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Estimation of the probable outbreak size of novel coronavirus (COVID-19) in social gathering events and industrial activities

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ABSTRACT

Background: The reproduction number (R_0) is vital in epidemiology to estimate the number of infected people and trace close contacts. R_0 values vary depending on social activity and type of gathering events that induce infection transmissibility and its pathophysiology dependence.

Objectives: In this study, we estimated the probable outbreak size of COVID-19 clusters mathematically using a simple model that can predict the number of COVID-19 cases as a function of time.

Methods: We proposed a mathematical model to estimate the R_0 of COVID-19 in an outbreak occurring in both local and international clusters in light of published data. Different types of clusters (religious, wedding, and industrial activity) were selected based on reported events in different countries between February and April 2020.

Results: The highest R_0 values were found in wedding party events (5), followed by religious gathering events (2.5), while the lowest value was found in the industrial cluster (2). In return, this will enable us to assess the trend of coronavirus spread by comparing the model results and observed patterns.

Conclusions: This study provides predictive COVID-19 transmission patterns in different cluster types based on different R_0 values. This model offers a contact-tracing task with the predicted number of cases, to decision-makers; this would help them in epidemiological investigations by knowing when to stop.

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1. Introduction

The outbreak of COVID-19 has currently spread to more than 217 territories (Hui et al., 2020) since December 2019 (Chang et al., 2020; Li et al., 2020; Roda et al., 2020; Wu et al., 2020). According to the latest statistics, up to May 1, 2020, there have been more than 3,389,933 confirmed cases found in more than 187 countries covering six continents (Johns Hopkins Coronavirus Resource Center, 2020). COVID-19 was officially declared by the World Health Organization (WHO) a pandemic on March 29, 2020 (WHO, 2020). COVID-19 causes Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) (Guliyev, 2020; Vega, 2020; Ceylan,

2020); COVID-19 can be considered the most significant public health threat caused by a respiratory virus since 1918 (Sen-Crowe et al., 2020). In addition to its consequences for public health, COVID-19 has a profound impact on affected nations' economic well-being.

Several studies have reviewed the impacts of COVID-19 on public health (Liu et al., 2020a,b), pathophysiology, clinical manifestation diagnosis, case management, emergency response, and preparedness (Di Gennaro et al., 2020).

The primary reason for the long-distance transmission of COVID-19 is migration. Wu et al. (2020) analyzed the relationship between the migration network and the virus's spread. Setti et al. (2020) studied the impact of the two-meter interpersonal distance, which was recommended by the WHO, on virus transmission. A work by Yasir et al. (2020), investigated the effect of e-Government and COVID-19 word of mouth on social presence while (Qeadan et al., 2020) used data from South Korea and Italy, who separately implemented public health actions to contain the spread of COVID-19, to build a naïve forecast for the outbreak of COVID-19 in the state of Utah in the USA.

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The reproduction number (R_0) is a measure used in epidemiology to estimate the number of new cases of infected people caused by contacting one infected person in the population (Zhao et al., 2020; Liu, 2020). If R_0 is more than one, infections will continue to spread whereas, if R_0 is less or equal to one the infection will eventually diminish; however, the COVID-19 virus is still new, many assumptions are needed to calculate COVID-19's R_0 , and researchers have not yet reached a consensus about this value. According to the published literature, the R_0 of COVID-19 ranges from 1.4 to 6.49 (Liu et al., 2020a; Wu et al., 2020; Shen et al., 2020; Read et al., 2020; Majumder and Mandl, 2020; Cao et al., 2020; Zhao et al., 2020; Imai et al., 2020; Riou and Althaus, 2020; Tang et al., 2020; Li et al., 2020).

Variations in the estimated values of R_0 for COVID-19 indicate that it is situation-dependent. Furthermore, the R_0 for COVID-19 varies based on the outbreak's start time and the control measures imposed by countries to combat the virus' spread. The virus' outbreaks in certain countries can be attributed to events that had several people present, such as wedding parties, religious events, scientific conferences, national festivals, etc. Henceforth, we use the word *cluster* to describe any event that involved an infected person with a group of susceptible people.

