Estimation, control and forecast of COVID-19 disease spread in Central Visayas, Philippines

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ABSTRACT

The current trend of infections from COVID-19 outbreak in Central Visayas (CV) is posing higher risk of continued spreading. When uncontrolled, swarming of infected individuals to hospitals puts a greater challenge to the health care systems in the region and may breakdown. It is imperative in this situation that data-driven decisions and policies are required the most. In response, this study provided estimates of the epidemiologically important parameters namely, reproduction metric (R_o) and infection (α), recovery (β) and mortality (γ) rates, by using a modified Susceptible-Infected-Recovered-Dead (SIRD) model. This modified model incorporated control parameters, σ and ω, associated with enhanced community quarantine (ECQ) implementation and observance of social distancing (SD), respectively. For the covered months from 27 March 2020–10 May 2020, results of the simulation estimated these parameters at: R_o=3.12, α=0.18, β= 0.029, and γ=0.029 with 90% confidence. Moreover, the reproduction metric can be effectively reduced with the combined effect of the control parameters at $\sigma, \omega \geq 0.5$ resulting to an effective R_o below unity. Similarly, this lowered the peak value of infection to 23% (or 7% of the total number of susceptible population) compared to when these measures are not observed and moved the peak time farther as well. While these estimates reflected the timely implementation of ECQ keeping its current level comparable with the country's estimates and the world, reducing the reproduction metric effectively requires strict observance to both ECQ and SD control measures. Lastly, the temporal dynamics of this metric may not be necessarily true in any given area, and hence geographically induced.

Keywords: Central Visayas, ECQ, social distancing, SIRD model, reproduction metric

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INTRODUCTION

The Philippines is among the hard-hit country in the ASEAN region from the COVID-19 outbreak which originated in Hubei, China. Approximately 12,400 cases have been recorded in the country as of 16 May 2020. This is 10% compared to the overall cases recorded in the ASEAN region and 0.3% compared to the world data during this time. It also recorded 2,561 recoveries and 817 deaths, hence there are 8,927 active cases in the entire country.

In the local setting, Central Visayas (CV) region has been considered a high-risk area in the country with 1,876 active cases 53 recoveries and 28 deaths or 1,957 recorded positive cases. With the increased turn out of active cases, the region has been recently placed in ECQ status quo and is constantly monitored by the regional interagency task force (RIATF). Putting the region at this quarantine level signals the inevitable increase of infections particularly in highly congested areas. The effects are, as Anderson et al. (2020) puts it, increased deaths and economic downturn are generally impacted with the viral spread. While measures of quarantine were put up as above, it is imperative in this situation that data–driven policies and decisions are needed in translating them into practical actions beneficial to people and the government. However, the challenge in the imposition of these measures may require stringent quarantine guidelines, such as social distancing measures and early implementation of quarantine, just as the Chinese government did when the COVID-19 outbroke in Wuhan City (Anderson et al. 2020; World Health Organization 2020).

Relative to these measures, it is vital that by using epidemiological models, decisions have better lensing of approaches in the control and forecast of disease spread (Dimitrov and Meyers 2010; Heesterbeek et al. 2015; Lutz et al. 2019; Morgan 2019; Skrip and Townsend 2019). Thus, we provide estimates on epidemiologically important parameters and forecasts on the infection dynamics in the region using the widely-used Susceptible (S) – Infected (I) – Recovered (R) – Dead (D) (SIRD) model for Central Visayas (CV), Philippines. The bias of using the SIRD model, while it is classic, is that it is commonly employed by most studies of COVID-19 disease spread tackling the different aspects of control and forecast (Ahumada et al. 2020; Anastassopoulou et al. 2020; Canto and Avila-Vales 2020; Fanelli and Piazza 2020; Shinde et al. 2020). In fact, Carletti et al. (2020) highlighted that COVID-19 outbreak belongs to the class of simple SIR model and its extensions while that of Canto and Avila-Vales (2020) showed that SIRD model have better predictive power over time. We have followed the method provided in Anastassopoulou et al. (2020) that provided reasonable picture of the disease dynamics at earlier stage. It is also reasonable to use the discretize SIRD model particularly when the element of time is on daily basis or equally saying that most statistical data were obtained in discrete time (Hattaf et al. 2015). In fact, there are several applications for the analysis of COVID-19 spread using a discrete SIRD model and their variants including that of Bertozzi et al. (2020), Carcione et al. (2020), Giordano et al. (2020), Marinov and Marinova (2020), and ud Din et al. (2020), among others.

