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INVESTIGATION THE CASES OF NOVEL CORONA VIRUS DISEASE (COVID 19) USING DYNAMIC STATISTICAL TECHNIQUES

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Abstract

This is the first to create concepts to examine the links between COVID-19 mortality and confirmed case, using both time series and Panel data models. We collected data each day in the 31 provinces, including deaths, confirmed cases, suspected cases and recoveries of four health indices. We examined the unrecognised elements including environmental expositions that contribute to the propagation of the illness through human-to-human transmission because of the intricacies of COVID-19. We have used estimate techniques to manage sectional dependency, endogeneity and heterogeneity uncontrolled. The estimates for the more effective dynamic reproduction number have also been calculated, showing that the gravity has typically declined since the initial instances were verified inside the individual nations. It was determined that the predictive capacity of the loglinear regression model was better suited and a basic daily estimate was calculated for both nations. The dynamic behaviour of COVID-19 infection by isolation class incorporation is developed in the mathematical model. First, it proposes the model formulation and then it discusses the positive nature of the model. The local stability of the suggested model and global stability dependent on the fundamental reproductive system are provided. The non-standard NSFD system and the Runge-Kutta 4th order approach are employed for the numerical solution of the suggested model. Finally there are some pictorial findings. Our data reveal that the likely source of COVID-19 outbreaks is human to human contact

Introduction

At the end of 2019, the new coronavirus that arose in Wuhan (China) swiftly expands across every Chinese province, and by 1 March 2020 it expanded to 58 other nations. Coronavirus 2 (SARS-CoV-2) (1, 2). Efforts to control the virus are underway; however, the efficiency of these efforts is unclear in view of the many uncertainties about pathogen transmissibility and virulence.

The undocumented and non-infected case proportion is critically epidemiological, modulating the pandemic potential of an emerging air virus (3-6). Undiagnosed as a result of mild, restricted and/or absence of symptoms these unrecognised infections may thus expose a considerably larger proportion of the population to the virus, depending on their contagiousness and quantity. In this context, we apply Modeling frameworks for estimating infections, and% of unpopular diseases in China, to assess the whole potential pandemic SARS-Cov-2 Weeks before and after the shutdown to and from Wuhan.

Coronavirus infections are varied and may cause moderate to severe respiratory infections in humans, and infect many other species. In 2002 and 2012, two zoonotic coronaviruses, Severe Acute Air Syndrome (SARS-CoV) and Coronavirus Respiratory Syndrome (MERS-CoV) in the Middle East have evolved in humans and lethal air illness and have brought forth new public health issues for the 21st century1. Diseases were very pathogenic between 2002 and 2012. In late 2019 a unique SARS-CoV-2 coronave virus created an outbreak of unusual viral pneumonia in Wuhan city, China. This new coronavirus disorder, known as the 2019 coronavirus illness (COVID-19), is widely transmitted and has spread quickly around the globe. 2.2.2. The number of affected persons as well as the size of epidemic zones has been dramatically exceeded by SARS and MERS. The current COVID-19 pandemic has presented an exceptional danger to public health worldwide4,5. We sum up the present knowledge of the SARS-CoV-2 and COVID-19 nature in this review. This complete review focuses on SARS-CoV-2 fundamental biology, including genetic traits, possible origin and its receptor binding, on the basis of current published discoveries. In addition, the diagnosis of, and countermeasures against COVID-19 will be discussed.

Mathematical modelling is important when entering a community to understand the behaviour of an illness and to examine the circumstances under which it is wiped out. The fast rate of infection spreading and the substantial number of fatalities now affecting COVID-19 is of tremendous concern to researchers, governments and everyone. Coronavirus, originally reported in December 2019, was a newly found coronavirus infectious illness in Wuhan, China. COVID-19 is mostly transferred by droplets caused by the toxicity, sneezing and exhalation of an infected individual. These goutlets are too heavy to fit into the air and fall rapidly on the surface or floors. Coronavirus-confirmed infections in 187 countries reached around four million, and almost 295,000 persons were killed. The most significant occurrences happened in the US, according to information collected by University Johns Hopkins. It also boasts the biggest death toll in the world as over 77,000 fatalities occurred.