The main objective of this study is to mathematically estimate R_0 of COVID-19 in clusters. We used published data from several events in different countries to estimate R_0 . Using the estimated R_0 , we develop a simple model that can predict the number of new COVID-19 cases as a function of time, where these cases emerge from such clusters.

We validate our predictive model by applying it to religious, social, and industrial clusters. Results show that decision-makers can rely on our model for estimating possible cases related to such clusters, which would in turn help them in epidemiological investigations by knowing when to stop.

2. Mathematical model

We use dynamic modeling to capture and predict the number of cases with time. Unlike previous research that relies on the classical SIR (susceptible-infectious-recovered) model and its extension (Calafiore et al., 2020), we have a new definition for the different compartments into which people in the cluster are divided (Fanelli and Piazza, 2020). Moreover, we present a new set of transition equations among the compartments. We assume that our mathematical model is only valid when the COVID-19 infection is transmitted in a cluster event of a homogeneous population with the same social contact pattern. For example, infected individuals were infected with the same transmission probability from the susceptible group of individuals. This can help with contact tracing when undertaking an epidemiological investigation.

On the other hand, with respect to tracking the spread of COVID-19 in heterogeneous populations with a no-contact social pattern, our model cannot perform in this situation with reasonable accuracy. Other mathematical models have been proposed to do this, for example, Liu et al. (2020b) developed the contact network and no-contact models to track disease spread in contact patterns such as unprotected and protected contact and airborne spread. This, in fact, was not our objective. Our mathematical model only predicts the spread in homogenous populations (e.g., event attendees) based on a contact model to offer the decision-maker in a contact-tracing task the predicted number of cases, which would help them in epidemiological investigations by knowing when to stop.

The population that we target in our model is only people attending an event, those in the cluster. The different compartments in which we divide the targeted population are:

- 1) suspected individuals (S) who are exposed to positive-infected individuals with symptoms of COVID-19 infection,
- 2) infected individuals (I) who have confirmed COVID-19 infection with a positive result by Polymerase Chain Reaction (PCR) testing of respiratory specimens, and quarantined infected individuals (Q) who are either quarantined or in hospitals.

An infected person in a cluster exposes S_0 individuals, who were present at the event, to the disease. Out of the S population, $I(t)$ individuals are identified by PCR testing to have the virus at the time t .

The Infection Rate (r_i) depends on R_0 and the incubation period (N), as shown in Eq. (1):

$$r_i = \frac{\theta R_0}{N} \quad (1)$$

where θ is empirically estimated as 0.035 for COVID-19 in the present study to best fit the actual cases (i.e., with an accuracy greater than 80%, given as a constraint in the model), representing the average transmissibility. Liu et al. estimated θ to be equal to 0.026 under no quarantine measures. The R_0 range given to the model was between 2 and 5, and N is 14 days for COVID-19 (range, 2–14 days) (Lauer et al., 2020; Linton et al., 2020).

At the time of the event, we divided attendees into S_0 and I_0 to show the starting numbers of susceptible and infected individuals. I_0 is either a given number or a percentage of S_0 , 2–4% of the S_0 , depending on the infection-source country. For example, for the religious event that took place in South Korea that caused thousands of infections, the infection source was a single individual; consequently, $I_0 = 1$ and $S_0 =$ all event attendees, except the infected individual.

