Insights from Early Mathematical Models of 2019-nCoV Acute Respiratory Disease (COVID-19) Dynamics

ABSTRACT

In December 2019, a novel coronavirus (SARS-CoV-2) has been identified to cause acute respiratory disease in humans. An outbreak of this disease has been reported in mainland China with the city of Wuhan as the recognized epicenter. The disease has also been exported to other countries, including the Philippines, but the level of spread is still under control (as of 08 February 2020). To describe and predict the dynamics of the disease, several preliminary mathematical models are formulated by various international study groups. Here, the insights that can be drawn from these models are discussed, especially as inputs for designing strategies to control the epidemics. Proposed model-based strategies on how to prevent the spread of the disease in local setting, such as during social gatherings, are also presented. The model shows that the exposure time is a significant factor in spreading the disease. As crowd density increases, the higher the chance an infected person could infect other people. The attendees of the social gathering should have effective protection or preventive measures (e.g., administrative and engineering controls) to minimize further disease transmission.

Key words: *coronavirus, Wuhan, infectious diseases, mathematical modeling, huge crowd*

Jomar F. Rabajante[1,2,3]

[1] Biomathematics Research Cluster, Institute of Mathematical Sciences and Physics, University of the Philippines Los Baños, (UPLB) 4031 Laguna, Philippines
[2] Computational Interdisciplinary Research Labs, UPLB, 4031 Laguna Philippines
[3] Faculty of Education, University of the Philippines Open University, 4031 Laguna, Philippines

corresponding author:
jfrabajante@up.edu.ph

INTRODUCTION

A new coronavirus has been identified to cause respiratory illness, such as an atypical pneumonia, in humans (*European Centre for Disease Prevention and Control 2020*). This disease, with the interim name '2019-nCoV acute respiratory disease (ARD)' [official name: COVID-19], is first detected in the winter month of December 2019 in a city of 11 million people – Wuhan in Hubei Province, China (*World Health Organization 2020a, Tweeten et al. 2020*). The 2019-nCoV ARD is believed to be zoonotic in origin, from bats to intermediate host to humans (*Zhou P. et al. 2020*); and its initiation is geographically associated, but with uncertainty, with the Huanan Seafood Market in Wuhan (*Cohen 2020a*). Human-to-human transmission of 2019-nCoV has been established, such as through respiratory droplets (*Chan et al. 2020*), and there is also a suspicion of asymptomatic infection (*Chan et al. 2020, Kupferschmidt 2020*). To contain the epidemics, the government of China has ordered cancellation of huge events for the Chinese New Year celebration, and the lockdown of Wuhan and other cities (*Tweeten et al. 2020*).

The disease has been exported to other parts of China and to other countries (Singapore, Thailand, Japan, South Korea, Australia, Germany, USA, Philippines etc.) generally via travel-related activities (*Johns Hopkins CSSE 2020, Gardner 2020)*. The World Health Organization (WHO) has declared the 2019-nCoV ARD outbreak as a 'Public Health Emergency of International Concern' on 30 January 2020, specifically to enhance the level of preparedness of countries that need additional support (*World Health Organization 2020b*). To prevent the global spread of the virus, many countries have imposed travel restrictions to and from China (*Whitley et al. 2020*). The Philippine government issued temporary travel ban starting on 02 February 2020 to flights coming from and going to China, including Hong Kong and Macau (*Whitley et al. 2020, ABS-CBN 2020*). During the travel ban, foreign nationals who have been to China within 14 days prior to their arrival to the Philippines will be denied entry; but Filipino citizens and those who have a permanent resident visa may enter Philippines, but they need to undergo a 14-day quarantine (*ABS-CBN 2020*).

The World Health Organization has requested all governments and public health institutions to "implement decisions that are evidence-based" (W*orld Health Organization 2020b*). However, there are limited data

and information on 2019-nCoV ARD, especially during the initial stage of its epidemics where antiviral treatment and vaccine are not yet available. To contribute in addressing the challenge of predicting the spread of novel diseases, and assessing the possible risks and interventions, mathematical models and simulation apps can be used (*Siettos and Russo 2013, Heesterbeek et al. 2015, Tuite and Fisman 2020*). Based on the results of the models, it is possible to prescribe possible epidemiological and social strategies to effectively and efficiently prevent or control emerging diseases that could initiate pandemics (*Heesterbeek et al. 2015*). Mathematical modelers can be valuable non-frontline members of the 'early responders' team during an outbreak.

MATERIALS AND METHODS

Preliminary models of 2019-nCoV ARD, published in official webpages of academic/research institutions, as preprints, or as journal articles on or before 08 February 2020 (with updates on 11 February 2020), are reviewed. Important insights from the results of these models are discussed.

Moreover, a model using a Susceptible-Exposed-Infected (SEI) framework is formulated to propose measures to prevent epidemics during social gathering events, e.g., during parties or concerts with huge crowds. The parameter values used in this model are based on the known information about 2019-nCoV ARD. The model is represented by a system of differential equations, and simulated using Berkley Madonna for Mac version 9.1.19.