Literature Review

Srikanth Umakanthan (2020) Because of its increased geographical expansion in the last two decades, coronavirus has emerged as a worldwide health hazard. This paper looks at current understanding of coronavirus illness origins, transmission, diagnosis and treatment in 2019 (COVID-19). In history, two pandemics have occurred: severe acute respiratory and Middle East syndrome and current COVID-19 from China. It has caused severe acute respiratory syndromes. It is hypothesised that the virus is obtained through zoonotic sources and transmitted by direct transmission and contact. The symptomatic phase shows a severe respiratory failure with fever, cough and myalgia. A reverse transcriptase PCR is used to confirm the diagnosis. COVID-19 is managed in severe patients mostly by support treatment with mechanical ventilation. The main function in preventing public transmission of the virus, as well as effective isolation from diseases and community control, is preventive techniques. A vaccination is still a constant challenge to develop to remove the virus from the host. This article is free for use for the duration of the Covid 19 epidemic or until otherwise determined by BMJ in accordance with the online limitations of BMJ. You may use the article for any valid non-commercial purposes, download it and print it.

Liu, Wei (2020) In Wuhan, Hubei Province of China, pneumonia epidemics have been triggered by the 2019 Novel Coronavirus Disease (KOVID-19). The purpose of this research was to evaluate the variables influencing pneumonia development in COVID-19 patients. Associated findings are utilised for prognosis assessment and the optimum therapy regimes for pneumonia COVID-19. For 78 individuals with COVID-19 pneumonia, the inclusion criteria were met. 2 weeks following hospitalisation, an efficacy evaluation indicated a decline (14.1%) in 11 patients and improvements and stabilisation (67). (85.9 percent). The improvement/stabilizement group in the condition (66[51, 70] vs. 37 [32, 41, 41] years, U = 4,932, P=0,001) was much older than the patients with progressions. In addition to the stability group, the progression group was significantly greater than the smoking pain group (27.3% vs 3,0% µ2 = 9,291; P = 0.018). The greatest body temperature was significantly higher in all 78 patients (38.3 [38.8, 38.6] vs 37.5 [37.0, 38.4]°C, U = 2.057 and P = 0.027]) and the initial symptom was the most common fever among the patients admitted to the treatment. The proportions of patients with respiratory disorders (54.5% vs. 20.9%), ·2=5,611, and P=0,028, respectively) and respiratory disorders (34[18,48] vs. 24[16,60] breaths/min; U+ = 4,030; P=0,004) were much higher in the progression group than in the improvement/stabilization group. The c-reactive protein has risen significantly in progression group compared to the improvement/stabilisation group (38.9 [1.9, 64.8] vs 10.6 [1.9, 33.1] mg/L, U = 1.315, P = 1.024). Progressive albumin in the stabilization/improvement group was significantly less (36.62 ± 6.60 vs 41.27 ± 4.55 g / L, U= 2,843, P = 0.006). In the advancement group patients were more likely to be than in the improve/stabilization group (ß2 = 16.01, P = 0.001). The likelihood was greater. Age of cigarette smoking (OD, 14.285; 85% of CI: 1.577–25.000; P = 0.018); body temperatures are not limited to admitted (OR, 8.999; 95% of CIs, 1036–78.147; P= 1.046). The albumin (OR, 7,353, 9,8,97, 96 percent CI, 1.846; P = 8.018) was reported by a multivariate logistic analysis. Seven indicators have been discovered, including age, smoking history, maximum body temperature, breathing failures, albumin, and C-reactive protein, which have contributed to advancement of COVID-19 pneumonia. These data may also be utilised to improve COVID-19 pneumonia management.

Pranab Chatterjee (2020) As a public health emergency of worldwide significance a new spillover coronavirus (nCoV) with epicentre in Wuhan, People's Republic of China. The outbreak of new coronavirus diseases in 2019 (COVID-19) started in December 2019 and, through February 28, 2020, 83,704 confirmed cases with 2,859 fatalities worldwide resulted in an overall mortality rate of 3,31 percent. 58 nations or territory and one international transport were impacted by this moment (28 February 2020). The main focus was on the generation of scientific insight to guide evidence-based responses to the virus, which was called SARS Virus 2, as its genetic similarities to SARS virus, were the managed and contained pands. The main focus was on managing and controlling the pandemic. This study presents new findings that may guide the response to public health, especially in India. Key areas in which research is required to provide crucial information for preventative and control activities have been highlighted. The development of SARS-CoV-2 has once again highlighted flaws in global healthcare systems, the capacity to address an infectious threat, the fast spread of diseases across global boundaries and the inefficacy of knee-based policy responses to new threats to infectious diseases. This evaluation concludes with essential knowledge from work on COVID-19 prevention and limitation and highlights the need for investment in health systems, community action channels and the need for preparedness and global safety.