The number of suspected and infected cases on the first day ($n = 1$) can be calculated using Eqs. (2) and (3). Two to 14 days after the event, the number of suspected and infected cases is found using Eqs. (4) and (5).

$$S_{i=1} = S_0 - I_0 \quad (2)$$

$$I_{i=1} = I_0 \quad (3)$$

$$S_{i=n} = S_{i=n-1} + I_{i=n-1} - I_{i=n} \quad (4)$$

$$I_{i=n} = I_{i=n-1} + (S_{i=n-1} * r_i) \quad (5)$$

To calculate the suspected cases per day after identification of infected cases and removing them (the infected cases) from the susceptible population for treatment, then Eq. (5) is substituted in Eq. (4), as shown in Eq. (6)

$$S_{i=n} = S_{i=n-1} - (S_{i=n-1} * r_i) \quad (6)$$

3. Study clusters

The cluster types are selected in the present study because they are considered a homogenous sample with running contact-based models in a specific time and location. The cluster event is bounded and well-identified. The social pattern and communication intensity are relatively varied; hence, it is expected that the R_0 varies. Most importantly, these cluster events were in the beginning of the virus spread worldwide and played a role in causing outbreaks in each of the considered countries in the present study.

We searched for data given in news and public health reports, an official website (WHO), and governmental reports that cited

COVID-19 infection data in the selected study cases. For each case, we extracted from the news and other sources the number of positive cases recorded each day after the event.

In most cases, the interval of possible COVID-19 virus exposure was selected between the time the event was held, and the latest reported positive cases related to the event. We assumed that the transmission is proceeding until the epidemiological teams reach all cases (generations) of the infection chains.

3.1. Religious events

Two religious events are analyzed in our work. The first event took place in a Malaysian mosque while the second event took place in a South Korean church.

3.1.1. Malaysia

A four-day Tablighi Jamaat event was held at Jamek Mosque in Sri Petaling, Kuala Lumpur, from February 27 to March 1, to which 16,000 attendees (including about 1500 from outside Malaysia (Barker, 2020)) were invited and at least 10,500 guests attended this event. The event was socially active (including sharing of food, sitting close to each other and holding hands, and no COVID-19 precautions were officially declared); however, most attendees washed their hands during the event (The New York Times, 2020).

The Tablighi assembly is considered the largest cluster that kicked off the second wave of COVID-19 infections in Malaysia. On March 16, 553 positive cases were reported, linked to this Tablighi assembly in Malaysia; also, 620 people, including those from other countries, who attended the event have tested positive, making it the largest-known center of COVID-19 transmission in Southeast Asia (Beech, 2020).

3.1.2. South Korea

The Shincheonji religious group was connected to the coronavirus outbreak on February 18 in South Korea. A 61-year-old South Korean woman, with no prior overseas travel history nor contact with other confirmed cases, attended two Shincheonji religious services before testing positive for the virus; she is believed to have spread the virus (Martin and Yoon, 2020). A cluster of infections followed. By February 20, the national tally had increased from 31 to 156, and the first death was reported. The religious group became involved in controversy during the COVID-19 pandemic in South Korea, reaching 4000 cases of COVID-19 within two weeks; roughly 60% of the total infections nationwide stemmed from the church services (KCDCP, 2020).

3.2. Social events

Two weddings, one in Jordan and the other in Uruguay, witnessed several COVID-19 outbreaks due to the presence of infected individuals.

3.2.1. Jordan

From March 14 to March 27 79 coronavirus cases were officially reported in Jordan (<https://corona.moh.gov.jo/ar>), who had been guests at a wedding party attended by 400–450 people held on March 13, despite a ban on large gatherings. This coronavirus cluster put Jordan at a crossroads in dealing with the pandemic and forced the government to seal off the City of Irbid, Jordan's second-biggest city, and the surrounding province after dozens of guests, who had attended the wedding, tested positive. Subsequently, the government announced a lockdown on March 17, a strictly-enforced curfew described as one of the world's strictest measures. However, after four days the curfew was relaxed, because government plans to deliver food to neighborhoods had failed; people were allowed to walk to buy groceries from local stores

from 10 am till 6 pm, when civil defense sirens were used to announce the time when people could no longer go outside (CNN, March 26, 2020).