DISCUSSION

Early Mathematical Models

Various international study groups have attempted to model the dynamics of the 2019-nCoV ARD. It is important to note that it might still be early to predict what will happen due to the complexity of the biomedical factors and social systems involved. Mathematical modelers are not fortune tellers, and in fact, modelers do not wish their worst-case prediction to happen. Models can be used as intelligent input during decision-making. Here are the preliminary models of 2019-nCoV ARD published on or before 11 February 2020. Most of these early models discuss the basic reproduction number R_0 which is the average number of people that one case can infect in a population full of susceptible individuals, excluding the secondary cases. An $R_0 > 1$ indicates potential outbreak.

Model by *Gardner (2020)*

The team of Lauren Gardner of the Center for Systems Science and Engineering, Johns Hopkins University used a stochastic simulation model which is intended to mitigate pandemics at the onset of the outbreak (*Gardner 2020, Zlojutro et al. 2019*). Their metapopulation model connects airport networks (connections are weighted based on travel volume) at global scale. In each airport, a discrete-time Susceptible-Exposed-Infected-Recovered (SEIR) model is implemented. To model the 2019-nCoV ARD spread, the parameters and assumptions used are

Assumption i. incubation period is 5 days
Assumption ii. effective contact rate (related to the basic reproductive number R_0) equals 2;
Assumption iii. recovery period is 5 days; and
Assumption iv. initial cases are only from Wuhan with no border control.

Gardner (*2020*) estimated the average number (based on 250 runs) of infected individuals in mainland China and the distribution of infected travelers worldwide. Their estimates are as follow:

a. Predicted cumulative number of cases in China by 31 January 2020 is 58,000 (actual reported number is 12,000). They attributed part of the discrepancy to reporting delays, suggesting that there can be mild or asymptomatic cases who do not seek medical care and are not reported.
b. The predicted start of the epidemics happened in November 2019, with hundreds of cases already present in early December.
c. Thailand, Taiwan, Hong Kong, South Korea, Singapore, Japan, Macau, USA, Australia and France are the top 10 countries with most number of predicted imported cases by 31 January 2020. The predicted number of imported cases in Thailand is approximately 25.

Gardner (*2020*) concluded that "the actual number of 2019-nCoV cases in mainland China are likely much higher than that reported to date." The outbreak control assumed is through passenger screening upon arrival at airports. The team from Center for Systems Science and Engineering, Johns Hopkins University also developed an interactive dashboard that map the 2019-nCoV ARD outbreak in almost real-time mode (*Johns Hopkins CSSE 2020*).

Model by *Imai et al. (2020a, 2020b)*

The team of Natsuko Imai and Neil M. Ferguson

from WHO Collaborating Centre for Infectious Disease Modelling, MRC Centre for Global Infectious Disease Analysis, Imperial College London published several sets of reports. One is on the transmissibility of 2019-nCoV (*Imai et al. 2020a*), and another on estimating the potential total number of 2019-nCoV ARD cases in Wuhan (*Imai et al. 2020b*).

In the first study (*Imai et al. 2020a*), the conclusions are as follow:

a. Estimated basic reproductive number R_0 is 2.6 with uncertainty range of 1.5-3.5 (as of 18 January 2020).
b. It is suggested to block more than 60% of transmission to effectively control the outbreak. This conclusion is probably because the rule of thumb for calculating critical elimination threshold in a well-mixed host population (minimum fraction of the susceptible individuals that needs to be successfully protected, e.g., by vaccination to attain herd immunity) is $p_c = 1 - \frac{1}{R_0}$ (*Heesterbeek et al. 2015*).

In the second study (*Imai et al. 2020b*), they concluded that the estimated total number of symptomatic infected individuals in Wuhan as of 18 January 2020 is 4,000 people with uncertainty range of 1,000-9,700. They used the following assumptions:

Assumption i. Wuhan International Airport serves 19 million individuals (catchment size) from the city of Wuhan and neighboring locations;

Assumption ii. delay between infection to detection is 10 days;

Assumption iii. incubation period is 5-6 days;

Assumption iv. international travels from Wuhan is 3,301 passengers per day;

Assumption v. exit screening implemented on 15 January 2020 has no impact on exported cases as of 16 January 2020; and

Assumption vi. infected individuals travelling outside mainland China are detected at their destinations.

Other models on estimating the basic reproductive number and its implications *(Zhao et al. 2020a, Shen et al. 2020, Li et al. 2020, Wu et al. 2020, Riou and Althaus 2020, Read et al. 2020, Zhou et al. 2020, Kucharski et al. 2020, Park et al. 2020)*

There are multiple models that aim to estimate the basic reproduction number R_0 of 2019-nCoV ARD even at the early phase of the outbreak. Shi Zhao from