Ayub Ahmed (2020) Coronavirus disease (COVID-19) is a worldwide health issue that has been presented and explored by worldwide initiatives to manage this illness. Although numerous study has been carried out on the basis of clinical data as well as documented instances of infection, more study is still possible since many difficult elements are involved in the future forecast. Mathematical modelling using computer simulations is thus a major tool for evaluating critical factors of transmission and predicting the dynamics of disease models. In this work we examine and present different COVID-19 models which may answer significant global health care concerns and provide crucial comments. We offer 3 well-known numerical solutions, Euler's approach, Runge–Kutta order two (RK2) method and four method of sequence (RK4). Results based on the proposed numerical methodologies and solutions provide essential answers to this worldwide problem. The number of persons sensitive, infected, recovered and quarantined may be estimated using numerical findings in future. The findings may also contribute to worldwide efforts to enhance preventative and intervention programmes. More interestingly, the fundamental reproductive numbers R0 of both nations, Turkey and Iraq, lately have been published by different organisations; by 9 April 2020, the study estimate showed that R0 is 7.4 for Turkey and 3.4 for Iraq. Furthermore, according to the WHO data, on 11 April the number of confirmations was 5138 for Turkey and, on 29 May, 416 for Iraq, which might be considered the highest figure since the onset of the epidemic. We thus examine, by means of the logistic model, the predicted epidemic magnitude for Turkey and Iraq. It may be concluded that the proposed model describes this epidemic sickness in a fair way.

Objectives

1. Analysing the mathematical Model to study COVID-19 problem
2. To Formulate model to study COVID-19 problem

Formulating Model

This portion of the study is about building the mathematical model for our issue. We have 3 cabinets here: S(t), I(t) infected and R recovered (t). We build the necessary model under convex incidence rate that the host population assumes to be convex to the infective class. The advantage of utilising a convex incidence rate is that two exposures over a shorter period are equivalent to an enhanced rate of infection: a single encounter creates CIS infection, while the new infectious people are the result of double exposures to CI2S. It gives the healed person more possibility of recovering from infection. The oscillation function (S,I) = CI(t)S(t)(1 + μ I(t)), where both C and α are positive constants, may be seen here. This is an intriguing example of the incidence rate that other writers already utilise. Figure shows the flow chart of the model. 1.