We have adopted the method provided in Anastassopoulou et al. (2020), we determine (i.e. estimate) these essential epidemiological parameters with emphasis on the reproduction metric and the decay pattern of infections. Besides the availability of literatures to anchor on, simplicity and ease of algorithm, the choice of the method described therein fitted the scenario in Central Visayas. The urgency of putting up data-driven measures to control the viral spread necessitated to use the simplest algorithm from which the method can provide. On the same note, their method provided a coarse estimate of the reproduction metric without the need to compute other parameters, i.e. infection (α), recovery (β) and mortality (γ) rates, however, valid only at the beginning of the disease spread. The latter justified the use of the model since the outbreak in Central Visayas was in its earlier stage during this time.

For policy directions, we introduced control parameters associated to the implementation of enhanced community quarantine and observance to social distancing measures were introduced providing a variety of perspective to effectively combat and reduce the COVID-19 disease spread (Lewnard and Lo 2020; Sen-Crowe et al. 2020). To note, these vital information are important in making sound decisions as the ongoing public health crisis has severe social and economic repercussions. These estimates and the forecasts provided herein can be used as guides to local executives in planning non-pharmaceutical interventions to control widespread disease spreading.

METHODS

In this paper, we start by employing the coupled system of equations of the discrete SIRD model which reads

$$S(t) = S(t-1) - \frac{\alpha}{N} S(t-1)I(t-1), \quad \text{Eq. 1}$$

$$I(t) = I(t-1) + \frac{\alpha}{N} S(t-1)I(t-1) - \beta I(t-1) - \gamma I(t-1), \quad \text{Eq. 2}$$

$$R(t) = R(t-1) + \beta I(t-1), \quad \text{Eq. 3}$$

$$D(t) = D(t-1) + \gamma I(t-1), \quad \text{Eq. 4}$$

where the number of susceptible, S(t), infected, I(t), recovered, R(t), and dead, D(t) as functions of discrete time points, t = 1, 2, 3…; and N refers to the population size which is a constant through time.

For the data resource needed in this study, we utilize the 54 data points for CV with reported cases of Infected (I), Recovered (R), Dead (D) from 27 March 2020 up to 10 May 2020. For Susceptible (S) data, we used an approximate value of **$\mathbf{S_{CV}}$ = 5M** susceptible in CV. This is approximately equivalent to the population in Cebu Province, hence this is also a reasonable estimate since almost all cases recorded in CV are in Cebu Province.

To determine whether the COVID-19 outbreak in the country and in CV can spread into the population or die out, we exploited the discrete method provided in Anastassopoulou et al. (2020) to estimate the essential epidemiological parameters, R_o, α, β, and γ given by the relation

$$R_0 = \frac{\alpha}{\beta + \gamma}, \qquad \text{Eq. 5}$$

where R_o (i.e. reproduction number) represents the average number of secondary cases resulting in the introduction of a single infections in a totally susceptible population; the parameters α, β, and γ are the corresponding rate constants associated to infected, I(t), recovered, R(t), dead, D(t) functions, respectively. Qualitatively, small values of R_o<1 translate to less turn out of secondary cases or equally saying that the spread dies out.

It is pointed, however, that one can encounter problems of estimations particularly in large-scale epidemics where the actual total number of infected, I(t), population often is unknown. Nonetheless, Anastassopoulou et al. (2020) provided a coarse estimation procedure of which the researcher had faithfully verified. The coarse estimation of these parameters is then solved by linear regression using least–square problem. The parameter estimation is a two-step process of which rate constants β and γ are obtained using linear regression while α is obtained from the SIRD simulator. Moreover, these parameters are obtained for t = {1, 2, ...} with a rolling window of 1 day using the available daily data of actual cases from 06 March 2020 to 10 May 2020. Estimates and time series plots of daily R_o were rendered using Matlab R2019b.

