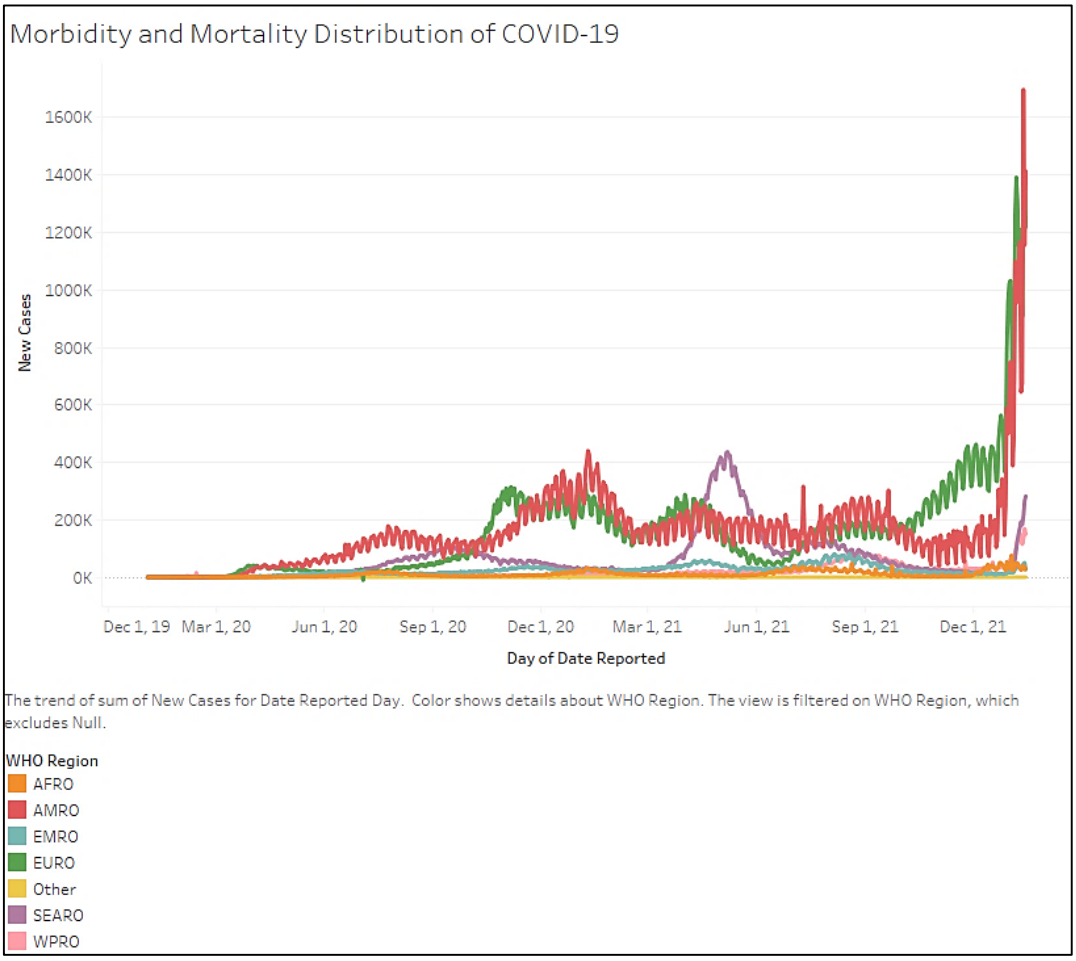


Figure 2. Global distribution of morbidity and mortality of SARS-CoV-2 based on the reported cases and deaths