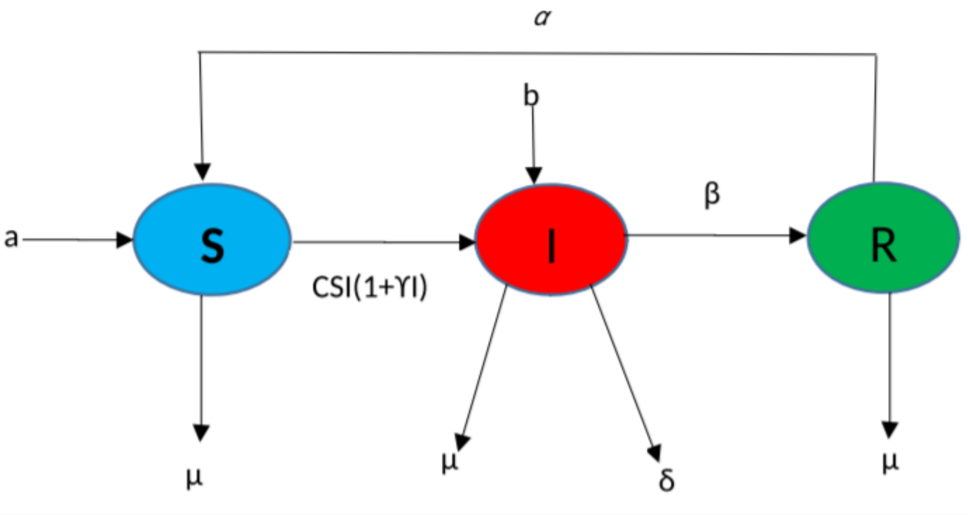


Figure 1: Proposed Flowchart

In this paper, a deterministic compartiment model is used to analyse the transmission mechanism of COVID-19. We have divided the population N(t) into seven mutually excluding bays based, for example: susceptible (S(t)), exposed (E(t)), infected with asymptomas (A(t)), symptomatic infected with but not quarantined (I(t)), infected with symptom and quarantine (Q(t)) and infected with hospital, isolated (H(t)) and rehabilitation models (R) (t). A sensitive individual might be infected with the diseased individual in close touch with him/her. The quarantined and isolated folks are generally unable to transfer the virus to other sensitive individuals. However, we realistically see that a large number of employees in quarantine and insulation centres such as doctors, nurses and health workers are infected with the virus. Let the quarantine and isolation persons in q1 and q2 proportions comply appropriately according to the norms of quarantine and centre. So that quarantine persons (1 − q1) and (1 − q2) do not comply correctly the norms of such the centre, and are accountable for transmitting the virus to their personnel. So, when an S-class person has infected any persons in class A, I, Q, H are transferred to the exposed class.

Positivity and boundedness of solutions

The fundamental characteristics of the COVID-19 model will be examined in this section (1). It will be of biological significance if all the variables are non-negative for T 0 — that is, for all times non-negative solution with non-negative start circumstances which we investigate on the following lemma.

Lemma 1 Suppose F(t) = (S, E, A, I, Q, H, R) along with starting F(0) = 0 and COVID-19 solution F(t) (1), are nonnegative for all t = 0.

Proof Suppose t1 = sup {t > 0, F(t) > 0}, which is a positive quantity. Now, multiplying the first equation of (1) by its integrating factor exp $\left\{\mu t + \int_0^t \lambda(\tau)\mathrm{d}\tau\right\}$ and arranging the equation, we get

$$\frac{\mathrm{d}}{\mathrm{d}t}\left[S(t)\exp\left\{\mu t + \int_0^t \lambda(\tau)\mathrm{d}\tau\right\}\right]$$

$$\pi \exp\left\{\mu t + \int_0^t \lambda(\tau)d\tau\right\}$$

$$\text{or } S(t_1)\exp\left\{\mu t_1 + \int_0^{t_1} \lambda(\tau)d\tau\right\}$$

$$S(0) + \pi\int_0^{t_1} \exp\left\{\mu y + \int_0^{y} \lambda(\tau)d\tau\right\}dy$$

$$\left\{S(0) + \pi\int_0^{t_1} \exp\left\{\mu y + \int_0^{y} \lambda(\tau)d\tau\right\}dy\right\}$$

$$\left\{\exp\left\{-\mu t_1 - \int_0^{t_1} \lambda(\tau)d\tau\right\}\right\} > 0$$

Likewise, E(t1)>0, A(t1)>0, I(t1)>0, 0, Q(t1) > 0, H[t1] >0, 0, R(t1) > 0, may be demonstrated. F > 0 for every t > 0, thus. In the viable closed area, the dynamic behaviour of the COVID-19 model (1) is investigated:

$$\Omega = \left\{(S, E, A, I, Q, H, R) \in \mathscr{R}_+^7 : S + E + A + I + Q + H + R \leq \frac{\pi}{\mu}\right\}.$$

It will be shown to be positive and attractive to the closed area of all the positive COVID-19 models solutions.

Log-linear model

A log-linear model (regression) is another easy way to describe the incidence of infectious illnesses. Infectious illness outbreaks may usually be divided into two phases: the growth and decline phase. In this study, we concentrate on the first growth phase, given the sample information. In the data section, the daily increment incidence shows an approximated exponential trend in Italy and Spain (nationally) and its most impacted areas. There is hence an almost linear trend in the daily incidence logarithm. This may be written as a simple linear regression in the simplest situation.

$\text{Log}(y) = b + rt_1$

If y is the daily incidence, r is the growth rate, t is the number of days after first confirmed incidence and b is a constant intercept. In order to adapt the log-linear model, we use the incidence package in R to reach optimal values. The model may be used to forecast the incidence trajectory till the peak incidence during the growing period using the estimated parameters. Although the log-linear model provides for incidence modelling and forecasting, it does not indicate the amount of people who can be sensitive or recovered in comparison with the SIR model. As is the case with the SIR model, R0 is also estimated using the loglinear model, which has a growth rate r as its main parameter indicate that a linear connection between the growth rate and R0

$$R_0 = 1 + \frac{r}{b}$$

If r is the exponential growth rate observed (or estimated) as per Eq (6) and b is the same as the μ rate in Equ. 1