Parameter Estimation from the Reported Confirmed Cases

We denote $\Delta I(t), \Delta\, R(t), \Delta\, (t)$ as the reported new cases of infected, recovered and deaths at time t respectively. The cumulative numbers of confirmed cases are then calculated as

$$C\Delta X(t) = \sum_{i=1}^{t} \Delta X(t)$$

where, $X = I, R, D$, and $\Delta X = X(t) - \Delta X(t-1)$.

We then denote $\mathbf{C\Delta X}(t)$ which is the $t \times 1$ column vector containing the cumulative numbers up to time t expressed as

$$\mathbf{C\Delta X}(t) = [C\Delta X(1), C\Delta X(2), \dots, C\Delta X(t)]^T$$

From these definitions, we can provide a coarse estimation of R_0 by using equations 2, 3, 4, and 5. We then substitute the terms $\beta I(t-1)$ and $\gamma I(t-1)$ with $\Delta R = R(t) - R(t-1)$ and $\Delta D = D(t) - D(t-1)$ and then add Eqs. 4 and 5. After careful manipulation of the equations, we then arrive at

$$\frac{C\Delta I(t) + C\Delta R(t) + C\Delta D(t)}{C\Delta R(t) + C\Delta D(t)} = \frac{\alpha}{\beta + \gamma} = R_0.$$

Note that we can directly compute R_0 with the use of regression without the need first to compute the other parameters. Using this equation, we can extract a coarse estimation of R_0 by solving the linear regression using the least-squares problem as

$$\hat{R}_0 = ([\mathbf{C\Delta R}(t) + \mathbf{C\Delta D}(t)]^T[\mathbf{C\Delta R}(t) + \mathbf{C\Delta D}(t)])^{-1} \\ [\mathbf{C\Delta R}(t) + \mathbf{C\Delta D}(t)]^T[\mathbf{C\Delta I}(t) + \mathbf{C\Delta R}(t) + \mathbf{C\Delta D}(t)],$$

Also, the coarse estimation of the mortality and recovery rate can be calculated using linear regression problem for corresponding cumulative functions by least square given as follows

$$\hat{\gamma} = \left[\left(\mathbf{C\Delta I}(t) - \mathbf{C\Delta D}(t) - \mathbf{C\Delta R}(t)\right)^T(\mathbf{C\Delta I}(t) - \mathbf{C\Delta D}(t) - \mathbf{C\Delta R}(t))\right]^{-1} \\ \left(\mathbf{C\Delta I}(t) - \mathbf{C\Delta D}(t) - \mathbf{C\Delta R}(t)\right)^T\mathbf{C\Delta D}(t),$$

$$\hat{\beta} = \left[\left(\mathbf{C\Delta I}(t) - \mathbf{C\Delta D}(t) - \mathbf{C\Delta R}(t)\right)^T\left(\mathbf{C\Delta I}(t) - \mathbf{C\Delta D}(t) - \mathbf{C\Delta R}(t)\right)\right]^{-1} \\ \left(\mathbf{C\Delta I}(t) - \mathbf{C\Delta D}(t) - \mathbf{C\Delta R}(t)\right)^T\mathbf{C\Delta R}(t).$$

Next is we estimate the infection rate, α, by running the SIRD simulator using $\hat{\beta}$ and $\hat{\gamma}$ as the initial conditions with one infected person from 27th of March until the last date available (10 May 2020). The value of α is then determined by wrapping around the SIRD simulator an optimization to solve the problem

$$\text{argmin}\left\{\sum_{t=1}^{M}(w_1 f_t(\alpha;\hat{\beta},\hat{\gamma})^2 + w_2 g_t(\alpha;\hat{\beta},\hat{\gamma})^2 + w_3 h_t(\alpha;\hat{\beta},\hat{\gamma})^2)\right\},$$

where

$$f_t = C\Delta I^{SIRD}(t) - C\Delta I(t)$$
$$g_t = C\Delta R^{SIRD}(t) - C\Delta R(t)$$
$$h_t = C\Delta D^{SIRD}(t) - C\Delta D(t)$$

and $C\Delta X^{SIRD}(t), (X = I, R, D)$ are the cumulative cases resulting from the SIRD simulator at time t. Whereas the constants w_1, w_2, and w_3 correspond to scalars serving in the general case as weights to the relevant functions. We can easily get the solution of the above problem by using the function "lsqnonlin" of matlab using the Levenberg-Marquard algorithm.