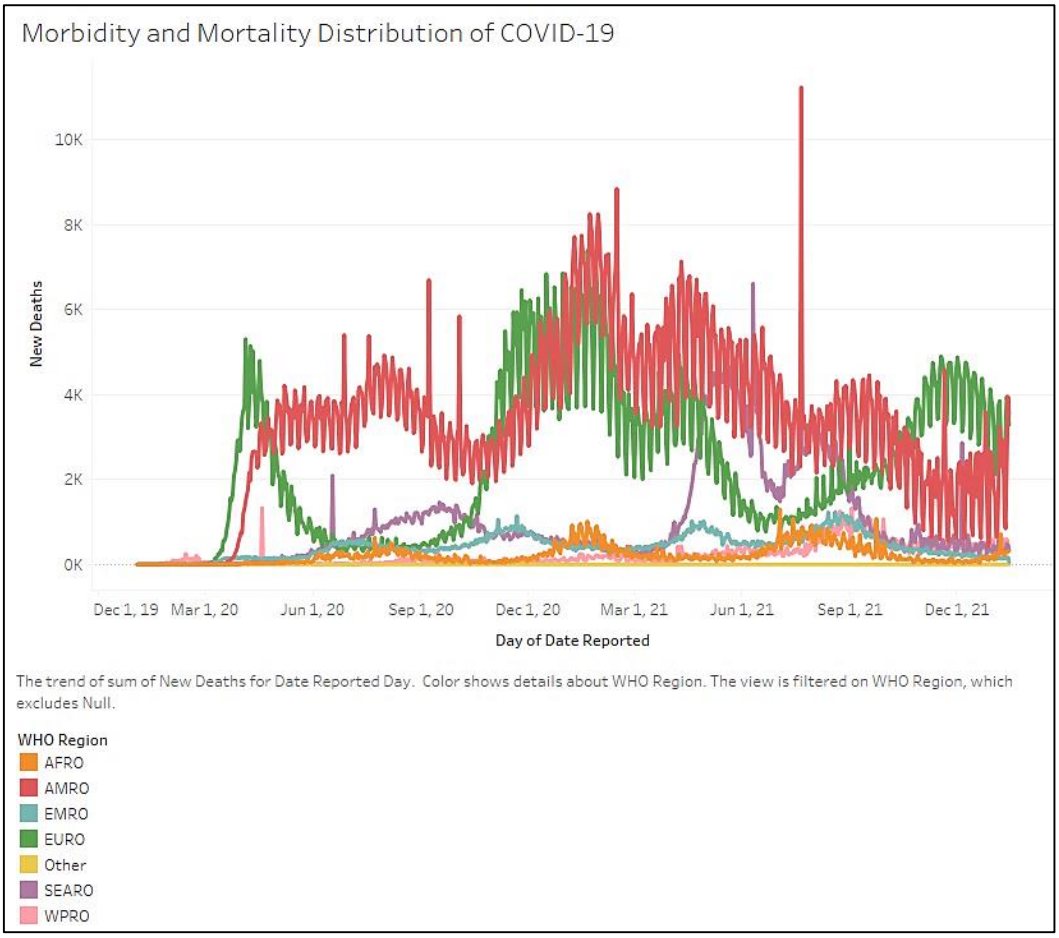
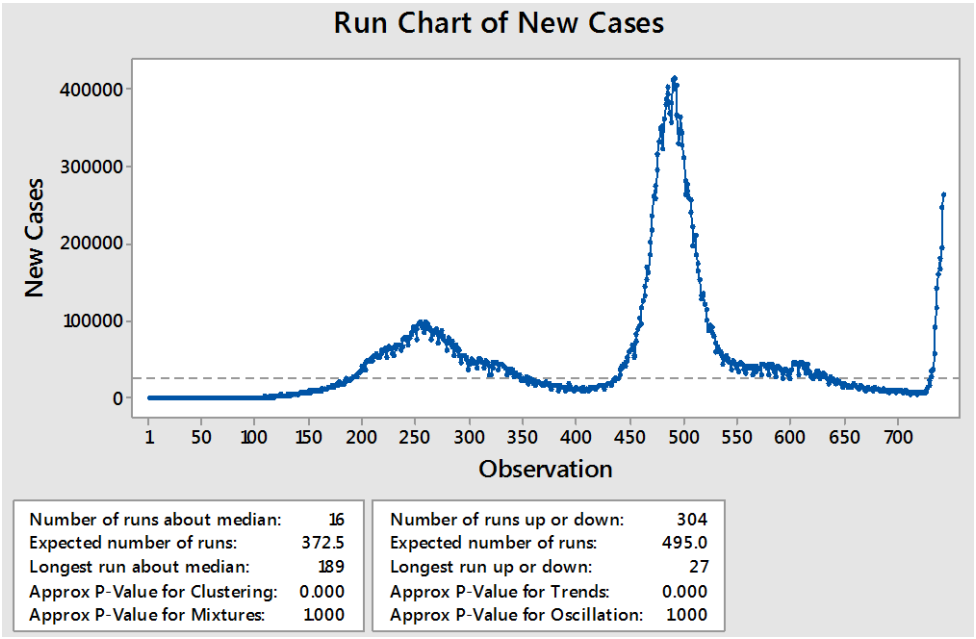