JC School of Public Health and Primary Care, Chinese University of Hong Kong and colleagues estimated R_0 using the exponential growth model (*Zhao et al. 2020a*). The model assumed serial interval for 2019-nCoV to be 8.0±3.6 days, which is estimated based on the serial intervals of MERS-CoV and SARS. Serial interval is the duration between the onset of symptoms of the primary case and the onset of symptoms of the secondary case infected by the primary. The results of the study are (*Zhao et al. 2020a*):

a. The estimated mean R_0 ranges from 2.24 to 5.71 based on the reporting rate of cases.
b. If there is no change in the reporting rate (as of 10-24 January 2020), the estimated R_0 is 5.71, which is estimated to be between MERS-CoV-like (5.31) and SARS-like (6.11) respiratory syndrome.
c. If the reporting rate will increase 2-fold, the estimated R_0 is 3.58, which is estimated to be between MERS-CoV-like (3.38) and SARS-like (3.77) respiratory syndrome.
d. If the reporting rate will increase 8-fold, the estimated R_0 is 2.24, which is estimated to be between MERS-CoV-like (2.16) and SARS-like (2.32) respiratory syndrome.

A comparison of the pathogenicity and transmissibility of 2019-nCoV with other viruses can be found in the paper by *Chen* (*2020*). Based on clinical studies, 2019-nCoV is less pathogenic than MERS-CoV and SARS, but there is still debate on the transmissibility of 2019-nCoV with estimated R_0 ranging 1.4-5.5 (SARS is 2-5 and MERS-CoV is less than 1) (*Chen 2020*). The estimated case fatality rate for 2019-nCoV is 3% (10% for SARS and 40% for MERS-CoV) (*Chen 2020*). Case fatality rate is the number of deaths due to the disease divided by the total number of cases having the disease. It should be noted that case fatality rate is not equal to an infected person's chance of death due to the disease (although many use this as approximation). Probability of death or survival is person- or situation-dependent. Also, a case fatality rate computed at global or national scale could be different from the case fatality rate computed at local scale. If 2019-nCoV ARD outbreak happens in a community with inferior health system, then case fatality rate in that community may be higher. The case fatality rate currently being computed is still an initial estimate since the epidemics is still ongoing, the number of deaths and total number of cases could still change.

Shen et al. (*2020*) predict epidemic of 2019-nCoV in China totalling to 8,042 infected individuals with case fatality rate of 11.02%. Their prediction used data prior

to 25 January 2020, and is not anymore accurate as of 8 February 2020. As of 08 February 2020, total confirmed cases in mainland China is 34,611, total deaths is 723 and total recovered is 2,370 (*Johns Hopkins CSSE 2020*). *Shen et al.* (*2020*) also estimated a basic reproduction number R_0 = 4.71 at the start of the epidemic on 12 December 2019 and the effective reproduction number R_e decreasing to 2.08 as of 22 January 2020. R_e is the average number of new cases caused by an infected when only a fraction of the population is susceptible.

Shen et al. (*2020*) predict that if effective intervention continues, the epidemics is expected to peak in March 2020. They suggested that every one day reduction in the average duration from disease onset to isolation of infected individuals will reduce the peak population size by 72-84%, and both the cumulative infected cases and deaths by 68-80%. Also, every 10% reduction in transmission rate could reduce the peak population size by 20-47%, and both the cumulative infected cases and deaths by 23-49%.

Li et al. (*2020*) estimated a mean incubation period of 5.2 days for 2019-nCoV ARD, mean serial interval of 7.5 days, and R_0 = 2.2. They also predict that cases in Wuhan is doubling in size approximately every 7.4 days.

Joseph T. Wu, Kathy Leung and Gabriel M. Leung of WHO Collaborating Centre for Infectious Disease Epidemiology and Control, School of Public Health, Li Ka Shing Faculty of Medicine, University of Hong Kong (*Wu et al. 2020*) presented their 'nowcast' and forecast of the 2019-nCoV ARD outbreak. They used a Susceptible-Exposed-Infectious-Recovered (SEIR) metapopulation model, considering the metropolitan-wide quarantine of Wuhan and neighboring cities, the international air travels to and from China, and the human mobility in mainland China. Using Markov Chain Monte Carlo method, the estimated posterior mean of R_0 = 2.68 (with 95% credible interval 2.47-2.86). The model predicts that there are 75,815 infected individuals in Wuhan as of 25 January 2020 which is way larger than the number of reported cases, and the epidemic doubling time is 6.4 days. They also predict that, if transmissibility in cities in mainland China is similar to Wuhan, then localized outbreaks are being sustained and the epidemics is already growing exponentially with a lag time of 1-2 weeks behind the Wuhan outbreak.

Wu et al. (*2020*) predict that large cities with close transportation links with China may become another epicenter of the epidemics unless effective control strategies are placed. Without reduction in mobility and transmissibility, daily 2019-nCoV ARD incidence will peak in the last week of March and early week of April 2020 with around 35 cases per 1,000 population. Reducing transmissibility by 25% will reduce the daily incidence to around 20 cases per 1,000 population and delay the peak of the outbreak to early May 2020.