SIRD Implementation

At the onset of the spread, we set S(t=0)=N−I_o, I_o =1, R(t=0)=0, D(t=0) = 0. For the purpose of this study, we have used the percentage of the population instead. We implemented the model in five (5) different scenarios by changing the percentage of susceptible population, S(t=0), as well as introducing a control parameter, ω, which we have associated to social distancing. For example, S(t=0)=N, the entire population is considered susceptible. With the implementation of the community quarantine, we assume that there is a reduction of the susceptible population using the relation

$$n = (1 - \sigma)\, N, \qquad \text{Eq. 6}$$

where σ=[0,1] is a constant factor related to the implementation of community quarantine. Qualitatively, a σ=0 means absence of ECQ implementation, 0<σ<1 means relative implementation of ECQ, and σ =1 strict observance of ECQ.

The last implementation of the model proposes a control parameter, $\omega = [0,1]$, on the infection rate, α, similar to that implemented in Lin et al. (2010). Qualitatively, we associate this control parameter to the adherence of social distancing, that is an ω=1 means strict social distancing is observed, ω=0 means the other extreme – no observance of social distancing, and $0 < \omega < 1$ means relative observance of social distancing. In control theory, the parameter ω modulates the interaction rate of the susceptible and infected variables in the model, hence Eq. (2) becomes

$$i(t) = i(t-1) + (1-\omega)\alpha\, s(t-1)i(t-1) - \beta i(t-1) - \gamma i(t-1) \quad \text{Eq. 7}$$

In principle, this control parameter has also an effect on the susceptible function of Eq. (1), that is

$$s(t) = s(t-1) - (1-\omega)\alpha\, s(t-1)i(t-1) \qquad \text{Eq. 8}$$

with the scaled susceptible and infected function are defined as $s = S/n$ and $i = I/n$, respectively. This is also true for Eqs. (3) and (4). We, then, make plots of Eq. (7) using different values of ω. We note, further, that the fraction of susceptible (S) to the population, N, is used for the simulation. In reference to van den Driessche (2017), the reproduction metric in Eq. (5) becomes the effective reproduction number given as

$$\mathcal{R}_0 = \frac{(1-\sigma)(1-\omega)\alpha}{\beta+\gamma} \qquad \text{Eq. 9}$$

RESULTS

Cumulative COVID-19 Cases in Central Visayas

The Department of Health (DOH) updates the country of the status COVID-19 infections in the country. From these datasets, we used data from 27 March 2020 to 10 May 2020 for Central Visayas data (Figure 1). It is self-explanatory that there is an exponential increase in the turn-out of confirmed cases while a linear trend is observed for recoveries and deaths. It is observed that during the intervals between 09 April 2020 (e.g. 36 cases) to 23 April 2020 (e.g. 363 cases), there is a 10-fold increase in the total number of infections with an average of 47 daily recorded infections over a span of five days.

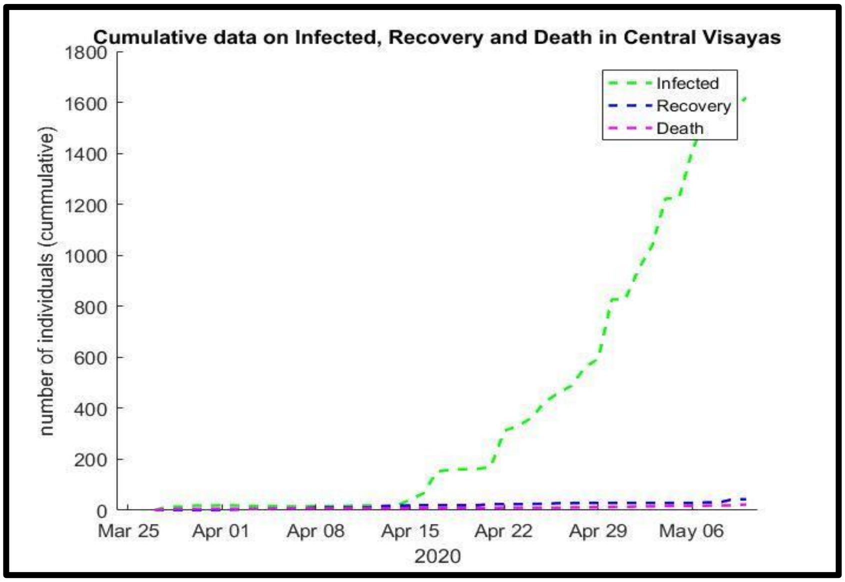

Figure 1. Time series data on recorded infection, recoveries, and death in Central Visayas, Philippines.