In order to calculate R0 from the r growth rate, we are able to utilise the epitrix R package for empirical distributions. Note, however, that the "epidemic model implies a generational distribution interval," also referred to as the "period between symptom onset in a main case and symptoms in subsequent cases"[85]. This is sometimes referred to as "the time interval distribution" Since COVID-19 patient data are not accessible to us, we cannot calculate serial interval distribution parameters directly. However, some The present COVID-19 analysis provides early assessments and matching model parameters of the best fitted serial interval distribution. This includes the following: ii) gamma mean $\mu = 7.5$; $\mu = 3.4$; ii) gamma mean gamma = 7; and $-\ \mu = 4.5$ standard; iii) gamma average $\beta = 6.3$, μ standard deviation= 4.2. Utilizing these three periods, we may calculate R0 using the above-mentioned methodology using rates estimates. It is important to note that the distributions for the Serial intervals are not only restricted to gamma distribution. Weibull and log-normal distributions are additional prominent distributions, and numerous factors, including period of isolation, are used.

Parameter Estimation and Model Validation

The model parameters are estimated using actual COVID-19 data in this section. The spread was really frightening over the world. Thus the management of the propagation of this virus is highly crucial for the survival of human civilisation as early as feasible. The new coronavirus, on the other hand, has unknown natural history and dynamics. Parameter estimation is a key issue to investigate its dynamics in this environment.

By adapting the reported instances of the ongoing COVID19 in India, we determined the essential model parameters associated with COVID-2019. This dataset is incomplete because of the epidemic, but after examining its early dynamics, we will utilise it to manage this epidemic. The COVID-19 epidemic in India really begins on 1 March 2020, and fresh infected patients are continually reported from then on. On the other side, by establishing a nationwide lockdown from 25 March 2020, the Indian government took a significant precautionary action, which was continued until 17 May 2020 and might extend if required. Thus two data sets are considered: The first case collection (set-1) for the period 1 March-24 April 2020 is reported. However, many exposed, symptomatic and asymptomatic individuals who have been infected in India originate from the other COVID-19 pandemic nations before lockdown (25 March 2020) who have not been adequately recognised and reported. Data recorded from 1 March to 24 March 2020 thus remain unknown. We thus take into account the second series (set-2) of data published during the period between 25 March and 24 April 2020, while excluding the above-mentioned data.

The methodology has been adapted to cumulative instances from India. Our model predicts the following cumulative new infected cases (q(t)):

$$q(t, \Phi) = q(0) + \int_0^t (\eta_i I(\tau) + \eta_q Q(\tau)) \mathrm{d}\tau$$

We numerically solve model equations and utilise the answers to define the most appropriate model parameters using a methodology that minimises the sum of the squared residues:

$$R(\Phi) = \sum_{J=1}^{n} \left(q_{t_j}(\Phi) - \overline{q}_{t_j} \right)^2$$

A collection of the parameters of the model to be evaluated is = (β, α, μq, α, βi, μq, β, p, d). According to model predictions and presented data, qt(j) and qtj represent a cumulative number of infected population. Here n refers to the total number of data points for the fitting procedure available. We have in India a general population of 1,352,642,280 deemed susceptible to COVID-19, which is the starting S(0) number of sensitive persons=1,352,642,280, in order to adapt the model to the reported Indian case reports. The annual rate of birth is 18.2 / 1000. So India is 67,446,82 in daily recruiting. India's average lifetime of 69.7 years is 0.000039074 death.

Initially, cumulative cumulative cases for the first data set dated 1 March 2020 were 3, first hospital and first cumulative cases H(0) = 3 and q(0) = 3. The first cumulative cases were 3. For all datasets, E(0), A(0) and I(0) are not calculated for the initial number of exposed asymptomatic and symptomatic, but non-quaranted infections (not reported) and q1 (0,94), q2 (1,90). The facts provided in the initial situation, the recruitment rate and the usual death rate suit our model. All other crucial metrics including the fundamental reproductive number have been computed. Our calculation reveals that A(0) = 16, I(0) = 10 and the fundamental value of reproductive activity of the infected is R0 = 2.397448678, with a R0A contribution = 1.317554127. This is the contribution to the asymptomatic class. Furthermore, the contribution from R0I is also provided by the symptomatic, but unquarantinated, class infected symptoms, the symptomatic, quarantine and the hospitalised class of infectants, 0,765798290, R0Q =,0,02241962187, R0H =,0.2915951005. Compared to the other parts, we need to focus on the declines in preventive approaches, which are discussed in full in the prevention part, in the contribution of the asymptomatic infecting classes (R0A).

