

# A modeling strategy for novel pandemics using monitoring data: the case of early COVID-19 pandemic in Northern Mindanao, Philippines

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## ABSTRACT

The COVID-19 pandemic has severely impacted individuals living in developing countries, including the Philippines. Possibly, COVID-19 might not be the last pandemic that can hit the country hard. To provide timely and evidence-based insights for health policymakers to control the spread of a novel infectious disease that might arise in the future, we proposed a mechanistic model that captures the dynamics of an infectious disease during its

early phase, when testing capacities are limited. Specifically, we aimed to understand the COVID-19 dynamics during its early phase by formulating a mechanistic model that uses the monitoring data (e.g. number of PUMs, PUIs from Northern Mindanao, Philippines), which are the available information on hand during that time. Closed-form formulas for the basic and effective reproduction numbers of the model were obtained to gain insights on the transmissibility of COVID-19. Sensitivity analysis was done to identify the epidemiological parameters that significantly affect the disease dynamics. We also provided numerical experiments to simulate COVID-19 dynamics. The results showed that the increasing basic reproduction number and disease transmission rate (from the susceptible to exposed

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population) were highly correlated. With limited testing capacities and unavailability of vaccines during the early phase of the outbreak, the combination of containment, lockdown, social distancing, and amplified efforts to quarantine exposed individuals can reduce the disease transmission rate. We further highlight that monitoring data, when modeled appropriately, can provide insights that can serve as a guide to our policymakers to craft evidence-based health protocols. Consequently, we note to use appropriate models when laboratory-based disease reports (e.g. those cases identified from RT-PCR tests) are available since the model is tailored fit to an early epidemic.

## INTRODUCTION

The coronavirus disease or COVID-19 has significantly impacted the healthcare system and everyone's life worldwide. It is caused by the coronavirus SARS-CoV-2 (Guo et al., 2020) and first emerged in late November 2019 in Wuhan City, Hubei Province of the People's Republic of China (WHO, 2020a). However, 2019-nCoV as formerly known, only received attention during the first week of January 2020 as the number of cases with respiratory disease grew in the city. On January 11, 2020, the first COVID-19-induced death in China was reported. Then, the first COVID-19 case outside China was confirmed two days later (WHO 2020b). The virus has continued to spread worldwide at a fast rate. Notably, the first COVID-19 death outside China was reported in the Philippines on February 2, 2020 (Center for Infectious Disease Research and Policy, 2020). On March 11, 2020, the World Health Organization (WHO) declared the COVID-19 outbreak a global pandemic (Cucinotta & Vanelli, 2020). As the year 2020 ends, the total global number of COVID-19 cases climbed to 70 million, with almost 1.6 million deaths, with 448,331 total cases and a death toll reaching 8,730 in the Philippines (Hasell et al., 2020).

As a novel pathogen, specific treatment for COVID-19 is scarce, especially during the early phase of the outbreak. In the Philippines, a series of non-pharmaceutical interventions (NPIs) have been put in place as means to reduce the time-dependent reproduction number (Flaxman et al., 2020), ever since the COVID-19 status was raised to Code RED (level 2) last March 7, 2020. These NPIs include, but are not limited to, closure of schools, working from home setup, implementation of border lockdowns, and community quarantines (Overseas Security Advisory Council, 2020; National Disaster Risk Reduction and Management Council [NDRRMC], 2020). During this time, the Philippines' Department of Health (DOH), the primary health agency tasked with monitoring the disease, reported only the number of people being monitored or investigated. This is due to limited testing facilities; the local government was careful about not letting the healthcare facilities be overwhelmed immediately. As of March 9, 2020, only around 200 to 250 tests per day were performed by the Research Institute for Tropical Medicine (RITM), which was the country's lone diagnostic lab for the coronavirus at that time (Magtulis, 2020). In the early part of the infection, DOH defined a person under monitoring (PUM) as someone who has a travel history for the past 14 days from banned countries or locations, and a history of exposure to a COVID-19 infected individual who does not exhibit symptoms of COVID-19. On the other hand, a person under investigation (PUI) refers to someone who exhibits similar symptoms as COVID-19 but has not been confirmed to have the disease. The PUMs are advised to undergo a 14-day home quarantine for observation while the PUIs, depending on how critical the symptoms are, can either be put to an isolation facility or be hospitalized (Department of Health, 2020a).

These PUMs and PUIs were considered as suspected COVID-19 cases which were subject to confirmation as testing was

heightened. Consequently, it implies that the reported number of confirmed cases is suffering from underreporting which is common to disease surveillance data (Guery et al. 2013; Lachica et al. 2019; Do Prado et al. 2020). It is noteworthy that in an early phase of a pandemic, projections pertaining to COVID-19 (e.g. cases, retrenched individuals) are deemed to be useful to aid policymakers in the extent of the implementation of NPIs (Fisman et al., 2013; Center for Strategic & International Studies, 2020; Gotinga, 2020). However, incidence data or laboratory-confirmed cases are the typical information used in projecting COVID-19 incidence (Bagal et al. 2020; IHME COVID-19 Forecasting Team, 2020; Loli Piccolomini & Zama, 2020). Thus, in the context of low testing-capacity countries (e.g. Sub-Saharan African countries, Madhi et al., 2020; and the Philippines) at the early pandemic period, a proactive modeling initiative that can use readily available information (e.g. the monitoring data) for disease projections is necessary to be formulated. It remains to show that these early datasets can be utilized to generate projections of COVID-19 cases in an affected location and derive epidemiological insights to help manage the healthcare system, in general.

The Philippines is an archipelago with 17 regions that have distinct geographical and socio-political landscapes. This poses a problem in implementing a uniform approach of the NPIs and other interventions for the entire country. Such archipelagic nature of the country is the reason why COVID-19 projection as a whole can have spurious results. As Dayrit et al. (2018) noted, the Philippines had a low quality of healthcare with limited and fluctuating testing capacity for COVID-19 surveillance (Albano et al., 2020; Sabillo, 2020). This challenges the fight to control the COVID-19 pandemic in the country. Northern Mindanao is one of the regions with no testing laboratory during the early phase of the COVID-19 outbreak. The region likewise lacked COVID-19 referral hospitals or healthcare facilities. This forces the suspected COVID-19 individuals to travel to the nearest facility to get tested and/or cater their healthcare needs. Northern Mindanao is situated around 129 mi. (207 km.) away from Davao City, Philippines, which happened to have a COVID-19 referral facility and was a testing center during the early phase of the outbreak.