Essential Epidemiological Parameters

From the datasets, we determine the coarse estimates of the essential epidemiological parameters α, β, γ, and R_o. The time series of these estimates were plotted with a rolling window of 1 day and a 90% confidence interval. Using the values of these parameters, we obtain the effective reproduction number $\mathcal{R}_0$ from Eq. (9) as shown in Figure 2 below. The computed $\mathcal{R}_0$ from the actual data resulted to approximately $\mathcal{R}_0 \approx 3.1$. It is also worth noting that this metric is kept at this level and is relatively comparable to the global metric of $R_o = [2.0, 4.5]$. Nonetheless, this is above the threshold value of 1. For purposes of comparison, the trend of the reproduction metric for the entire country is relatively the same, however, showing a down trend as shown in Figure 2d.

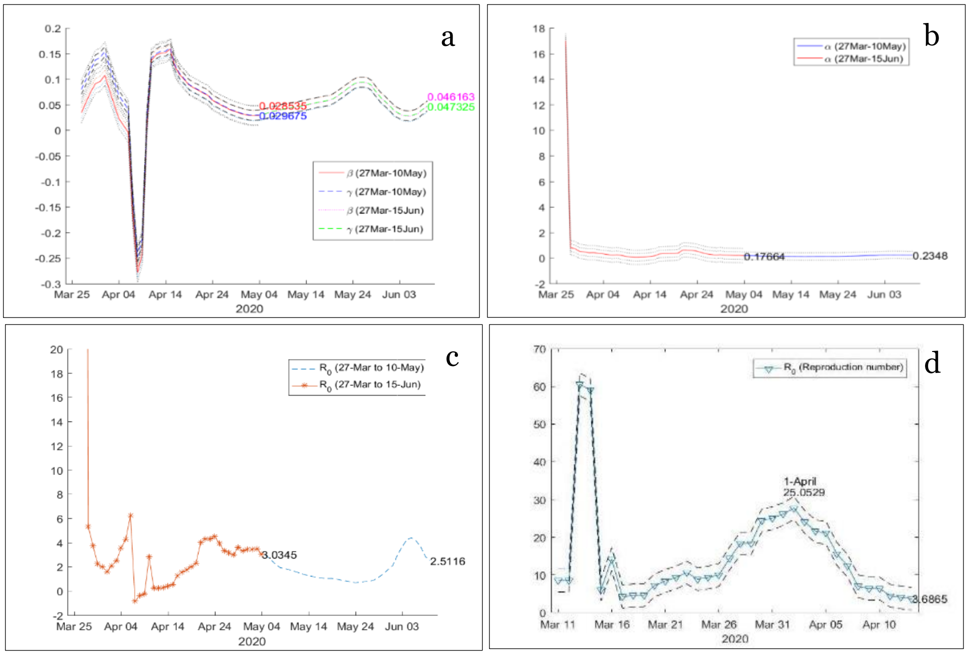

Figure 2. a) Estimated daily recovery and mortality rates (Central Visayas); b) estimated daily infection rate (Central Visayas); c) daily R_o values for Central Visayas with rolling window of 1 day from 27 March 2020 to 15 June 2020; and (d) daily R_o values for the Philippines (for comparison purposes) with a rolling window of 1 day from 11 March 2020 up to 17 April 2020. These estimates are obtained using linear regression at 90% confidence.

Modified SIRD Model for Central Visayas

The forecast on the percentage of susceptible (s), infected (i), recovered (r), and dead (d) individuals is shown in Figure 3. From the model, the critical points we look into are peak values of these parameters and when it will occur when the control parameters, σ and ω, are implemented particularly the infection function, *i(t)*. We have implemented this in different scenarios depicting the control of susceptible population and the observance of social distancing as presented below.