Figure 3. Time series plot showing the trend line of COVID-19 cases and deaths with time demonstrating multiple waves for different WHO regions

USA and Brazil have been subjected to distinctive statistical examination and mathematical modeling as primary affected countries by the epidemic in later studies [32, 45]. Along the same line, this work is focusing on India's situation as a part of a series of investigations concerning outbreak profile and behavior in a quantitative manner in different geographical areas that showed major contributions to the reported morbidities and mortalities [34]. The initial stage involved an overview of the disease progression using the run chart as a primary indicator for the outbreak progression in terms of daily cases and deaths as could be seen in Figure 4. Except for a single observation, the points vary randomly around the median (center line).



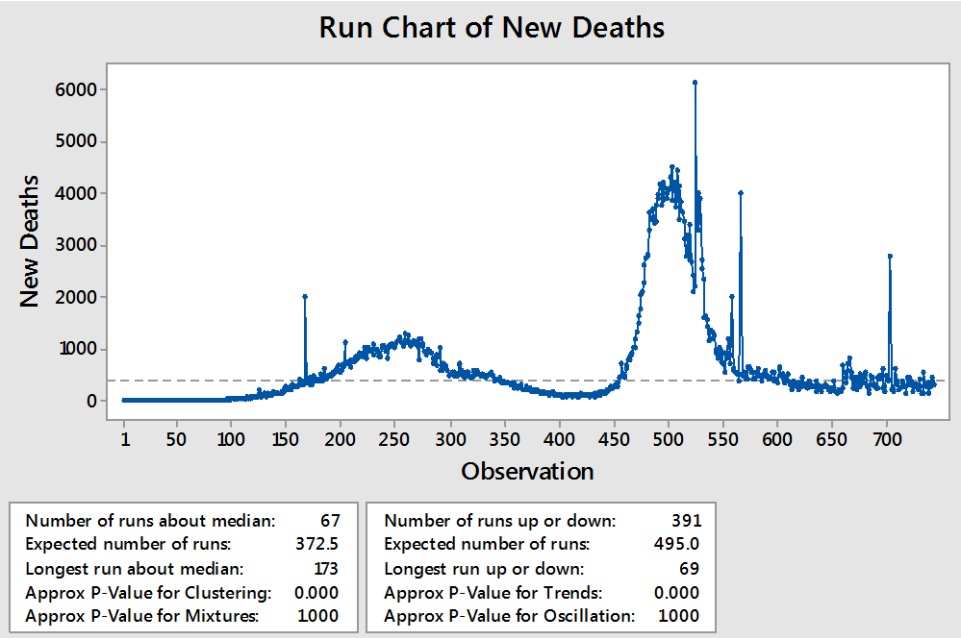


Figure 4. Time series plot of SARS-CoV-2 morbidity and mortality over two years displaying outbreak waves

The approximate p-values for mixtures and oscillation are all greater than the significance level (α) of 0.05, in contrast to the clustering and trend patterns which are below 0.05. Hence, the P-value is 1.000 in the first two and < 0.001 in the last two parameters. Accordingly, failure to reject the null hypothesis (H_0) because the means do not differ appreciably and vice versa could be concluded, respectively [46]. Therefore, there is an indication of special-cause variation or non-randomness for the latter two inspection parameters. Plot subgroup means the centerline is the midpoint of all the subgroup means and the blue plotted points are the subgroup means [46]. If the subgroup size equals one, then the centerline is the midway of all data, regardless of the option selected for the plotted points.