Northern Mindanao region is composed of five provinces that hold 4.61% of the entire nation's population, making it the 2<sup>nd</sup> most populous region in Mindanao and the 3<sup>rd</sup> highest in population density. Northern Mindanao, the second-largest regional economy in Mindanao, also includes Cagayan de Oro City which serves as the regional center and business hub of the region. With large populations and high population density, human-to-human disease transmission is quick and COVID-19 transmission is catalyzed (Chen et al. 2020; Rocklöv & Sjödin, 2020). Hence, there is a need to understand the early COVID-19 dynamics to provide more insights into the implementation of the NPIs especially at the early phase of its outbreak. This could further guide the policymakers in anticipating budgetary, logistics, and human resource-related needs in the planning of mitigating actions for the surge of cases.

In doing so, we developed a compartmental model as popularized by Brauer et al. (2012) to describe COVID-19 dynamics, contextualized on the readily available data. The model considered the implementation of the following strategies: 1) social distancing, 2) containment period/quarantine duration, 3) testing/detection, and 4) hospitalization availability (i.e., beds capacity), and analyzed its effect on the reproduction number numerically. We also estimated unknown epidemiological rates that can plausibly describe the trends in the number of PUIs and PUMs. Finally, we used these estimated rates as baseline parameter values which can be helpful to provide projections for the number of

hospitalized PUIs that can be used as a metric to determine if the healthcare system will be overwhelmed. A case in point is when the projected hospitalized PUIs are greater than the number of hospital beds.

There are still numerous pathogens out there, either undiscovered or not fully understood. Each decade, these viruses appear and create havoc to the populace. The emergence of public health concerns from these pathogens can be linked to human activities that disturb the environment, thereby increasing the risk of transmission of pathogens that humans are unfamiliar with (Morand et al., 2014; Flandroy et al., 2018; da Silva et al., 2020). With such unprecedented human activities, new infectious diseases or epidemics can potentially emerge. Hence, developing a mathematical model that can be used at an early phase of an outbreak will be of great significance because, according to Lie et al. (2020), COVID-19 will not be the last disease to be caused by a novel virus. To our knowledge, this is the first to document the use of early monitoring data (e.g. PUM/PUI) to study the COVID-19 dynamics in the Philippines leading to new empirical work by giving new insights to old information.

## MATERIALS AND METHODS

### Monitoring Data

In this study, we used only the monitoring data provided by the Center for Health Development Northern Mindanao, Department of Health. These data were also posted on the official social media site of the said office and are for research purposes or public consumption. Henceforth, ethical approval is not required. We have processed the data for Northern Mindanao along with its provinces namely Misamis Occidental, Misamis Oriental, Bukidnon, and Lanao Del Norte, which are part of the mainland Mindanao. The monitoring dataset includes the daily count of PUM, PUI/Hospitalized, discharged, and quarantined individuals. Furthermore, the dates reflected in this report were the arrival dates of the individuals within the region.

### Mathematical Model

The model developed in this study to describe the dynamics of COVID-19 infection in Northern Mindanao was an extension of the compartmental model presented by Murray (2002) and Brauer et al. (2012) to use the early available data sets. In the model, the individuals are classified into five types:

1. Susceptible ( $S$ ) - individuals at risk of contracting the disease;
2. Exposed ( $E$ ) - individuals who has been exposed to the disease but not entirely infected;
3. Hospitalized ( $H$ ) - individuals that are under investigation (PUI), who have COVID-19 symptoms and are hospitalized;
4. Quarantined ( $Q$ ) - individuals that are under investigation (PUI) who are negative with COVID-19 symptoms or are under monitoring (PUM) being quarantined; and
5. Removed ( $R$ ) - individuals that recovered from the disease, hence removed in the system assuming they gained immunity for a time of interest.

Individuals in the Hospitalized ( $H$ ) and Quarantined ( $Q$ ) compartments are assumed to be isolated, hence cannot infect individuals in the Susceptible ( $S$ ) compartment. The parameter  $\kappa_h$  is the carrying capacity of the hospital in terms of the number of hospital beds and has a constant value per province. A schematic diagram of the mathematical model is shown in Fig 1. The model has five population compartments and each of them is a dynamic state variable – i.e. each subpopulation is a

function of time  $t$  (in days). The total population size,  $N(t)$ , is given by  $N(t) = S(t) + E(t) + Q(t) + H(t) + R(t)$ .

From Fig 1, the model equations of the well-mixed system are

$$S'(t) = -\beta_e ES + \alpha_d E + \delta_q Q \quad (1)$$

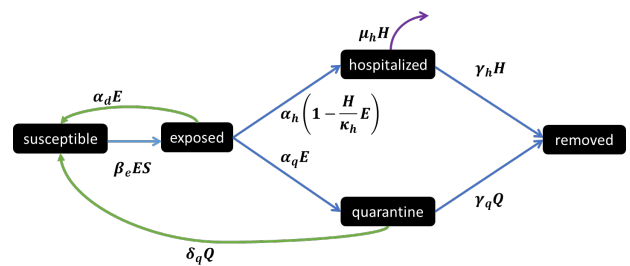
$$E'(t) = \beta_e ES - \left( \alpha_h \left( 1 - \frac{H}{\kappa_h} \right) + \alpha_q + \alpha_d \right) E \quad (2)$$

$$H'(t) = \alpha_h \left( 1 - \frac{H}{\kappa_h} \right) E - \gamma_h H - \mu_h H \quad (3)$$

$$Q'(t) = \alpha_q E - \gamma_q Q - \delta_q Q \quad (4)$$

$$R'(t) = \gamma_h H + \gamma_q Q \quad (5)$$

and the total living population follows  $N'(t) = -\mu_h H$ . The model parameters, their definitions, and units are described in Table 1.