Julien Riou and Christian L. Althaus of the Institute of Social and Preventive Medicine, University of Bern predict that R_0 is around 2.2 (90% high density interval 1.4–3.8) (*Riou and Althaus 2020*). *Riou and Althaus* (*2020*) also estimated the median dispersion parameter k = 0.54 that measure the chance of super-spreading (*k* is a parameter of the negative-binomial offspring distribution where value near zero denotes overdispersion). They indicated that transmission characteristics of 2019-nCoV is similar to SARS and to the 1918 pandemic influenza. They suggested heightened screening, surveillance and control at airports and other travel hubs to prevent further global outbreak.

Read et al. (*2020*) estimated an R_0 between 3.6 and 4.0, with corresponding critical elimination threshold p_c between 72-75%. This means that containment of the virus could be challenging. *Read et al.* (*2020*) estimated that only 5.1% of infected individuals in Wuhan are reported, and by 4 February 2020, there are more than 190,000 cases in Wuhan. Major cities like Shanghai, Beijing, Guangzhou, Chongqing and Chengdu are predicted to have large outbreaks. Thailand, Japan, Taiwan, Hong Kong and South Korea have high risk of disease importation via air travel. The lockdown of Wuhan is estimated to contribute only to 24.9% reduction in epidemic size in locations outside Wuhan.

Zhou et al. (*2020*) used SEIR to estimate R_0 which is in the range of 2.2 and 3.0. Moreover, the group of Adam J. Kucharski also estimated median R_0 fluctuating between 1.6-2.9 (*Kucharski et al. 2020*). *Kucharski et al.* (*2020*) used an SEIR-based stochastic transmission model to determine transmission over time, prevalence of symptomatic cases, and importation of the disease as of 23 January 2020. The assumptions of the model by *Kucharski et al.* (*2020*) are as follow:

Assumption i. incubation period is Erlang distributed (rate=2) with mean of 5.2 days;

Assumption ii. delay from symptom onset to isolation follows an Erlang distribution (rate=2) with mean of 2.9 days;

Assumption iii. delay from symptom onset to reporting follows an exponential distribution with mean 6.1 days;

Assumption iv. proportion of reported cases is 16% of total cases (including unreported);

Assumption v. probability of disease being exported from Wuhan to a certain location depends on the number of cases in Wuhan, the air travel connections and volume between the two places (3,300 passengers per day) before the lockdown on 23 January 2020, and the probability of reporting an imported case;

Assumption vi. transmission is modeled as geometric random walk process as:

$$d \log \beta = \alpha \, dB_t$$

where β is the transmission rate in the force of infection, α is the volatility and B_t is Brownian motion;

Assumption vii. sequential Monte Carlo is used to estimate the evolving transmission rate and daily effective reproduction number;

Assumption viii. the outbreak is initiated by a single case on 02 December 2019 (sensitivity analysis is also done by changing to 10 initial cases);

Assumption ix. super-spreading is modeled using a branching process with negative-binomial offspring distribution. The probability that an outbreak will occur after n introductions is computed as

$$1 - (1 - P_e)^n$$

where P_e is the probability that a single case will initiate an outbreak;

Assumption x. latent period is equal to the incubation period (which means asymptomatic cases are non-infectious); and

Assumption xi. the model has two sets of compartments: one for the population in Wuhan, and one for international travelers. The compartment for the population in Wuhan has SEIR sub-compartments; while EIR sub-compartments for the international travelers.

Combining multiple sources of data, the results of *Kucharski et al.* (*2020*), in addition to the R_0 estimate, are as follow:

a. their model replicated the reported temporal trend of epidemics in Wuhan and other countries as of 30 January 2020;

b. if there are more than 3 cases in a location with similar transmissibility as in Wuhan, then there is more than 50% probability of outbreak in that location; and

c. there will be substantial variation in the transmissibility of 2019-nCoV over time, which suggests that effectiveness of control measures is setting-dependent.

Due to the uncertainties in the early stages of an epidemic that could lead to pandemic, estimating transmissibility and severity (e.g., by analyzing data of the first few hundred cases) can be a challenging task. *Black et al.* (*2017*) proposed a way to do an early estimation. This could help authorities in estimating the impact and level of risks. To reconcile the different R_0 estimates for the 2019-nCoV ARD epidemics, *Park et al.* (*2020*) proposed a framework to compare and integrate the different R_0 values estimated using different models.

Models by *De Salazar et al. (2020)* and *Chinazzi et al. (2020)*

The team of Pablo M. De Salazar and Rene Niehus from Center for Communicable Disease Dynamics, Department of Epidemiology, Harvard T.H. Chan School of Public Health used simple regression analysis to predict imports of 2019-nCoV cases from Wuhan to other countries outside China (*De Salazar et al. 2020*). The goal of their study is to determine possible countries that are under-detecting the number of imported cases. The assumptions of their model are:

Assumption i. only direct air travel volume from Wuhan to other countries are considered; and

Assumption ii. the observed case counts follow a Poisson distribution. This means that *De Salazar et al.* (*2020*) assumes that the case counts are random and have equal mean and variance.