There is an observable rise in the trend line of morbidity and mortality, in addition to the aggregation tendency that appeared to be stemmed from remarkable two major peaks with signs of multiple overlapping smaller waves and the second peaks are almost four times higher than the first broad peak that shows roughly evidence of at least three combined waves. At the start of the year 2022, there is a sharp rise in daily cases preceding the death. The similar series plot chart of daily mortality report – but with much lower intensity - showed intermittent spiking surge in death incidents along the observation period.

Tailing of peaks in cases and deaths charts were detected following all peaks in the charts. Figure 4 demonstrates the number of runs and the longest daily runs [47]. The count of cases and deaths daily runs that had crossed the median line were 16 and 67 times, respectively. The longest run about the median showed 189 and 173 points falling below the centreline for cases and deaths, respectively. The total count of upward and downward runs equals 304 and 391, respectively [47]. Since data points of daily record are not randomly distributed and there is an observable rising trend pattern, the expected number of runs is significantly different from that found practically.

Linear regression analysis of Log C.D. versus Log C.C. showed satisfactory results as reported in previous cases [48]. The regression equation is Log C.D. = - 0.6288 + 0.8281 Log C.C. with S = 0.182314, R-Sq = 98.9% and R-Sq(adjusted) = 98.9%. The Analysis of Variance (ANOVA) for sources of variability of Degree of Freedom (DF) 742 and Sum of Squares (SS) 2261.08 showed error factor DF 741, SS 24.63 and Mean Squares (MS) of 0.03. The regression with DF of unity, SS and MS 2236.45 demonstrated F 67285.08 (P < 0.001). However, the model fitting should be evaluating the data and mathematical best-suiting equation in terms of the epidemic metrics [38]. Looking at the fitted curve plot to be sure that the dataset adequately covers the range of logarithmically transformed cumulative cases (X) values, the model properly fits any curvature in the data (avoid over-fitting). And the line fits well in areas of special interest [49]. With this respect, the quadratic fit might appear more appropriate when R-Sq(adj) = 99.21% with a lower residual standard deviation of 0.155. The fitted equation for the quadratic model that describes the relationship between *Y* and *X* is $Y = - 0.3926 + 0.6241\ X + 0.02420\ X^2$.

Mitigation of possible large and unusual daily record points – which were mainly caused by a lagging period of deaths behind the reported cases - could be sought by surveying a better fit which was found to be Morgan-Mercer-Flodin (MMF) model which was found to explain other processes [50 - 52]. If the model fits the data well, this equation can be used to predict Log C.D. for a value of Log C.C. or find the settings for Log C.C. that correspond to a desired value or range of Log C.D. values. It should be noted a statistically significant relationship does not imply that X causes Y. The relationship between Log C.D. and Log C.C. is statistically significant (p < 0.05). Hence, 99.91% of the variation in Log C.D. can be explained by the regression model. Since the amount of sample is large enough (n =

743) then a precise estimate of the strength of the relationship could be attained. Because more than 15 data points were available, normality is not an issue. The dilemma occurs if the number of data points is small and the residuals are not normally distributed, the p-value used to determine whether there is a significant relationship between X and Y may not be accurate. Moreover, the last model does not reduce error and improve regression only, it minimized unusual (X) values and large residuals and hence demonstrated the best fit under the current condition.