3.2.2. Uruguay

A 500-guest wedding party was held on March 7 and was reported then to have caused an explosive growth of COVID-19-positive cases. It was traced back to a traveler who, deciding to attend the wedding event just hours after arriving from Spain, later tested positive (The Guardian, 2020). Subsequently, confirmed cases jumped from four on March 12 to 79 on March 20; 44 cases were traced back to the 500-guest wedding party. As a result, various containment measures were introduced in mid-March, and additional restrictions on movement followed in late March.

3.3. Industrial event

After suppressing the infection rate to below 1%, parts of Australia started easing restrictions (i.e., social distancing); subsequently, a relatively small COVID-19 cluster emerged on April 2, 2020, at a meat factory in Victoria (Kelly, 2020). Forty-nine positive cases were reported in a meat processing plant, out of 350 employees, on April 29, 2020. The physical layout of meat factories is relatively challenging for maintaining physical distancing since workers have to be in relative proximity.

4. Results

4.1. Reported cases

Table 1 shows the confirmed case of COVID-19 infection for wedding party events in Jordan and Uruguay, religious gathering

Table 1
Reported actual cases of COVID-19 in the selected cases.

Days	Actual cases				
	Jordan	Malaysia	Uruguay	South Korea	Australia
16-Feb		4		1	
17-Feb				21	
18-Feb		11		91	
19-Feb				635	
20-Feb		15		804	
21-Feb		18		879	
22-Feb		32		1008	
23-Feb		37			
24-Feb		65			
25-Feb		75	1	2000	
26-Feb		81			
27-Feb		100		4200	
28-Feb		112			
29-Feb		131			
1-Mar		158			
2-Mar		197	4		
3-Mar	2	238	6		
4-Mar	9	428	8		
5-Mar	16	553	16		
6-Mar	16	1173	26	4482	
7-Mar	16		44		
8-Mar	17				
9-Mar	20				
10-Mar	25				
11-Mar	30				
12-Mar	36				
13-Mar	42				
14-Mar	47				
15-Mar	73				
16-Mar	79				
2-Apr					1
28-Apr					45
29-Apr					49

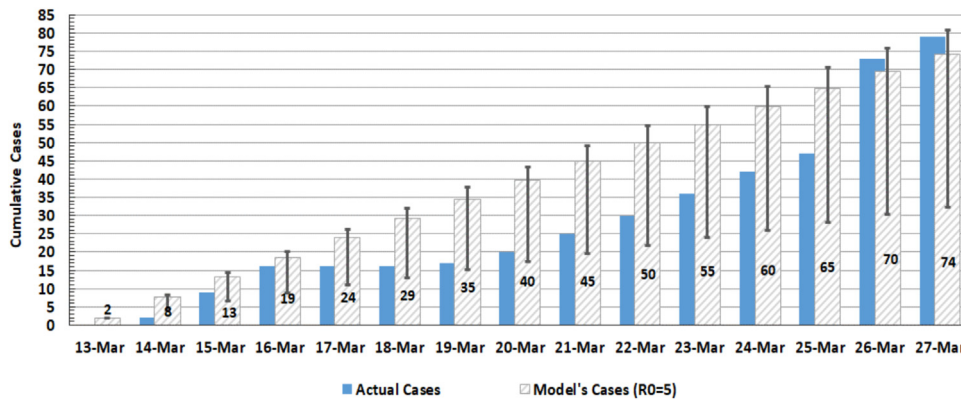


Fig. 1. The cumulative cases for COVID-19 in Wedding event-Jordan (March 13, 2020, and March 27, 2020).