De Salazar et al. (*2020*) used generalized linear regression, which may only detect linear but not the nonlinear relationship in the data. The regression model with coefficient β is as follows:

$$C_i \sim Poisson(\lambda_i)$$

$$\lambda_i = \beta(x_i + 1)$$

where C_i is the observed case count in the i-th country which is assumed to follow a Poisson distribution with estimated mean λ_i. The variable x_i is the number of daily flight passengers from Wuhan to the i-th country. Inferring from the results of *De Salazar et al.* (*2020*), the maximum likelihood estimate of β is 0.07 with bounds 0.04-0.13 (95% prediction interval). Based on the model by *De Salazar et al.* (*2020*), Indonesia and Cambodia as well as Thailand may have undetected cases.

Other models have also considered importation of 2019-nCoV ARD from Wuhan to other countries using transportation data (*Gardner 2020, Yuan et al. 2020, Chinazzi et al. 2020*). *Chinazzi et al.* (*2020*) ranked cities based on associated risk of disease importation, with Shanghai (risk value = 5.7%) and Beijing (risk value = 5.1%) as the top two in mainland China; and Hong Kong (risk value = 6.6%), Bangkok (risk value = 1.4%), Seoul (risk value = 0.6%), Taipei (risk value = 0.6%) and Tokyo (risk value = 0.5%) as the top 5 cities outside mainland China. Assuming that 20 million passengers is the catchment size of Wuhan International Airport, the estimated median outbreak size is 31,200 cases (95% credible interval 23,400-40,400).

Model by *Nishiura et al. (2020)*

It is important to know the proportion of reported cases vs total number of cases (*Nishiura et al. 2020, Zhao et al. 2020b*). *Nishiura et al.* (*2020*) estimated the ascertainment rate of infection in Wuhan at 9.2% (95% confidence interval 5.0-20.0). This rate informs us that 90% of the cases is potentially undiagnosed or unreported. The infection fatality risk is estimated at 0.3-0.6%, comparable to 1957-1958 Asian influenza pandemic (*Nishiura et al. 2020, Jung et al. 2020*).

In the model by *Nishiura et al.* (*2020*), they used the data from the 565 Japanese passengers evacuated from Wuhan who were screened for symptoms using portable thermo-scanners. There were 63 who showed symptoms. The passengers were also tested for the presence of 2019-nCoV using reverse transcription polymerase chain reaction (RT-PCR). Eight were positive with five of them are asymptomatic. Assuming the population size in Wuhan is 11 million, the balance equation for the risk of infection used by *Nishiura et al.* (*2020*) is

$$\frac{8}{565} = \frac{c(t) \times T}{q \times 11 \text{ million}}$$

where $c(t)$ is the cumulative number of reported cases in Wuhan as of time t (as of 29 January 2020, there were 1,905 confirmed cases), T is the window of virus detection based on the serial interval (e.g., $T = 7.5$ days), and q is the ascertainment rate. The cumulative incidence can be estimated by $c(t)/q$. Due to the limitations of diagnosis techniques, small T (short detection window) may result in low value of q.

Model by *Ming et al. (2020)*

The model by *Ming et al.* (*2020*) aimed at forecasting the actual number of infected individuals in order to estimate the number of beds needed in isolation wards and intensive care units (ICUs) in Wuhan. They used a Susceptible-Infected-Recovered model. The results of their model are as follow:

a. Assuming 50% detection rate without public health interventions, the actual number of cases could be greater than the number of reported cases. The forecast is 88,075 cases as of 31 January 2020 where 34,786 cases in isolation wards and 9,346 in ICUs.

b. If public health interventions are implemented with 70% efficacy, the forecast can be reduced (26,498 total cases as of 31 January 2020). The implication of this is that continued large-scale anti-transmission controls should be executed across all members of the population (e.g., closure of schools and suspension of public transport).

An outbreak may disrupt the activities of a community. From the models discussed above, it can be observed how mathematical modelers can help in crafting decisions or policies to prevent or control infectious diseases. In the next model to be presented, the author formulated a model that can be used to recommend auxiliary strategies to prevent the spread of 2019-nCoV ARD in large social gatherings, especially during the early period of a possible outbreak. The following model can be used to inform the public on possible scenarios that may happen during social events, and the quantitative insights drawn from the model results can be translated to actual strategies.

Disease Transmission Model in Social Gatherings

A simple Susceptible-Exposed-Infected (SEI) framework (**Figure 1**) is used to propose measures to prevent epidemics during social events, e.g., during parties or concerts with huge crowds. The aim of the model is prevention during the event so the Recovered compartment in SEIR framework is not considered, which indicates that the simulation runs do not predict the whole disease outbreak in a community. The focus of the model is on disease transmission during an event that is short in duration (maximum of 24 hours) in a population that is formed randomly (well-mixed).