$$y = \frac{(a.b+c.x^d)}{(b+x^d)} \quad (1)$$

MMF Model equation is expressed by Equation 1, where coefficient data are a = -8.91820960555E-002, b = 6.72289251559E+001, c = 9.23111203690E+000 and d = 2.30513775705E+000 with standard error of 0.0724608 and correlation coefficient equals 0.9991478. It could be commented that the fit converged to a tolerance of 1e-006 in 32 iterations without weighting used. Curve fitting of the association between logarithmically transformed daily cumulative morbidities and mortalities is shown graphically in Figure 5. The same model applied also for the dynamic transformed morbidity and mortality. In the same line, Figure 6 shows the modeling of the transformed cumulative morbidity and mortality kinetics in India. The coefficient data were a = -1.23467033978E-001 and -2.69762762526E-001, b = 2.77470698130E+004 and 6.21376241498E+005, c = 7.57261466140E+000 and 5.54932635252E+000 and d = 2.20826909113E+000 and 2.80789683049E+000 with no weighting used, in addition to the fit converged to a tolerance of 1e-006 in 67 and 1e-006 in 69 iterations, respectively. The best curve fitting using FFM equation for the transformed cumulative outbreak markers showed standard errors of 0.1454407 and 0.1879990 and correlation coefficients of 0.9976246 and 0.9942497, respectively.

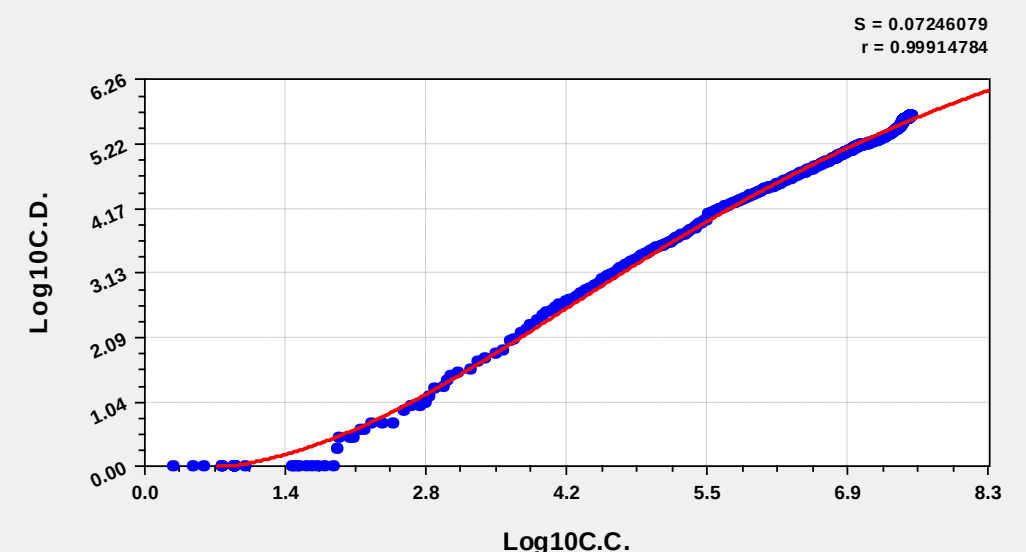
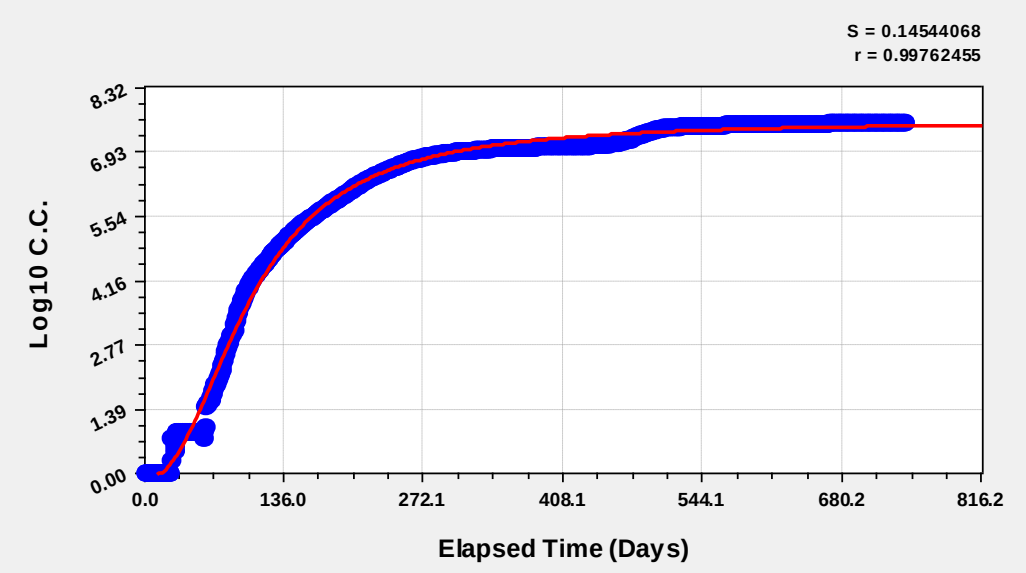