**Figure 1: Compartmental representation of the model. Blue arrows represent disease progression. Purple arrow denotes death. Green arrows indicate returning to a susceptible state.**

**Table 1: Descriptions of the model parameters.**

Parameter	Description	Unit
$\beta_e$	Transmission rate	per individual per day
$\alpha_h$	Hospitalization rate	per day
$\gamma_h$	Recovery rate from hospitalization	per day
$\mu_h$	Death rate from hospitalization	per day
$\alpha_q$	Rate of being quarantined	per day
$\gamma_q$	Recovery rate from being quarantined	per day
$\alpha_d$	Transition rate of an exposed to susceptible	per day
$\delta_q$	Discharging rate of a quarantined*	per day
$\kappa_h$	Hospital carrying capacity*	hospital beds

\*These parameters have predetermined values from the data

Note that  $\beta_e$  scales with the constant area  $A$  in sq. km., i.e.,

$\beta_e = \frac{\kappa}{A}$ , where  $\kappa$  is the contact rate. Scaling was done to reflect the transmission rate of COVID-19 per province and collectively as a whole (Ferrari et al., 2011).

### Sensitivity analysis

There is a scarcity of information of the uncertainty of the model parameters during the early phase of the pandemic and novel

pandemics. Hence, the sensitivity of  $\mathfrak{R}_0$  to its key epidemiologic parameters was evaluated using the methods of Latin Hypercube Sampling and Partial Rank Correlation Coefficient (LHS-PRCC) (McKay et al., 2020; Iman & Conover, 1979). In LHS-PRCC, 1000 parameter values for the key epidemiologic parameters were sampled from uniform and triangle distributions. After which, these samples were randomly paired in a Latin hypercube scheme and ran 1,000 Monte Carlo simulations. From these simulation results, the PRCC for each model parameter and the reproduction number (i.e., the outcome measure of interest) were computed (Massey et al., 2020). The typical rule of thumb to assess the parameters that significantly

influence  $\mathfrak{R}_0$  is when the magnitude of PRCC values is at least 0.5000 (Alam et al., 2020).

### Parameters estimation

Parameter estimation was applied using a fitting procedure that minimized the cost function of a nonlinear least square function given by

$$J(\theta) = \sum_{i=1}^T (H_{obs}(t_i) - H(t_i, \theta))^2 + (Q_{obs}(t_i) - Q(t_i, \theta))^2 + (D_{obs}(t_i) - D(t_i, \theta))^2, \quad (6)$$

where  $\theta = (\beta_e, \alpha_h, \gamma_h, \mu_h, \alpha_q, \gamma_q, \alpha_d)$ ,  $\theta \geq 0$ . Here,

$H_{obs}(t_i)$ ,  $Q_{obs}(t_i)$ , and  $D_{obs}(t_i)$  are the given observation (i.e., data on the number of hospitalized, quarantined, and dead

individuals) in  $T$  days and  $H(t_i, \theta)$ ,  $Q(t_i, \theta)$ , and  $D(t_i, \theta)$  denotes the output of the mathematical model at time

$t_i$  computed with the parameters  $\theta$ . The optimization problem was solved using Approximate Bayesian Computation (ABC) (Csilléry et al. 2010) via Python version 3.7. In the Bayesian framework, determining the posterior probability density of the model parameters given an empirical dataset involves the prior probability of the model parameters and the likelihood function. However, the explicit form of the likelihood functions are often unavailable and such a framework is often confronted with computational issues. The posterior probability density of the model parameters using the ABC framework only involves the prior probability of the model parameters and a distribution of the discrepancy between the actual and simulated data with a tolerance threshold  $\varepsilon < 0$ . When  $\varepsilon$  approaches zero, the approximated posterior distribution becomes a good approximate of the true posterior distribution (Abdessalem et al., 2019). Furthermore, numerical simulations were done to show projections for each subpopulation considering various intervention scenarios.

## RESULTS

### Reproduction Numbers and Model Solution Behavior

It is typical to ensure that the domain

$$\Omega = \{(S, E, H, Q, R) \in \mathbb{R}_+^5; 0 \leq S + E + H + Q + R \leq N(0); H \leq \kappa_h\} \quad (7)$$

is positively invariant. We deduce, for an initial datum in  $\Omega$ , that there exists a unique global in time solution  $(S, E, H, Q, R)$  in  $C(\mathbb{R}_+; \Omega)$ . Since the infected individuals are in  $E, H$ , and  $Q$ , the rate of appearance of new

infections in each compartment  $f$  and the rate of other transitions between all compartments  $v$  can be rewritten as

$$f = \begin{pmatrix} \beta_e ES \\ 0 \\ 0 \end{pmatrix}, \quad v = \begin{pmatrix} \left( \alpha_h \left( 1 - \frac{H}{\kappa_h} \right) + \alpha_q + \alpha_d \right) E \\ -\alpha_h \left( 1 - \frac{H}{\kappa_h} \right) E + (\gamma_h + \mu_h) H \\ -\alpha_q E + (\gamma_q + \delta_q) Q \end{pmatrix} \quad (8)$$

Thus,

$$F = \begin{pmatrix} \beta_e S & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, \quad V = \begin{pmatrix} \alpha_h \left( 1 - \frac{H}{\kappa_h} \right) + \alpha_q + \alpha_d & -\frac{\alpha_h}{\kappa_h} E & 0 \\ -\alpha_h \left( 1 - \frac{H}{\kappa_h} \right) & \frac{\alpha_h}{\kappa_h} E + (\gamma_h + \mu_h) & 0 \\ -\alpha_q & 0 & \gamma_q + \delta_q \end{pmatrix} \quad (9)$$

Therefore, the next generation matrix is

$$FV^{-1} = \begin{pmatrix} \beta_e S \left( \frac{\alpha_h}{\kappa_h} E + \gamma_h + \mu_h \right) & \frac{\alpha_h \beta_e ES}{\kappa_h W} & 0 \\ W & \kappa_h W & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, \quad (10)$$

where

$$W = -\alpha_h^2 E \left( 1 - \frac{H}{\kappa_h} \right) \left( \frac{1}{\kappa_h} \right) + \left( \alpha_d + \alpha_h \left( 1 - \frac{H}{\kappa_h} \right) + \alpha_q \right) \left( \frac{\alpha_h}{\kappa_h} E + \gamma_h + \mu_h \right)$$

We deduce that the effective reproduction number (Nishiura & Chowell, 2009) is given by,

$$\mathfrak{R}_{eff}(t) = \frac{\beta_e S \left( \frac{\alpha_h}{\kappa_h} E + \gamma_h + \mu_h \right)}{W} \quad (11)$$

In particular, the basic reproduction number  $\mathfrak{R}_0$  evaluated at

the Disease-Free Equilibrium  $DFE(S^*, 0, 0, 0, R^*)$  is

$$\mathfrak{R}_0 = \frac{\beta_e S^*}{\alpha_d + \alpha_h + \alpha_q} \quad (12)$$

**Theorem 1.** The  $DFE(S^*, 0, 0, 0, R^*)$  is the unique positive equilibrium and it is globally asymptotically stable.