It can be observed from the different scenarios in both peak values of infections and peak times when social distancing is introduced in the model. The peak values had reduced to around 23% from scenario III and V (Figure 3). These amounts to reducing the total infections to 7% (i.e. from 1.5M to around 105K infections) when social distancing is observed. We also point out that when both ECQ and SD are strictly observed, i.e. scenario I, infections are reduced to almost nil and peak value occurs in a much-delayed time. We point out, however, that the 1.5M infected individuals is a large number to reach by September 2020. This large value may be caused by the computational process, particularly, on the assumed initial number of susceptible individuals, which is 5M. It would be possible that only 10% or 1% of the total population is susceptible to the disease because the information on how to stop the spread of the coronavirus has been widely disseminated throughout the country. The latest report in our timeline, i.e. 30 June 2020, suggested that between 33.52% to 40.97% of the population were observed to be susceptible corresponding to the number of infections of 8,660 at 90% confidence interval.

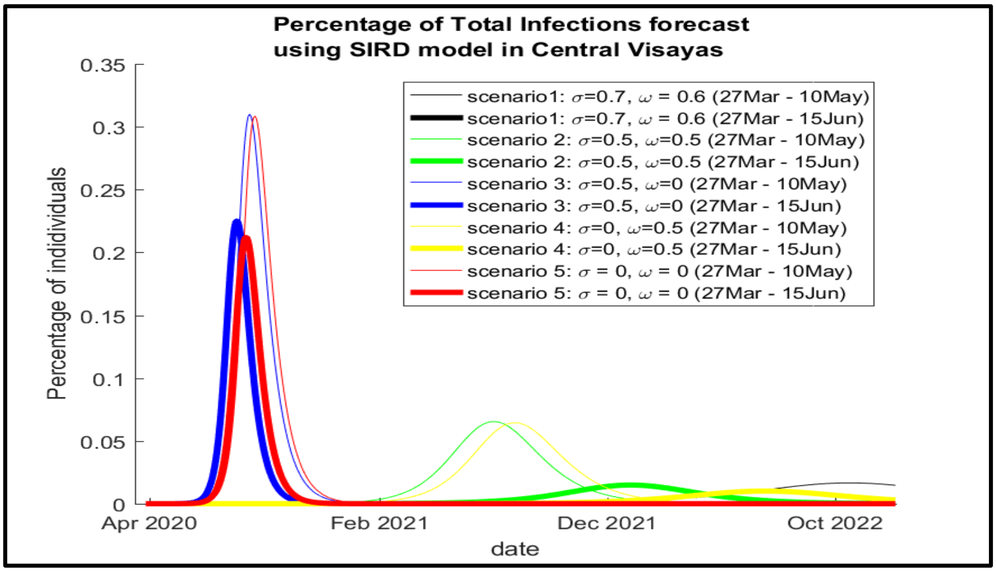

Figure 3. The infection curve simulated using modified SIRD model for Central Visayas in different scenarios. Thinner lines are infection curves of the earlier stages of the outbreak in Central Visayas. Thicker lines are infection curves with the inclusion of data until 15 June 2020.

Considering a totally susceptible population, i.e. s(t=0)=100%, i(t=0)=1/N, we obtained the effective reproduction metric from Eq. (9) for the different scenarios (Table 1). Clearly, when both ECQ and SD are observed, a flattened curve of infection is realized. Stricter implementations of these measures significantly reduce the number of infections as described by scenario I.

Table 1. Qualitative description in using control metrics.

Sample metrics used in the Modified SIRD Model				
Scenario	**ECQ Metric**	**SD Metric**	**Effective Reproduction Metric (R_o)**	**Description**
I	$\sigma = 0.7$	$\omega = 0.6$	$\mathcal{R}_0 = 0.37$	high ECQ and SD; flattened curve
II	$\sigma = 0.5$	$\omega = 0.5$	$\mathcal{R}_0 = 0.78$	moderately high ECQ and SD; flattened the curve
III	$\sigma = 0.5$	$\omega = 0.0$	$\mathcal{R}_0 = 1.55$	moderately high ECQ and absence of SD; approaching a flattened curve
IV	$\sigma = 0.0$	$\omega = 0.5$	$\mathcal{R}_0 = 1.55$	absence of ECQ and moderately high SD; approaching a flattened curve
V	$\sigma = 0.0$	$\omega = 0.0$	$\mathcal{R}_0 = 3.10$	absence of ECQ and SD; not flattened the curve