Figure 5. MMF best model fitting for both transformed cumulative mortality versus morbidity for Coronavirus disease outbreak in India



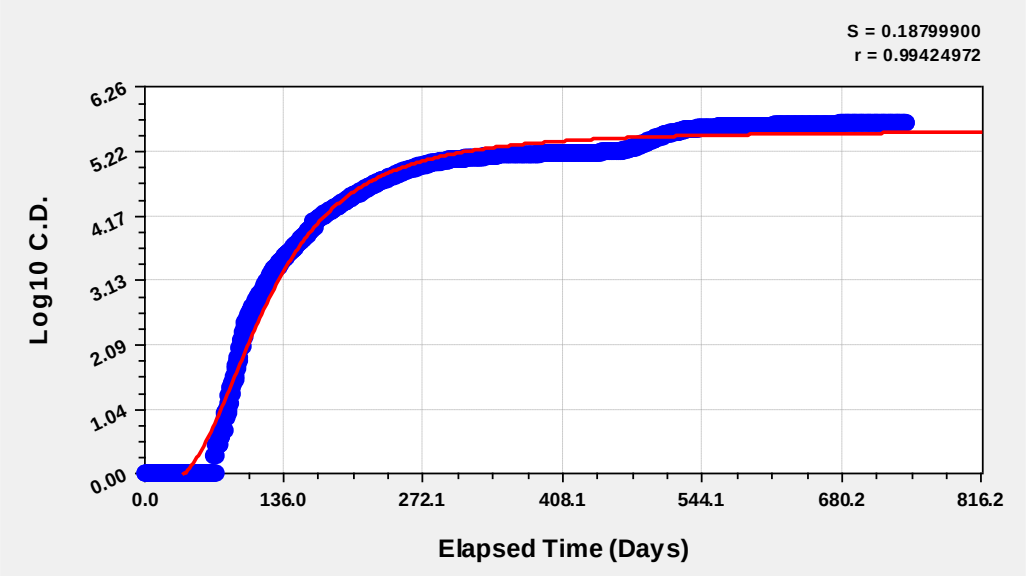


Figure 6. MMF modeling of the kinetics of the transformed Cumulative Cases (C.C.) and Deaths (C.D.) for COVID-19 reported in India

MMF model was previously implemented in contagious diseases by scientists and researchers [53, 54]. Derivatization of the kinetics equations for the epidemic metrics yields a dissemination risk factor (F) when x equals unity or other time values (Table 3). This factor could be used as an index for measuring the level of the epidemic in terms of the transformed cumulative morbidities and mortalities. According to this metric, the kinetics for cases and deaths is variable with time length and not fixed. Updating this value would be dependent on the dynamic change with the time factor. In addition, other countries might be included in this survey analysis to examine the relative challenge from the outbreak between different political regions. The first-order Derivatization Equation 2 is shown:

$$\frac{dy}{dx} = \frac{b.d.x^{d-1}(c-a)}{(b+x^d)^2} = f \qquad (2)$$

Table 3. Differential time-risk Factor (F) of the cumulative morbidity and mortality rates for two examined distinct political regions following MMF dataset modeling