**Proof.** By computing the eigenvalues of the Jacobian matrix, we

deduce that if  $\mathfrak{R}_0 < 1$ , then the DFE is locally asymptotically stable.

We will then prove that global asymptotic stability is independent of  $\mathfrak{R}_0$ . From the last differential equation in our

system of ODE, we can deduce that  $R$  is an increasing function bounded by  $N(0)$  and thus  $R(t)$  converges to  $R^*$  as  $t$  goes to  $+\infty$ . Then integrating over time this equation provides

$$R(t) - R(0) = \int_0^t \gamma_h H(s) + \gamma_q Q(s) ds \quad (13)$$

and

$$R^* - R(0) = \int_0^{+\infty} \gamma_h H(s) + \gamma_q Q(s) ds, \quad (14)$$

which is finite. Moreover,  $H(t)$  and  $Q(t)$  go to 0 as  $t \rightarrow +\infty$ , because of the positivity of the solution. Similarly,

integrating the fourth equation in the system gives  $E(t) \rightarrow 0$  as  $t \rightarrow +\infty$ . Finally, the first equation points to the decreasing of  $S$  that is bounded below by 0 and thus  $S(t) \rightarrow S^*$  as  $t \rightarrow +\infty$ .

Theorem 1 means that the asymptotic behavior does not depend on  $\mathcal{R}_0$ . For all initial data in  $\Omega$ , the solution converges to the DFE when time goes to infinity.

### Sensitivity analysis

It can be inferred from Fig. 2 that the key epidemiologic parameters contribute significantly to the basic reproduction

number. In particular,  $\mathcal{R}_0$  is strongly positively correlated with the transmission rate  $\beta_e$ . This means that the changes in the average number of new secondary infections is most sensitive to the contact rate of susceptible and exposed individuals. Hence, control measures that limit the contact among the individuals are deemed as effective measures in mitigating the spread of the disease. Such an approach is common not only to existing studies on COVID-19 but also to other infectious diseases (Jurado et al., 2018; Lachica et al., 2020; Logrosa et al., 2021;

Shaw et al., 2021). On the other hand,  $\mathcal{R}_0$  is strongly negatively correlated on the three parameters: hospitalization rate  $\alpha_h$ , transition rate of an exposed to susceptible  $\alpha_d$ , and

the rate of a PUM or PUI to be quarantined  $\alpha_q$ . These model parameters are associated with the efficiency and readiness of a healthcare system which is an integral part when responding to emergency situations such as disease outbreaks (Christopher et al., 2020).

### Model fitting estimates

To calibrate the model parameters, the model fitting started on March 8, 2020, which is the hospital admission of the first confirmed COVID-19 case in the region (MindaNews, 2020). Specifically, day 0 is assigned to January 31, 2020, which is the confirmation of the first COVID-19 case in the country (Edrada et al., 2020). Hence, March 8, 2020 is treated as day 37. The fitting stops on March 23, 2020 when the quarantine in the region started (Department of Agriculture Regional Field Office X, 2020). We assume that the whole population of Northern Mindanao is susceptible to the infection. The estimated values for the epidemiological parameters are shown in Table 2. Furthermore, the relative cost function  $J$  is also presented to provide an insight on the fitting of the model to the dataset.

Fig. 3 to 7 show different estimates and simulations fitted from the data of Region 10 and its provinces. The top and left-most panel of each figure shows the boxplot for posterior distribution for each epidemiological parameter. Meanwhile, the model fittings on the hospitalized, quarantined, removed, and discharged individuals as well as the effective reproduction number can also be seen in each figure. The grey curves are the fitted solutions from the posterior distribution. The colored dotted line represents the mean solution while the solid color line represents the median solution.

### Strategies to control the spread during the early stage of the epidemic

As remarked by Lie et al. (2020), COVID-19 will not be the last pandemic that can hit the country hard. In the presence of a new pandemic where knowledge about its cause (e.g. the virus) is limited, four strategies were commonly used in practice to

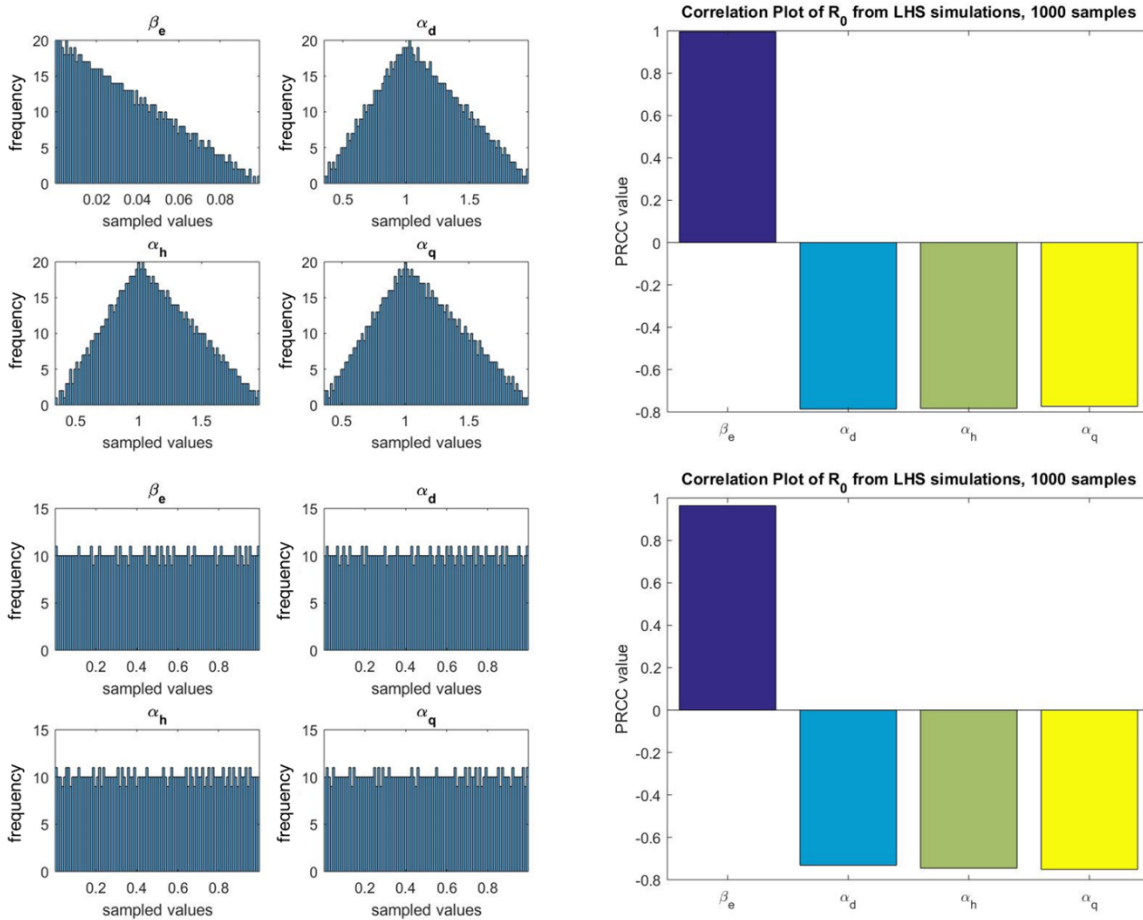
reduce the value of  $\mathcal{R}_{eff}$ . The four strategies are the following (Jones et al., 2020; Department of Health, 2020c; Hellewell et al., 2020):