Validation and Prediction

We validate the model by utilising both set of parameters to compare the model forecast to reported data not utilised to fit the process. With the use of a daily case bar chart published in India from 25 April to 10 May 2020, we compared each of the projected daily cases with the projected daily cases.

The blue colour bar here indicates new cases projected everyday, while the red colour bar indicates instances recorded. It is obvious that the second produces a better estimate than the first one.

The standard error in both circumstances may also justify the best estimate. The default for the first set of parameters for the model was 2.8264954 AT107, while the default for the second set was 1.630582 AT107. The second set, compared to the first set, is thus the better fit. Second, before 25 March 2020 (pre-lockdown), numerous exposed asymptomatic sick individuals arrived in India from other COVID-19 impacted nations that are not fully diagnosed. In the reports before 25 March 2020 there is thus ambiguity. Thus, we don't consider the data previously published. Thirdly, Fig. 4a and b show that the prediction based on the second set is better than the first. This is why we will choose from the data from 25 March to 24 April 2020 the second parameter set of estimates to investigate the trending of the epidemic and model predictions in the future.

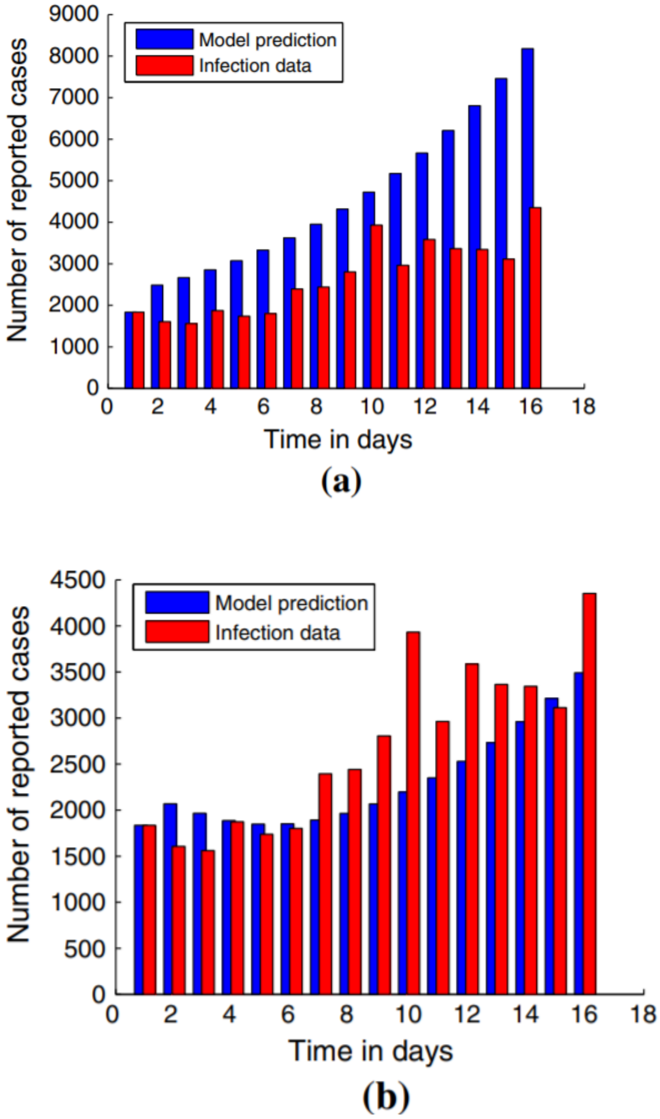


Fig. 2 Bar diagram of the daily infected cases where red bar denotes the reported case and blue bar denotes the model predicted case

Predictive ability of models

Along with important signals of COVID-19 infectivity and temporal variability in the results for the estimated reproductive values (R0 and Re), the models also provide a prediction capability, particularly in the drop after daily incidents peak and drop. During the decadition phase, daily incidence forecasts may assist to establish if medical interventions are working but may also give time frames for certain thresholds when there is a daily incidence of, for example, disease under control. For predictive capabilities of the SIR and log-linear models, we use the projection package in R. Since this portion is just designed for providing a brief overview of the predictive abilities of models, we urge our readers to a thorough description of the complications. The first step is to analyse which of the two models is best predicted during the increasing stage of the COVID-19 outbreak. We blend them from the above-mentioned Sir models and log-linear model with the three previously reported serial distributions based on the planning R0 values for Italy and Spain. We then use the prediction algorithms to predict the daily impact of India from 14 days till the day of peak incidence.