Model Constants	Arbitrary Category	Brazil Cases*	Brazil Deaths*	India Cases*	India Deaths*
a		-3.57E-01	-2.51E-01	-1.23E-01	-2.70E-01
b		2.85E+05	1.56E+07	2.77E+04	6.21E+05
c		7.21E+00	5.57E+00	7.57E+00	5.55E+00
d		2.78E+00	3.58E+00	2.21E+00	2.81E+00
F_d**	Low Short-Term	7.3811E-05	1.3358E-06	6.1373E-04	2.6335E-05
F_w**	Intermediate Short-Term	2.3716E-03	2.0415E-04	6.4915E-03	8.9714E-04
F_m**	High Short-Term	3.2254E-02	8.9733E-03	3.8274E-02	1.2750E-02
F_{2m}**	Low Medium-Term	1.1077E-01	5.3655E-02	8.8542E-02	4.4707E-02
$F_{1/4y}$**	Intermediate Medium-Term	2.2796E-01	1.5273E-01	1.4462E-01	9.3131E-02
$F_{1/3y}$**	High Medium-Term	3.8041E-01	3.2082E-01	2.0483E-01	1.5676E-01
$F_{1/2y}$**	Low Long-Term	7.8288E-01	9.1323E-01	3.3455E-01	3.2656E-01
F_y**	Intermediate Long-Term	2.6886E+00	5.4321E+00	7.7395E-01	1.1451E+00
F_{2y}**	High Long-Term	9.2335E+00	3.2470E+01	1.7904E+00	4.0150E+00

* Morgan-Mercer-Flodin (MMF)

** F-factor showed Derivatization of the transformed cumulative cases of India then Brazil

It should be noted that the exponential association model was found to be the next candidate for modeling with slightly lower regression and higher standard error for both mortality and morbidity of COVID-19 in the Indian outbreak despite being used in other studies involving this viral disease [32, 55]. Nevertheless, this exponential association model could be used as the primary choice and fits better with the American outbreak indices as was favorable empirically [32]. Extrapolation of the outbreak metrics with F values versus time showed that the Brazilian

epidemic of the pathogen was deadlier with the greater surge in the infection attribution reported over the investigation duration which appeared clearly after an intermingling period of the two countries that started to resolute at about 152 days ± one month (Figure 7) [56]. The finding in Figure 7 was supported by the pattern of run charts in Figure 5 and the trending graph of the Brazilian outbreak waves [56]. The acceleration in the cumulative morbidity and mortality rates of the outbreak in Brazil started lower (short-term) but ended higher (long-term) than the Indian epidemic during the monitoring time frame. At low medium-term outbreak duration, the flipping started in the infection rates with respect to cumulative cases and deaths. The switching occurred at about day 49 between the rates (risk factors) of the two countries. The Indian fingerprint showed narrower high amplitude peaks while the Brazilian timeline demonstrated lower magnitude but much broader waves.