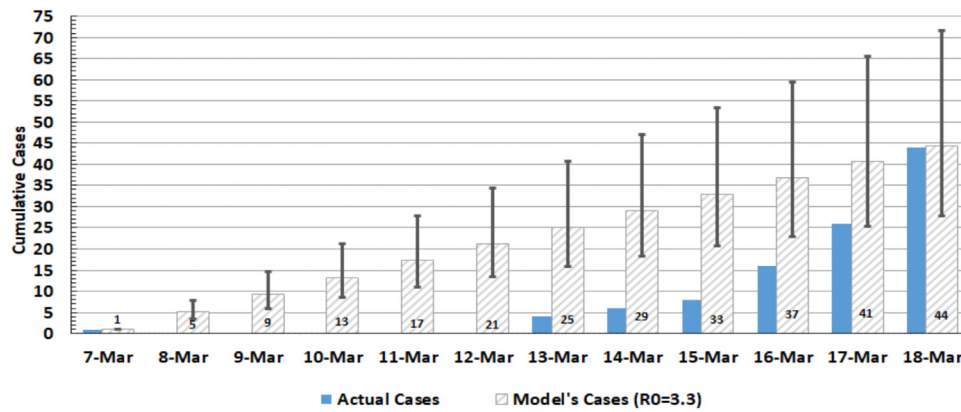


Fig. 2. The cumulative cases for COVID-19 in Wedding event – Uruguay (March 7, 2020, and March 18, 2020).

events in Malaysia and South Korea, and an industrial activity cluster in Australia.

4.2. R_0 estimation

To evaluate the transmissibility of COVID-19 in the selected clusters, as stated before, we applied our mathematical model to estimate the R_0 in such types of events. Accordingly, we calculated the expected infected cases, comparing our model's accuracy with the actual reported cases in the events mentioned above.

We assumed the interval values of the corresponding parameter (R_0) of this mathematical model, by which COVID-19 at an early stage of spread in each country, without intervention scenarios (curfew, lockdown, restricted social distancing, etc.) is modeled. The R_0 values were selected in an interval between 2 and 5.5; then, the best-fit R_0 value was determined for each event.

4.2.1. Wedding party events

The two wedding events held in Jordan and Uruguay, as stated before, were selected to evaluate the transmissibility of COVID-19 in such types of clusters. There was insufficient information about these two cluster cases, so we relied on the limited daily data published in official reports and daily news websites. This limited our ability to undertake sound statistical analysis.

Using the existing data of reported cases and the mathematical model incorporating these data, we estimated the R_0 of COVID-19 in these wedding events. We estimated that R_0 was about 5, as shown in Figs. 1 and 2, while modeling different ranges of R_0 (2.0–5.5) where the values of modeled cases are shown in the bars above the modeled cases of $R_0=5$. Fig. 3 compares the modeled

(predicted) and actual cases at the wedding events in Jordan and Uruguay, at $R_0 = 5$. The correlation coefficient between the two is 0.7303. It is noteworthy that it is quite difficult to precisely calculate the R_0 since it is difficult to determine actual daily cases during any cluster event due to the delay in epidemiological tasks, cases sampling, and PCR testing, as well as other parameters that might delay case-reporting, such as demographic variations, etc. (Delamater et al., 2019; Zhang et al., 2020). Moreover, our model assumes that all suspected cases (exposed cases and cases with close contact with confirmed cases) have been identified and PCR-tested, including asymptomatic cases.

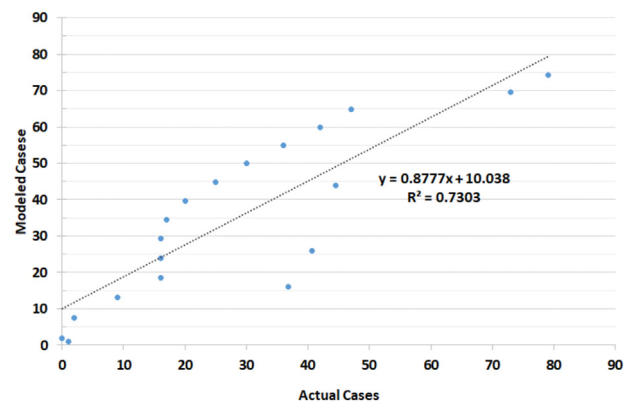


Fig. 3. Modeled (predicted) and actual COVID-19 cases in the two wedding events.