- decreasing  $\beta_e$  by lessening contact between individuals such as social or physical distancing;
- increasing  $\kappa_h$  by adding hospitalization availability;
- decreasing  $\delta_q$  by extending quarantine duration; and
- increasing  $\alpha_q$  by improving detection via testing then do isolation.

Figure 8 sums up the possible effect of the aforementioned strategies on reducing disease transmission, by varying the values of the above-mentioned parameters. The four parameters correspond to the whole Region 10 given in Table 2. The y-axis represents the effective reproduction number while the x-axis represents the parameter values.

The model presented here was created to possibly understand the dynamics of COVID-19 and how to combat its transmission in its early phase. First, we have seen in Table 2 that the estimated disease transmission rate was small in each province and the region itself. Likewise, referring to Fig. 3 to 7, the reproductive number is nearly 1.0 with a variance of about a tenth. However, such basic reproduction numbers ultimately rose in the succeeding months and caused an outbreak (Umel, 2020; CNN Philippines, 2020). As in any mathematical model, we cannot account for all the factors from the ground. One thing we would like to note is the scantiness of the regional and provincial data on COVID-19 incidences which were publicly available during the early phase of the pandemic. The limited testing capacity and the late reporting of the cases are also predominant at that time since only a few cities (e.g. Davao City, Philippines) had the capacity to process the swabbed samples (Perandos-Astudillo, 2020). These greatly contributed to the uncertainty of the estimated epidemiological parameters. Such an instance could result in the underreporting of cases coupled with the presence of asymptomatic individuals who are left undetected.

As reflected in Figure 8, our result pointed out that the best strategy to mitigate the disease spread is by reducing the transmission rate  $\beta_e$ . Our sensitivity analysis also showed that the transmission rate,  $\beta_e$ , has a positive and the highest correlation to the spread of the virus,  $\mathcal{R}_0$ . A typical action to



**Figure 2: LHS-PRCC output: 1000 sampled values of parameters from uniform and triangle distributions via Latin Hypercube Sampling method (top left and bottom left); Computed PRCC values of  $\mathcal{R}_0$ , for  $S^* = 2.56 \times 10^6$ , in terms of parameters  $\beta_e$ ,  $\alpha_d$ ,  $\alpha_h$ , and  $\alpha_q$ , sampled from uniform and triangle distributions (top right & bottom right), respectively.**

**Table 2: Parameters calibrated according to data from Region 10 and its province. Discharging parameter  $\delta_q$  is constant across all the locations with an assumed value of 1/14 (i.e., two-week quarantine government protocol).**

Parameter	Region 10	Lanao del Norte	Misamis Oriental	Misamis Occidental	Bukidnon
Population	5,089,061	736,222	783,442	345,048	1,134,878
$A$	19,031.9	3,346.57	3,131.52	2,055.22	10,498.59
$\beta_e$	$1.44 \times 10^{-7}$	$1.28 \times 10^{-6}$	$7.37 \times 10^{-6}$	$3.27 \times 10^{-6}$	$6.97 \times 10^{-7}$
$\alpha_h$	$3.25 \times 10^{-3}$	$5.98 \times 10^{-3}$	$1.72 \times 10^{-3}$	$1.13 \times 10^{-3}$	$5.52 \times 10^{-4}$
$\gamma_h$	0.04409	0.20965	0.11749	0.03242	$1.66 \times 10^{-17}$
$\mu_h$	0.03888	0.34951	0.21769	0.03031	$2.39 \times 10^{-17}$
$\alpha_q$	0.71694	0.91183	5.49945	1.03567	0.73106
$\gamma_q$	0.11882	0.23148	6.82494	0.49462	0.23852
$\alpha_d$	0.00760	0.00608	0.00226	0.01063	0.02358
$K_h^*$	6,407	1,177	1,838	1,187	1,642
Relative Cost function $J$	$5.76 \times 10^{-2}$	$7.83 \times 10^{-2}$	$2.90 \times 10^{-2}$	$1.83 \times 10^{-1}$	$2.03 \times 10^{-1}$

\*Source: Department of Health, 2020b.

reduce  $\beta_e$  is by containment of confirmed and suspected individuals with COVID-19, implementing border controls and/or community lockdowns, and by practicing physical distancing (Kucharski et al. 2020; MacIntyre, 2020; Di Domenico, 2020). The finding of this study also echoes the findings of Greenstone and Nigam and (2020) and Lewnard and Lo (2020), published during the first few months of the pandemic. Another alternative approach that can be done based

on Fig 2 and Fig 8, is by increasing the rate at which exposed individuals are quarantined ( $\alpha_q$ ). Higher quarantine rate means a more substantial proportion of exposed individuals (PUMs and/or PUIs) with COVID-19 are isolated. Isolating these PUMs and PUIs could slow down the spread of the disease by impeding the potential chain of transmission (Stuart et al., 2021). It is noted that during the early time of the pandemic, tests were limited. Hence, an isolation approach coupled with efficient