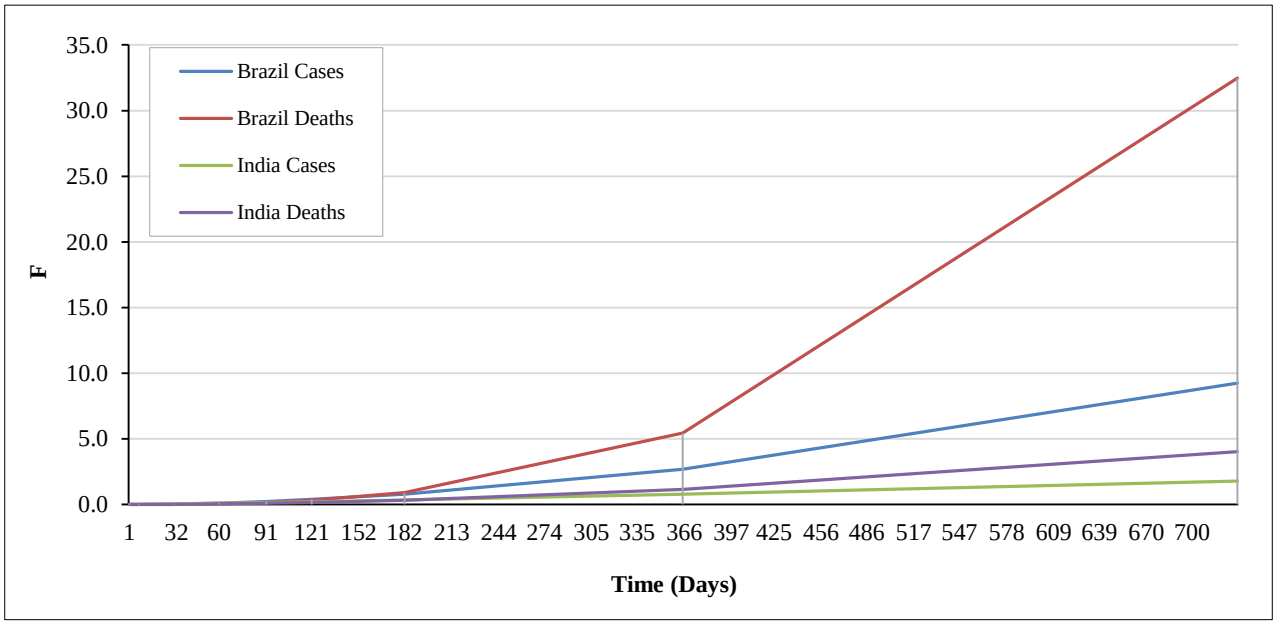


Figure 7. Dissemination rate Factor (F) at different time intervals showing the kinetics for the acceleration of the epidemic indices of two countries from two distinct WHO regions that showed major affection by COVID-19 outbreak

4. Conclusion

Our results show that the COVID-19 outbreak is still in its flourishing stages and that it is spreading rapidly despite vaccination and other public measures that have been established to halt the dissemination. However, we believe that with proper intervention, the spread of the disease can be controlled. We also believe that our novel approach to data analysis can be used to track and predict the spread of other diseases. The results of this analysis suggest that the COVID-19 outbreak is following a typical pattern of morbidity and mortality for outbreaks of the MMF model shape. However, further research is needed to confirm these findings. Since the metrics of the epidemic are highly dynamic, close monitoring and recording should be continued by the official and regulatory authorities to update the extrapolated morbidities and mortalities to provide an update on the status of the disease and to evaluate the usefulness of the measures and actions for any required modifications. The dissemination rate factor could be used as a dynamic index to assess the epidemic risk and the acceleration level over time and measure its kinetics.

5. Declarations

5.1. Author Contributions

Conceptualization, D.E.E. and E.R.R.; methodology, M.E.E.; software, D.E.E.; validation, M.E.E., E.R.R. and D.E.E.; formal analysis, M.E.E.; investigation, E.R.R.; resources, D.E.E.; data curation, E.R.R.; writing—original draft preparation, M.E.E.; writing—review and editing, D.E.E.; visualization, E.R.R.; supervision, E.R.R.; project administration, M.E.E.; funding acquisition, D.E.E. All authors have read and agreed to the published version of the manuscript.

5.2. Funding

The authors received no financial support for the research, authorship, and/or publication of this article.

5.3. Ethical Approval

Not applicable.

5.4. Data Availability Statement

The data presented in this study are available on request from the corresponding author.

5.5. Conflict of 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.

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