Let us suppose α is the level of protection of exposed persons. The β in the force of infection is derived based on the known R_0 (e.g., $R_0 = 2$) and population size of the susceptible class (S_0). The τ is a timescale factor to adjust the force of infection to the unit of time used (i.e., 'hours'). The value $\tau = \delta \times 24$ is assumed if R_0 is computed for a δ-day infectious period (e.g., 2 to 14 days) with 1 day = 24 hours (*World Health Organization 2020c*). The expression $\frac{s_0}{s_{max}}$ is the crowd

Figure 1. Susceptible-Exposed-Infected Model Framework. An infected may shed virus during the social gathering and a susceptible may be exposed. An exposed individual can be protected from being infected by having a protection (e.g., by washing hands or using face mask).

density in the area, where S_{max} is the maximum number of people that the event venue can accommod $\frac{s_0}{s_{max}}$ without overcrowding. Overcrowding happens when $\overline{\frac{s_0}{s_{max}}} >1$. To account for the assumptions stated above, the expression for β is

$$\beta = \left(\frac{R_0}{\tau}\right)\frac{S_0}{S_{max}}.$$

All parameters and state variables are nonnegative (**Table 1**). The model is represented by

$$\frac{dS}{dt} = -\beta S \frac{I_0}{N} + \alpha E$$

$$\frac{dE}{dt} = \beta S \frac{I_0}{N} - (1 - \alpha)E - \alpha E = \beta S I_0 - E$$

$$\frac{dI}{dt} = (1 - \alpha)E$$

where N=S+E+I, and N is less than or equal the maximum capacity of the event venue. The initial condition for I (I_0) is assumed to be one infected. In the Philippines, there are few confirmed cases but more than 200 persons underinvestigation as of 07 February 2020 (*Modesto 2020*). The probability of having this one initial case couldbe low in a country where the disease is possibly contained; but to account for the uncertainty, it is assumed that there is one possible case.

Insights that can be drawn from the model are as follow:

Insight A. The exposure time (number of hours the infectious and susceptible people are staying in the event venue) is a significant factor in spreading the disease. The risk of disease transmission increases through time (**Figure 2**).

Insight B. The level of risk increases when population size of the susceptible class increases, as reflected by the crowd density. The higher the crowd density, the more the disease can spread (**Figure 2**). A crowd density greater than 1 denotes that there is overcrowding. To minimize disease spread, physical distancing is essential. However, in an overcrowded place, physical distancing is often unattainable.

It should be noted that if the people in the social gathering interact very close to each other, the infection risk is still high even if the initial population size of the susceptible class is low. This means that a social gathering, irrespective of population size, where people have high rate of encounter with other individuals is similar to a social gathering with high crowd density. Moreover, social gathering where people have high chance of leaving respiratory droplets in the environment can be considered as a scenario with high exposure rate with the virus, which can be considered as similar to the case with high crowd density.

Insight C. An exposed person could be protected from being infected depending on the level of protection against virus transmission (**Figure 3**). Protection here means that an exposed individual has an opportunity to inhibit the transfer of his/her state from exposed compartment (**Figure 1**) to the infected compartment, i.e., the person will be transferred back to the susceptible compartment. In practice, knowing the level of protection (i.e., the actual percentage of effectiveness of an equipment or practice against transmission of the virus) is difficult to calculate. Different individuals have different commitment to the health standards set by the government; and different behaviors result in different preventive practices (e.g., washing of hands, wearing of face masks). However, using multiple preventive strategies, such as adding engineering controls on top of administrative controls (change in procedures or behavior of individuals), is more effective than just using one type of control. Example of engineering controls include setting up a well-ventilated event venue.

All in all, the model suggests that to prevent disease transmission in a social gathering, exposure time or the number of hours the people are staying in the event venue should be minimized. Physical distancing should also be observed, which also means avoiding overcrowded social gatherings. Protective equipment or practices should be used as preventive measures, which include not only change in behavior but also sustainable engineering (physical or environmental) controls. In addition, themodel presented here can also be used in investigating other scenarios, such as inside mass transportation vehicles, office workspaces, and classrooms.

Table 1. Definition of parameters and variables.