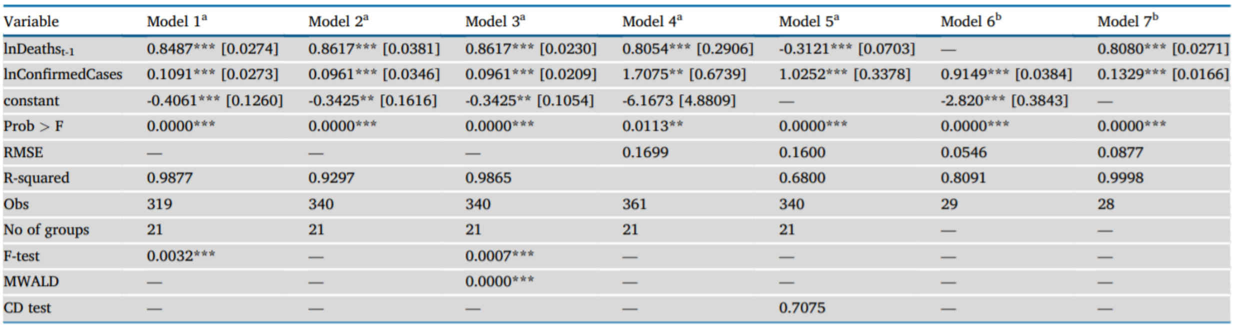
During the period of decrease there were around 1 month per incidence data for Spain and Italy (after the daily high incidence). Similarly, the log-linear model methodology has been followed, but it is now used to deal with the daily impact of decay. The model is also suited for the daily incidence and parameters of the decay stage are derived. Please note: during the decay phase the values and significance of the expected parameters vary, the growth rate is negative and the half time doubles.

The projected incidence of the daily sampling in both countries is compared to 1 to 2 months following the conclusion of the decay phase. During the remainder of the degrading period, the observed daily incidence was achieved. It generally appears that future daily incidence predictions in Italy and Spain are much higher than the daily incidence observed for all three serial distributions. With a month (21 May 2020), Italy's daily projections are about double the current incidence; Spanish daily forecasting is around double the current incidence. The daily incidience projects in Italy are around two to three times higher than the actual two month incidence (22 June 2020), with Spanish daily incidence forecasts up to double the actual incidence. However, the projected Spanish incidence for everyday life is almost equal to the actual incident with the average μ=6.3 and standard − ′= 4.2 deviations of the Serial Gamma distributive interval.

While the findings reveal that both Italy and Spain will typically estimate their future daily incidence, they do give some extra information on reproductive values with respect to daily incidence patterns. These estimates should not be accepted immediately at face value, however, since there are many setbacks which affect the expectations. At the time of the initial research, limited data on the incidence of decay were available, which likely contributed to lower R0 estimates and thus forecasts. The projections are based on the data until the end of the sample decay phase data and are hence unaccountable of any afterwards adopted health policies or interventions, which are likely to contribute to overestimation.

Table 1 provides the estimation of the parameter of the link between new coronaviral deaths and confirmed COVID-19 cases. The statistically significant figures were assessed to be 5% (95% CI) with a corresponding prediction power (R-square) of 68 to 100%. The Modified Forest Statistics of Model 3 (MWALD) refutes the concept of zero homosexuality. In other words, in China there is a varied influence of confirmatory cases on new coronaviral mortality. The two time series models showed that the lagging coronavirus (LDV) variable (lnDeathst-1) was positively and statistically significant, except from Model 5 with an extensive negative (99 percent CI-related) coefficient. The LDV models for managing omitted variable bias have been incorporated and the inertia effects of reported deaths linked to coronavirus are taken into account. In practically of these models, the positive lnDeathst-1 coefficient illustrates the persistence of past impacts that may have impacted future reporting coronaviral deaths. Instead, if unnoticed common factors determining coronaviral fatalities in Model 5 negatively influence the LDV coefficient. This reduces the inertia impact of previous deaths and reduces the impacts of verified incidents. The coefficients in both estimated panels and time series models are positive and statistically significant for the verified estimated cases in Table 1. (95 percent CI). Empirical study reveals an increase in the death rate from coronavirus by 1% in confirmed cases by ~0,10% ~1,71%. (CI of 95%).