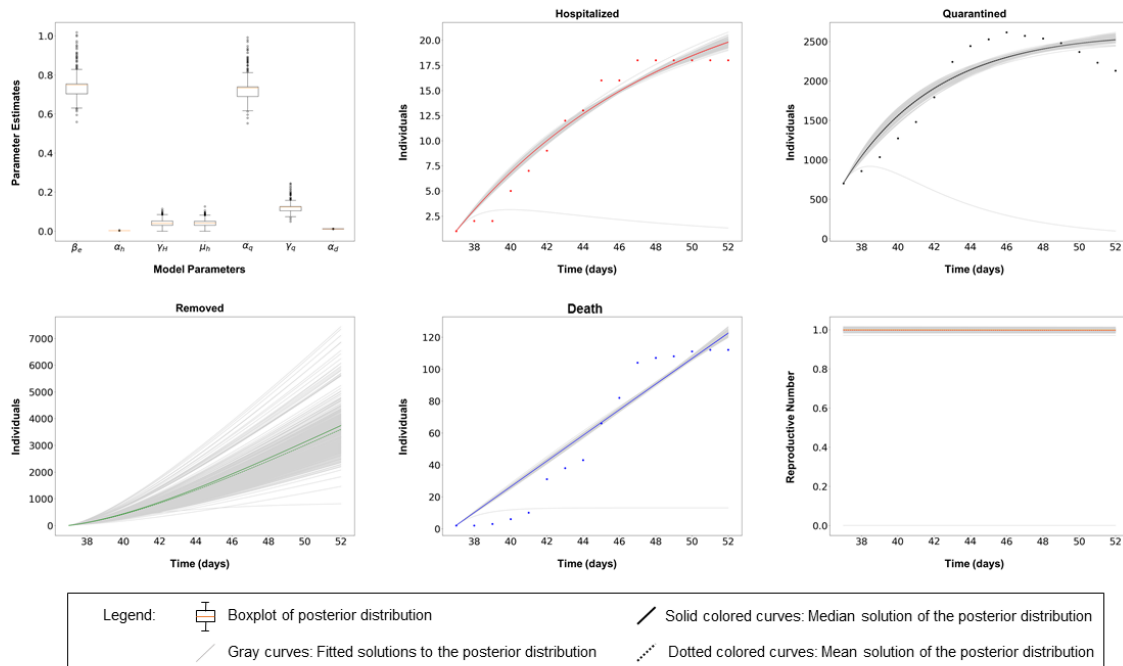


Figure 3: Fitting results for the whole Region 10, Philippines.

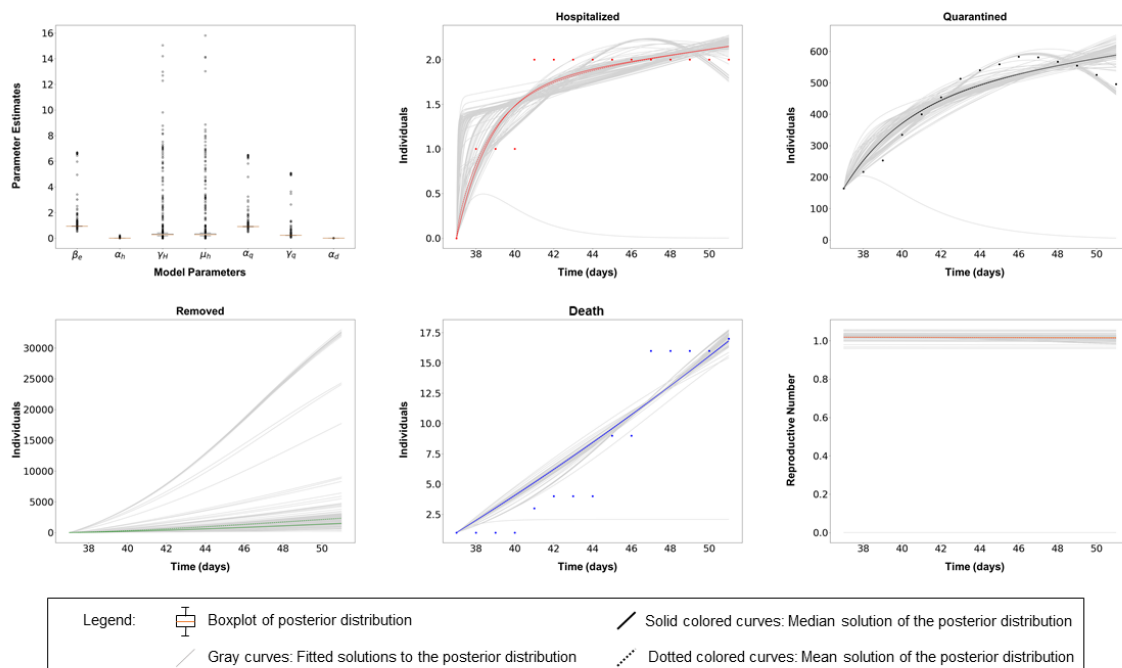


Figure 4: Fitting results for the Lanao del Norte, Region 10, Philippines.

mass testing (e.g. targeted testing to PUMs), if performed accordingly, could be a powerful weapon against COVID-19. Such strategies should be prioritized until a mass vaccination can be done so that we can expect an  $\mathcal{R}_0$  that is at a minimum level. Vaccination has been the central tenet of controlling some infectious diseases (Rafferty et al. 2018; Evangelio et al. 2020), yet remains a challenge for novel diseases. This echoes the similar findings of other studies such as Anderson et al. (2020), Mahase (2020), and Wilder-Smith and Freedman (2020). On the other hand, varying the values of hospital carrying capacity,  $K_h$ ,

and discharging rate of a quarantine,  $\delta_q$  produce little or no change to the  $\mathcal{R}_{eff}$ . This is because  $\mathcal{R}_{eff}$  does not depend explicitly on parameter  $\delta_q$ . Additionally, the parameter  $\frac{1}{\delta_q}$ , i.e., time to become susceptible again, does not affect too much the number of susceptible individuals ( $S(t)$ ).