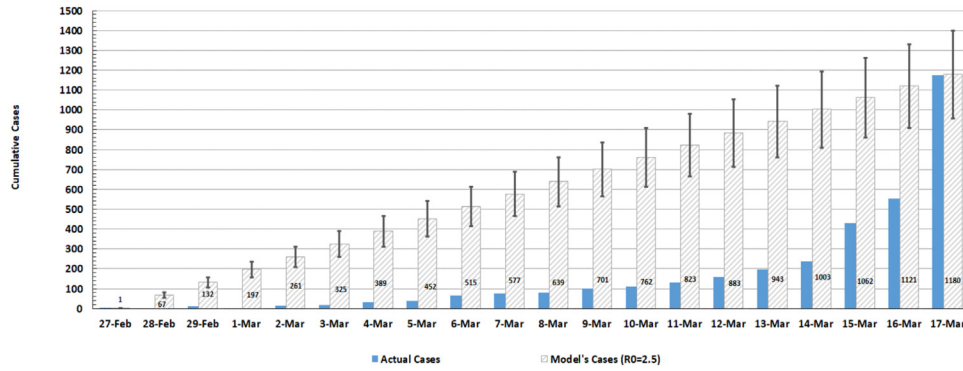


Fig. 4. The cumulative cases for COVID-19 in religious gathering event – Malaysia (February 27, 2020, and March 17, 2020).

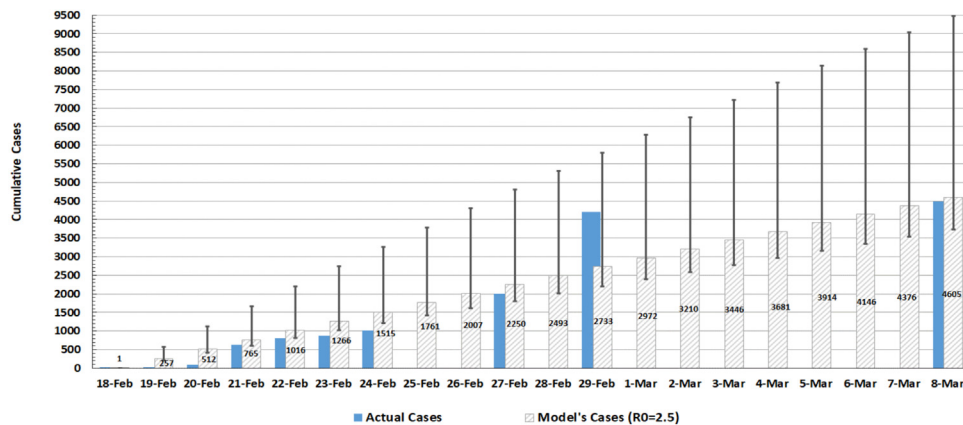


Fig. 5. The cumulative cases for COVID-19 in religious gathering event – South Korea (February 18, 2020, and March 8, 2020).

4.2.2. Religious gathering events

Two religious gathering events held in Malaysia and South Korea, as stated before, were selected to evaluate the transmissibility of COVID-19 in such types of clusters. There was insufficient information about these two cluster cases, so we relied on limited daily data, which were published in official reports and daily news websites, and hence, this limited the capability to undertake sound statistical analysis.

As shown in Figs. 4 and 5, the R_0 estimates based on the officially reported cases and after incorporating these data in our mathematical model, while modeling different ranges of R_0 (2.0–5.5) as shown in the bars above the modeled cases. We estimated that R_0 was about 2.5, which fits the actual data in good agreement. Fig. 6 compares the modeled (predicted) and actual cases at the religious gathering events in both Malaysia and South Korea, at $R_0=2.5$. The correlation coefficient between the two is 0.8755.

4.2.3. Industrial activity cluster

The meat and poultry processing industry is considered a medium to large industry worldwide, and an essential component of any country’s food infrastructure. Hence, it is of great importance to predict COVID-19 spread in such an industrial sector.