| Parameter/ Variable	Definition	Unit
β	rate at which susceptible individuals are exposed to the infectious disease	1 hr^{-1}
R_0	basic reproduction number	dimensionless
τ	infectious period	hour
S_0	initial number of susceptible individuals	person
S_{max}	maximum number of people that the event venue can accommodate without overcrowding	person
I_0	initial number of infected individual (default value: 1)	person
α	rate of protection of exposed persons	1 hr^{-1}
S	population size of the susceptible class	person
E	population size of the exposed class	person
I	population size of the infected class	person
N	total number of people in the event venue	person
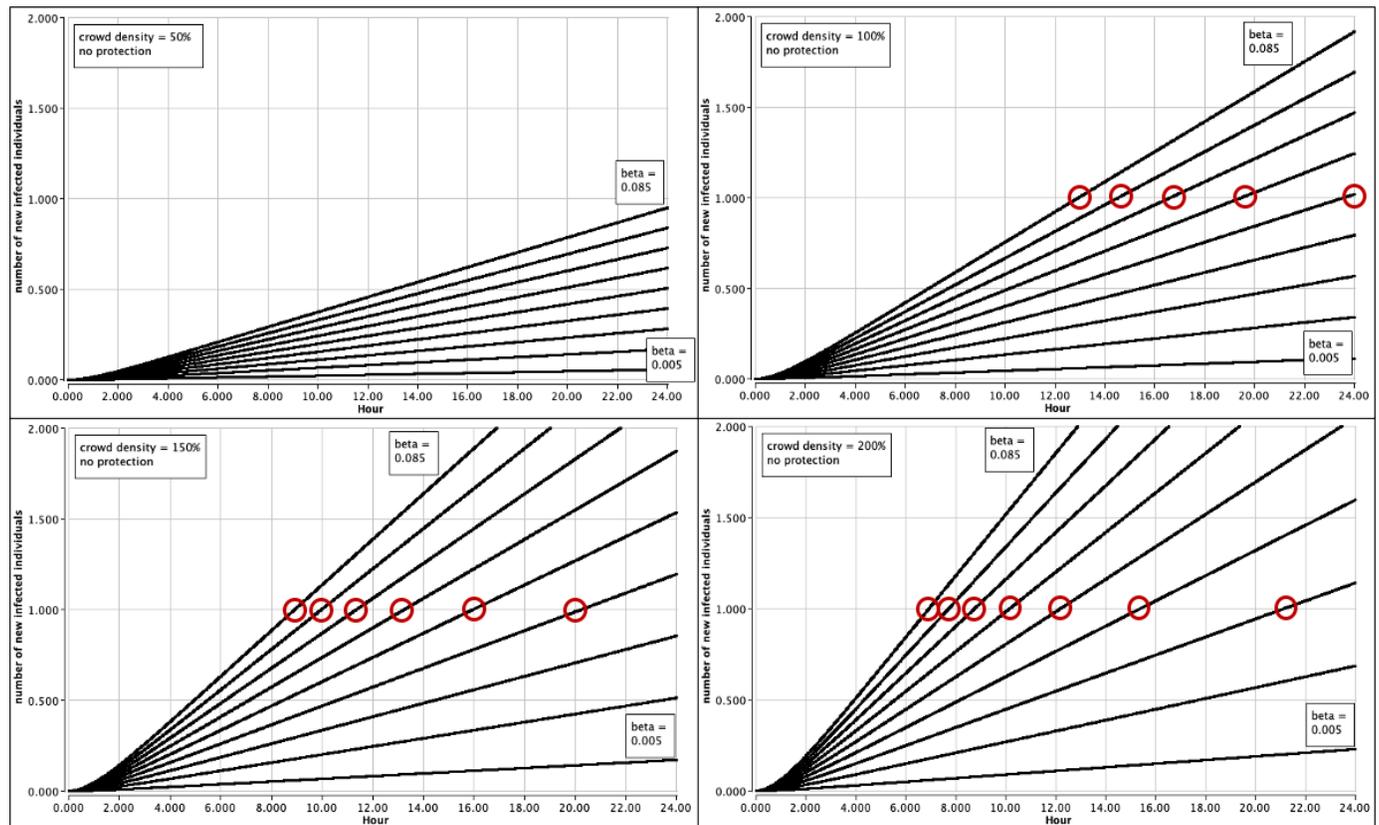
Figure 2. Transmission dynamics during an event with 50 to 200% crowd density (no protection level assumed). Number of new infected individuals greater than or equal to 1 means that there is a substantial risk of spreading the disease to other people. However, number of new infected individuals less than 1 does not mean that there is no infection risk. Different scenarios with varying values of β (0.005 to 0.085 with increments of 0.005) are simulated. β=0.005 is equivalent to the case with R_0=1.5 and 14-day infectious period. β=0.085 is equivalent to the case with R_0=4 and 2-day infectious period. Different combinations of R_0 and infectious period can be calculated for values of β between 0.005 and 0.085.