Here, we discuss the remaining two model parameters: the hospitalization rate  $\alpha_h$ , and the transition rate of an exposed to

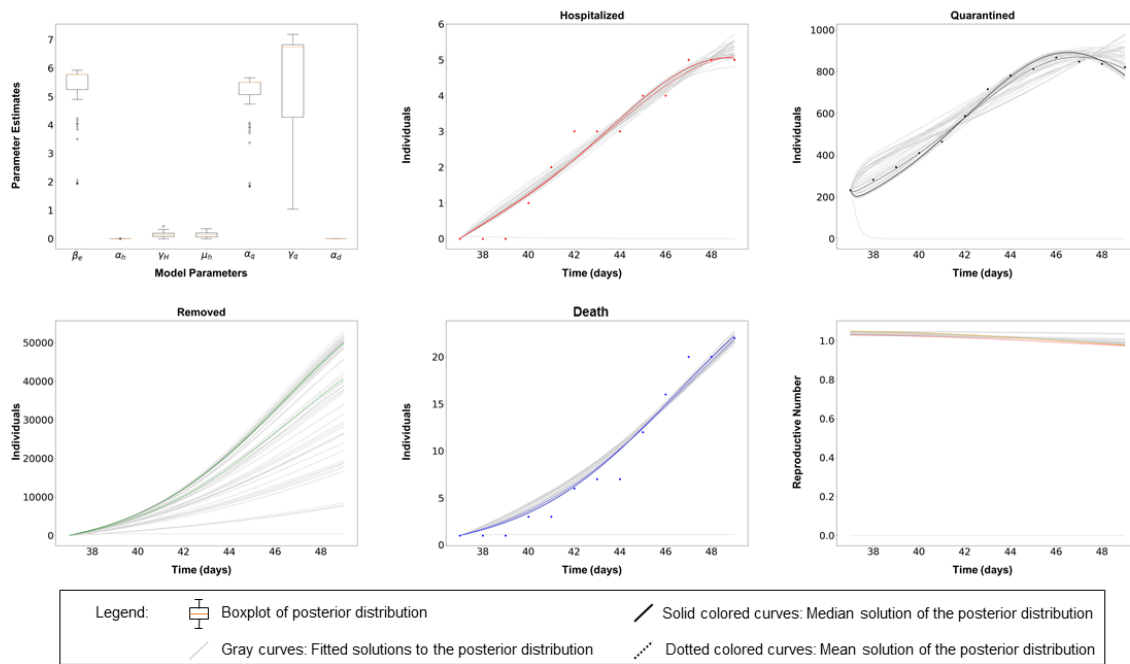


Figure 5: Fitting results for the Misamis Oriental, Region 10, Philippines.

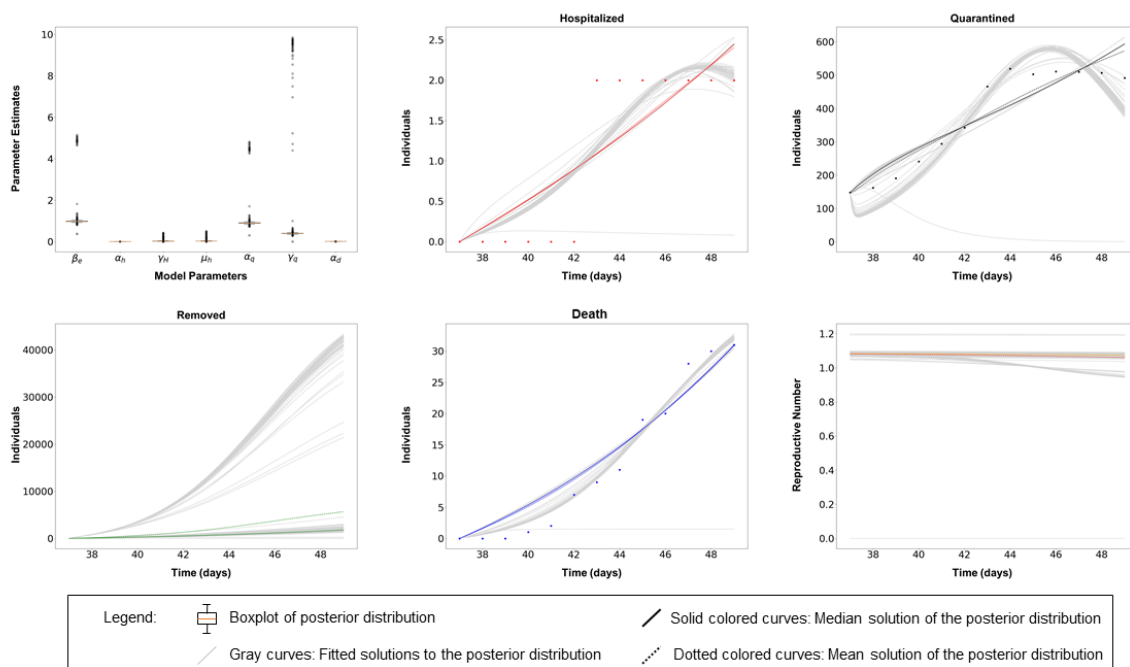


Figure 6: Fitting results for the Misamis Occidental, Region 10, Philippines

susceptible  $\alpha_d$ . Remarkably, our sensitivity analysis in Fig. 2 reveals that these parameters strongly influence  $\mathcal{R}_0$  negatively.

Higher hospitalization rate  $\alpha_h$  means that individuals with COVID-19 are treated, thereby lowering the number of infected individuals. Consequently, a reduction in the number of infected individuals could result in the breakage of the chain of disease transmission. Lower hospitalization rate could hasten the disease spread, which is possible through the unreported positive individuals, individuals with mild symptoms, and asymptomatic individuals. These individuals remain in the exposed class and have a chance to interact with the susceptible population and

infect others as what happened. Lower hospitalization might also be a result of improper and untimely monitoring. Improper and untimely monitoring can be a result of logistical concerns such as below-minimum number of contact tracers (Department of Interior and Local Government [DILG], 2020) and the non-compliance of individuals to the contact tracing due to the negative impression and being discriminated against after being tagged as PUM or PUI (Mercado, 2020). Improper and untimely monitoring leaves infected individuals to remain untested or undetected. These can be seen in the case of Singapore (Beech, 2020; Low, 2020). On the other hand, a higher transition rate of an exposed to susceptible means more hospital beds are readily available and the health system is stable (Bruni et al., 2020),