Therefore, we incorporated the existing data of reported cases in Australia, as stated before, and we calculated an estimation of the R_0 of COVID-19 in the meat processing case. We estimated that the R_0 was about 2, as shown in Fig. 7 while modeling different ranges of R_0 (2.0–5.5) where the values of modeled cases are shown in the bars above the modeled cases of $R_0=2$.

5. Discussion

Since most of the increasingly transmitted COVID-19 outbreaks started with clustering events, then a transmission-trends analysis based on daily positive-cases data using mathematical modeling is crucial. It can be employed as an early warning system for non-pharmaceutical interventions and the need for imposing restrictive measures (i.e., lockdown, confinement or quarantine), to combat and weaken the outbreak chains. Our proposed model may be a convenient tool to track the COVID-19 by testing and reporting changes over time and benchmark the cases within and after

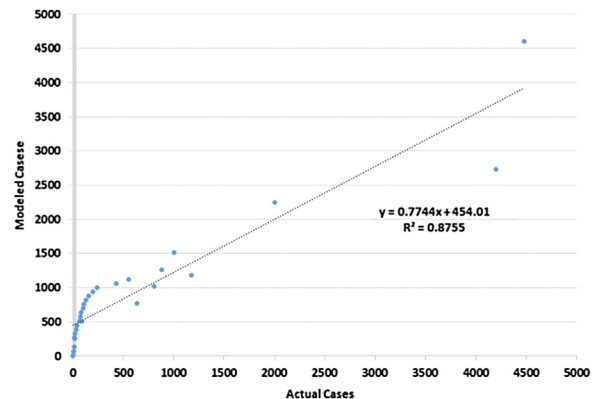


Fig. 6. Modeled (predicted) and actual COVID-19 cases in the two religious gathering events.

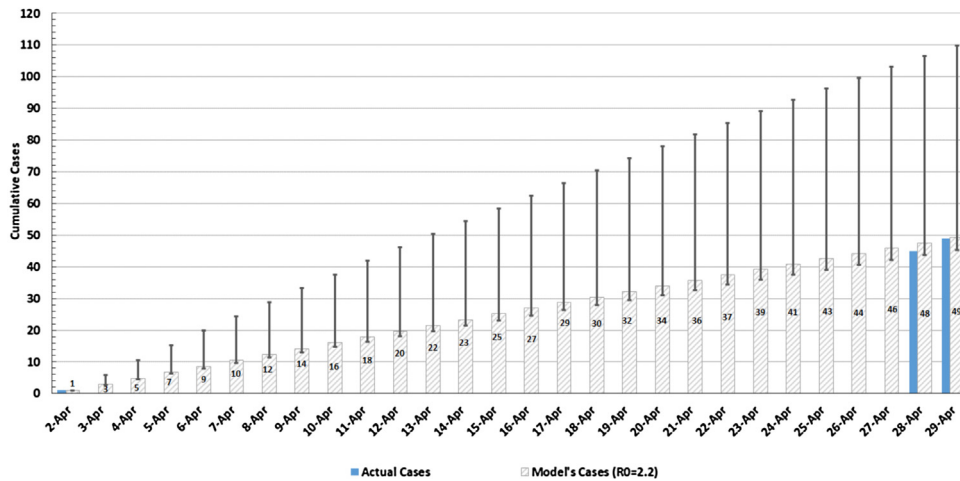


Fig. 7. The cumulative cases for COVID-19 in the meat processing factory (industrial cluster) in Australia (April 2, 2020, and April 29, 2020).

imposing control measures (i.e., either restricted or intermittent). Despite the limited data at the beginning of any cluster-causing-outbreak, the timely prediction of pattern variations might provide the responsible agencies with more information on the varied spread momentum, trend pattern, and outbreak size. Thus, this helps to decide on control measures ahead of time that could lead to flattening the COVID-19 epidemic curve.

The R_0 estimates for different types of clusters events can be used for predictive purposes, and based on these, healthcare authorities may assess their capabilities and resilience to absorb such outbreak wave events.