Table 1. Parameter estimation of COVID-19



Variable	Model 1[a]	Model 2[a]	Model 3[a]	Model 4[a]	Model 5[a]	Model 6[b]	Model 7[b]
$\ln Deaths_{t-1}$	0.8487*** [0.0274]	0.8617*** [0.0381]	0.8617*** [0.0230]	0.8054*** [0.2906]	-0.3121*** [0.0703]	—	0.8080*** [0.0271]
lnConfirmedCases	0.1091*** [0.0273]	0.0961*** [0.0346]	0.0961*** [0.0209]	1.7075** [0.6739]	1.0252*** [0.3378]	0.9149*** [0.0384]	0.1329*** [0.0166]
constant	-0.4061*** [0.1260]	-0.3425** [0.1616]	-0.3425** [0.1054]	-6.1673 [4.8809]	—	-2.820*** [0.3843]	—
Prob > F	0.0000***	0.0000***	0.0000***	0.0113**	0.0000***	0.0000***	0.0000***
RMSE	—	—	—	0.1699	0.1600	0.0546	0.0877
R-squared	0.9877	0.9297	0.9865		0.6800	0.8091	0.9998
Obs	319	340	340	361	340	29	28
No of groups	21	21	21	21	21	—	—
F-test	0.0032***	—	0.0007***	—	—	—	—
MWALD	—	—	0.0000***	—	—	—	—
CD test	—	—	—	—	0.7075	—	—

In order to determine the clinical characteristics, pattern of transmission, severity, and risk factors in new coronavirus diseases, many new methods for clinical and epidemiological studies were defined. Our estimated findings show that heterogeneity and common variables have not been discovered that promote new coronavirus related fatalities resulting from an increase in confirmation cases. But the function and common elements in facilitating COVID-19 communication remain unknown. The heterogeneity is understood. This confirms the conclusions of the WHO-published Status Report – 33. The function of environmental risk factors in the transmission process COVID-19 is questionable, according to the paper. However, the transfer of people to humans is confirmed by the expansion of communities, homes, medical establishments and environment. In the course of this transmission, our research shows that there is a completely linear link between proven and new mortality due to coronavirus, as safety precautions and preventative measures are essential to avoid human-to-human transmission.

Conclusion

Our provided research is not based on a clinical method but on phenomenological models, thus the interpretation of the result should be cared for. We showed that the influence of the confirmed cases on the attributable COVID-19 fatalities is rather linear, but in the case of recovery the influence of the confirmed cases is non-linear. Our study has limited early case research and historical data, such that in the later stage of a new coronavirus illness our assessment findings may vary (COVID-19). In order to boost the sensitivity and strength of models, we used an estimation battery strategy. The lack of accurate clinic data from COVID-19 has served to estimate the fundamental reproductive number using the log-linear modell with the present results for serial COVID-19 distribution from the literature. In Italy and the most affected regions of Lombardy, this value was assessed between 2.1 and 3 and in Spain and between 2.5 and around 4, the most affected regions of Madrid and Catalonia. Analysis of the effective number of reproductive illnesses indicated that in both countries the number of infectious illnesses of COVID-19 fell and the favourable health impact of measures such as national lock-outs. In order to provide fundamental predictions of a future daily incidence in Italy and Spain, the logrinear regression model for an epidemic decrease. In future, the predicted daily incidence was sometimes 2 to 3 times higher than the actual daily incidence. These findings show that the estimations can only provide acceptable signals in the short run since they are based on data from the past that may or may not account for short-term changes – e.g., new health interventions, public policies, etc.

Although our findings are simple, we feel that they give an intriguing glimpse into COVID-19 outbreak data in two of Europe's wors-hit nations. The results of our survey indicate that both the growth and decline phase of the COVID-19 and other infectious disease incidence may be better suited to the loglinear model and the number of new cases in short term predictions when no recent intervention measures are implemented for the growth (or decay) of the new cases. The data may also serve to make a contribution to decision making on health policy or government involvement, particularly in the event of a major second wave of COVID-19. These conclusions should nevertheless be used in combination with other, more complicated models of mathematics and epidemiology.

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