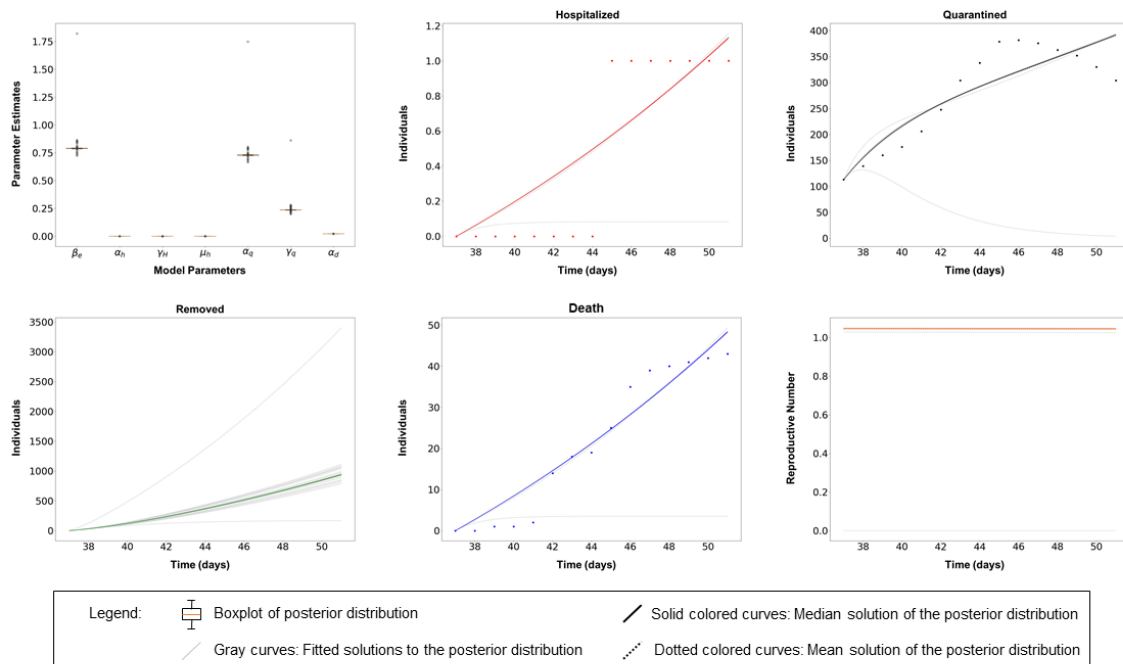


Figure 7: Fitting results for the Bukidnon, Region 10, Philippines.

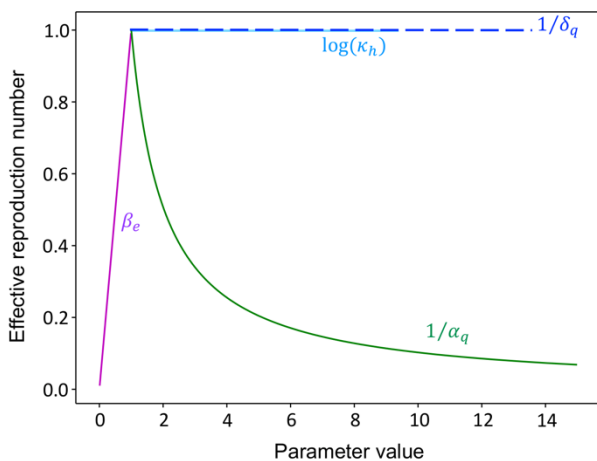


Figure 8: The marginal changes in the effective reproduction number according to the varying parameter values at  $t = 104$ . The simulations in Figure 8 are done with the parameters for the whole Region 10 given in Table 2, while the number of beds  $\kappa_h$  varies from 10 to 10000, the infection rate  $\beta_e$  from 0 to 1, and the parameters  $1/\delta_q$  and  $1/\alpha_q$  vary from 0 to 14 days.

thereby reducing transmission and thus, the value of  $\mathcal{R}_0$ . A low transition rate of an exposed to susceptible could lead to an inefficient health system due to either slow recovery of the patients or hospital intake is also apparently low.

We see from this analysis that when we obtain a value for  $\mathcal{R}_0$  at a time  $t$  (e.g. day), it should be taken into consideration that such a value is influenced by those aforementioned rates. Hence, we can expect a lower value of  $\mathcal{R}_0$  when the contact rates of infected and susceptible individuals are low (e.g. stricter community quarantine), coupled with high rates of hospitalization and high quarantine rates of exposed individuals.

Lastly, we note that the number of hospitalized individuals in the provinces are too small. It is suggested for future studies to explore the reliability of the estimated model parameters.

## CONCLUSION

The Philippines is not exempt from the widespread contagion of COVID-19. The possible emergence of new infectious diseases brought by human activities and the challenge of an early and timely disease surveillance bring the country to the realm of high-risk exposure to such diseases. To combat this, proactive approaches are deemed necessary to either fully prevent a pandemic or buy enough time so that the healthcare capacity will not be overwhelmed. In this study, we studied the dynamics of COVID-19 in Northern Mindanao, Philippines during its early phase by formulating a mechanistic model which uses the available data (i.e., monitoring data) on hand during that time. One should take note that novel diseases require new diagnostic techniques in order to fully detect it. Hence, with limited testing capacity and no vaccine especially during the early phase of the outbreak, the combination of containment, lockdown, social distancing, and amplified efforts of quarantine exposed individuals can reduce the disease transmission rate. We further highlight that monitoring data, when modeled appropriately, can provide insights that can serve as a decision-making guide to our policymakers. Consequently, we note to use appropriate models when laboratory-based disease reports are available since this model is tailored fit to an early pandemic.

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## CONTRIBUTIONS OF INDIVIDUAL AUTHORS

JP Arcede, RL Caga-anan, and ME Mata did the early conceptualization of the model. ICA Gonzales provided the ideas and insights to the model under conceptualization in the context of the Department of Health and provided the monitoring dataset. Y Mammeri finalized the model, did the parameter estimation, and generated results on strategies in the result and discussion. JP Arcede and ME Mata likewise wrote the results and discussion section. ME Mata performed the sensitivity analysis. RL Caga-anan derived the closed-form formula for the basic reproduction number and provided the qualitative results. RA Namoco prepared and cleaned the data ready for simulation. ZT Lachica checked and enhanced the results and discussion section. ZT Lachica also revised and finalized the entire manuscript.

## CONFLICT OF INTEREST

The authors have declared that no competing interests exist.

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