Our results indicate that the daily predicted infected cases and the outbreak's size are fundamentally dependent on the R_0 value. When no lockdown measures were imposed, the R_0 value was relatively high at the beginning of the COVID-19 spread, despite awareness dissemination campaigns and directives that were promulgated by governments worldwide.

Based on different values of R_0 (according to cluster type), we carried out a prediction of daily incidence and the probable size of the outbreak for 14 days, for each selected case. Our mathematical modeling results show the values of R_0 for the selected outbreaks clusters are 2 for industrial activity, 2.5 for religious events, and 5 for wedding events. These values are within the range of 2–5.5; these values are acceptable when compared to published literature. The estimated cases presented in Figs. 2, 4, 5 and 7 are also modeled for R_0 values between 2 and 5.5, as shown in the bars, while the actual cases are within these bar values above the selected predicted value.

6. Study limitations

In cluster types of outbreak infection, typically, the susceptible population is more or less the same as the exposed population, which is decreasing rapidly. Hence, the modeling period is relatively short (i.e., less than a month) depending on contacts tracing, epidemiological activity and performance. Moreover, the prediction of new cases cannot be performed until some cases are identified as infected cases and removed from the susceptible population for treatment. Hence, this might affect the infection transmission within the modeling period; in this case, the R_0 is expected to change, but its variation cannot be modeled.

Since our mathematical model aims to be used as a tool for the contacts-tracing team in an epidemiological investigation, the target is to provide the overall cumulative infected cases after 14 days (the modeling period). Accordingly, the R_0 was estimated by

the model to give excellent compatibility between the actual and predicted cases in the modeling period's final days.

A comparison with the actual reported cases cannot be made daily due to the delays in positive cases sampling, testing, and official recording. This might influence the accuracy between the actual and predicted cases on a daily basis and the precision of R_0 value estimation. However, the R_0 was selected to reflect the overall cases after 14 days, or the modeling period.

Regarding the sensitivity analysis of our model, only one parameter is used in our model, which is θ ; it is empirically estimated as 0.035 for COVID-19 in the present study to best fit the actual cases (i.e., with an accuracy of more than 80%, given as a constraint to the model). The value estimation of θ was based on the reported infection rate in the Lombardi region (Italy) and New York (USA) while comparing the number of infected bases to the total population of the cities as mentioned earlier (Lombardi and New York) and after subtracting the infected cases from the total susceptible population of these areas. Transmissibility is believed to have a high value at the beginning of an outbreak, because of the lack of public awareness of COVID-19 throughout February–March 2020 in the selected cases in the present study. Note that θ influences the infection rate (r_i) in our mathematical model. However, based on the actual data reported, $\theta=0.035$ was found to be the best fit (i.e., Liu et al., 2020a,b; we estimated θ to equal 0.026 under no quarantine measures).

Finally, to enhance our model's accuracy, there is a need to indicate the testing capacities for each country at the time of an outbreak. Unfortunately, we could not find a reliable source of references or data while investigating these points (i.e., testing capacities at outbreak timing, bias reporting, etc.) at that time of outbreak (February–March 2020).

7. Conclusions

The present study provides predictive COVID-19 transmission pattern clusters for different activities (i.e., wedding parties, religious events, industrial activities, etc.) based on different R_0 values. Moreover, the proposed mathematical model offers a tool to benchmark the impact of non-pharmaceutical intervention measures and operational responses, and their spread pattern towards flattening the epidemic curve for specific outbreaks induced by such types of cluster activity.

Our findings showed that the R_0 is higher in wedding clusters, followed by religious gatherings; the lowest value was found in the industry clusters. Accordingly, the present model can be used as a

tool to predict the expected number of infected cases based on the type of outbreak cluster, enhancing plans for close contact tracing of positive PCR cases; consequently, epidemiological activities can be directed efficiently towards exposed cases with optimal logistics.

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Conflicts of interest

The authors declare no conflict of interest.

Ethical approval

Not required for this type of study.

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