CONCLUSIONS AND RECOMMENDATIONS

Results of the mathematical models agree with the recommendation of *World Health Organization* (*2020b*) that "it is still possible to interrupt virus spread, provided that countries put in place strong measures to detect disease early"- e.g., development of rapid diagnostic tests, and increasing effectiveness of passenger screening in airports in which thermal screening for 2019-nCoV infection is estimated using simulation to be 46% (95% CI 36.0-58.0) ineffective (*Quilty et al. 2020*), – "isolate and treat cases, trace contacts, and promote social distancing
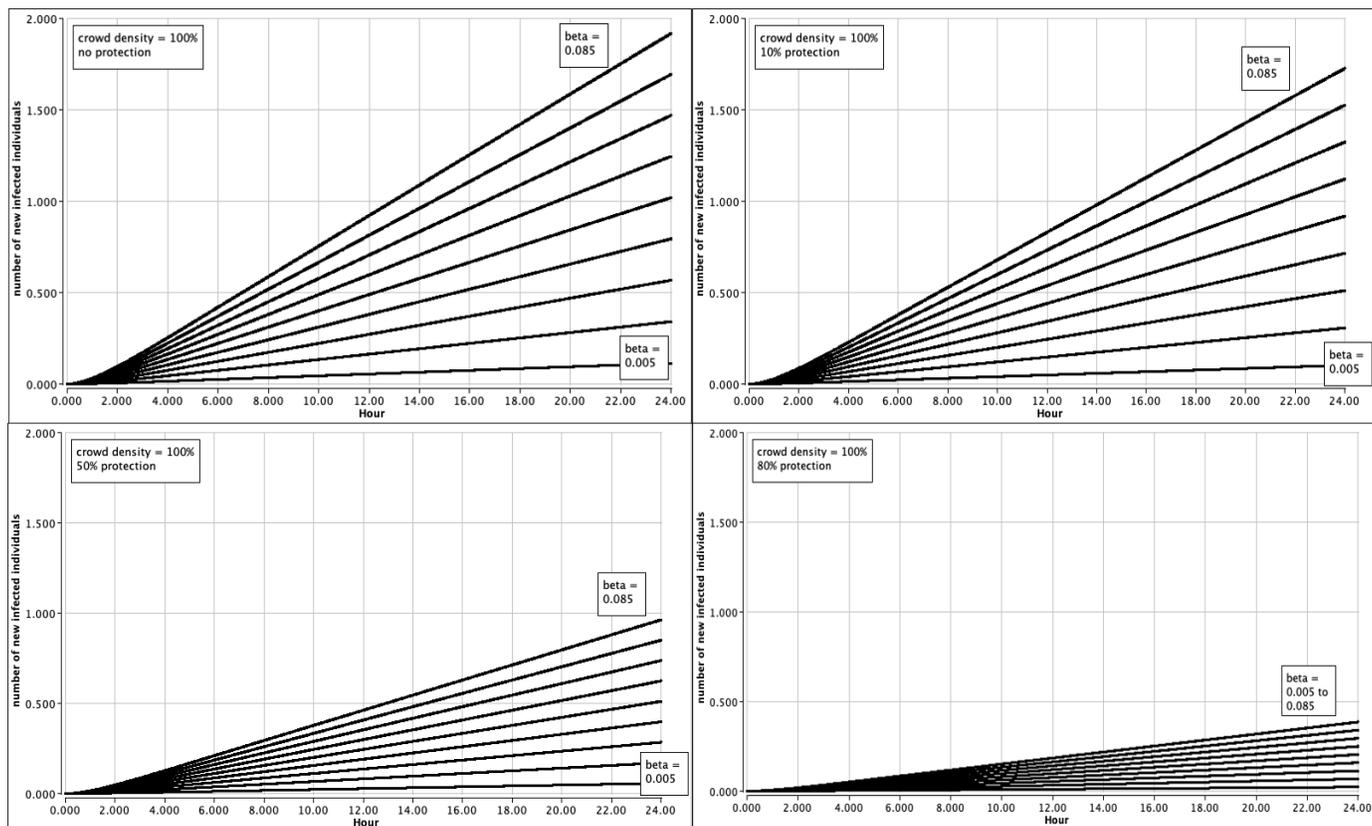
Figure 3. Transmission dynamics during an event with 100% crowd density (protection level from 0% to 80% effectiveness is assumed). Number of new infected individuals greater than or equal to 1 means that there is a substantial risk of spreading the disease to other people. As protection level increases, the risk of disease transmission decreases, as expected.

measures commensurate with the risk." Individuals can also practice basic protective measures, especially in high risk areas (*World Health Organization 2020d*). In the Philippines, many big events are cancelled because of the risk (*Malasig 2020*). In Singapore, the government raised its Disease Outbreak Response System Condition (DORSCON) level to Orange (*Mohan and Baker 2020*), which means there will be moderate disruption on daily life because "disease is severe and spreads easily from person to person, but the disease has not spread widely in Singapore and is being contained."

This study formulated a model that can be used to recommend auxiliary strategies to prevent the spread of 2019-nCoV ARD in large social gatherings, especially during the early period of a possible outbreak. The model shows that the exposure time is a significant factor in spreading the disease. An infected person staying in the event for long hours could infect other people. The crowd density and level of protection of the people are essential to be monitored during social gatherings.

Users of the models should be critical in reviewing the model structure, assumptions and results before applying

the insights drawn to decision making. Preliminary models can be too simplistic due to limited information available (*Cohen 2020b*), and do not consider detailed effect of the heterogeneity in susceptible and patient profiles. There can be infected individuals who are super-spreaders or super-virus-shedders, and there can be infected individuals who are isolated. Virus transmission in different settings or locations may also vary, e.g., transmission inside households, hospitals, offices, cruise ships and airports may have higher transmission rates compared to an open space such as park. A continuously updated global risk assessment model, e.g., using network science (*Robert Koch Institut 2020*), can be useful in visualization and drawing 'intuition'. Socio-economic and political factors (e.g., long duration of lockdown and travel ban) as well as influence of media can also affect the dynamics of the epidemics. In the midst of uncertainties, an effective risk communication and community engagement (RCCE) is essential to prevent infodemics, an excessive amount of information including disinformation and misinformation, that can be detrimental to public health control strategies. Moreover, the virus itself can mutate as it circulates from human to human, and other routes of transmission

maybe possible (e.g., fecal-oral transmission, aerosol transmission). As the situation continuously progresses, continuous surveillance and updated predictions are necessary, hence, prescriptions of models may change.

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DECLARATIONS

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