DISCUSSIONS

There are several reasons in the increasing trend of infections in CV, one of which is the increased turn out rate as caused by a) increased number of accredited testing centers, b) availability of testing kits, and c) the country-wide deployment of testing kits resulting to expanded testing activities. In perspective, these suggest that there could be more unrecorded and/or under reported positive cases in the country. In most pandemic studies, under-reporting seemed to be more likely as people experiencing mild symptoms often do not present themselves to health care as in the pandemic influenza (H1N1) (Mishra et al. 2010; Oberle et al. 2017) and TB epidemic (Zhou et al. 2019). Mathematically, it is non-normal to observe a sudden increase/spike in the number of cases. With COVID-19 infections, the actual number of cases may be two – or three – times more since infected persons are often asymptomatic. This increasing trend is, in fact, not unique to Central Visayas and the country as a whole, rather this is true worldwide. The severity of the spread reflects the imposed measures to curb the outbreak in the region. To note, the dynamics of the spread of any disease may not necessarily be the same in any given area. This reflects, further, the increasing trend of the reproduction metric in the region compared to the reproduction number in the entire country, although, the estimates are approximately the same (e.g. $R_{o,CV} = 3.1$ while $R_{o,PH} = 3.7$). This, further, showed that the implementation of ECQ region-wide is relatively effective keeping the reproduction metric at

R_0 ~ 3.10. While these values are relatively comparable worldwide and the earlier reported estimates in China between 2–7.1 (Lai et al. 2020a; Li et al. 2020; Mizumoto et al. 2020; Read et al. 2020; Zhang et al. 2020a; Zhou et al. 2020), an increasing trend suggests higher risk of continued spreading. Consequently, this may cause social and economic instability in the region as the possibility of swarming of infected persons may overwhelm its health care facilities (Sen-Crowe et al. 2020; UPC-19PRT 2020). Moreover, our results complimented that of Ridenhour et al. (2018) suggesting that reproduction metrics varies according to geographical location affected by changes in the environment, population structure, viral evolution and immunity, to include geopolitical influences (Katz et al. 2019; Kassem 2020; Peirlinck et al. 2020). When these geopolitical influences cater disagreement in the implementation of ECQ measures, such as the earlier transition to GCQ experienced in Central Visayas, resulted to sudden spike in the number of infections.

The uncertainties, however, of the actual number of infections (Lai et al. 2020a; Li et al. 2020; Zhang et al. 2020a) and of the nature and etiology of the virus (Andersen et al. 2020; Cascella et al. 2020; Zheng 2020) arrested the government and local government (LGU) leaders to implement drastic quarantine policies (i.e. home quarantine and social distancing) to contain the virus and control of the increasing loss of lives and of the continuing economic stress (Lim 2020). As reported in Pueyo (2020), these measures can isolate population to be exposed to the virus that slows down disease spreading. On preventing a wider spread of infection, we have shown here the effectiveness of how faithful adherence to the ECQ guidelines particularly on the number of exposed individuals as well as stricter observance to social distancing can reduce the reproduction metric below the threshold value. In Shim et al. (2020), they put prime on social distancing as measures to rapidly control the outbreak. This agreed well in our simulations of SD control parameter, ω, which significantly reduced the number of infections to 7% of the initially assumed total susceptible population. The same observations had been reported in many studies of historical pandemics such as in Caley et al. (2008). On the contrary, Reluga (2010) pointed out that social distancing is most beneficial to individuals when the reproduction metric is around two and larger values of metric requires a more efficient social distancing measures. These were implied in our simulation of SD parameters in scenarios I and II which the effective reproduction numbers were less than unity. More importantly, reducing the reproduction metric effectively requires strict observance to both ECQ and SD control measures and/or their combined effects.

We note that our predictions were proximate that of reported flattened curved for the number of infections in the country (Nepomuceno 2020; Parrocha 2020), the total number of predicted number of infections was relatively high given the initial number or susceptible individuals. This can be justified since latest analyses suggested that it may be 10 to 40% lower where majority of cases were never confirmed (Annastassopoulou et al. 2020; Killeen and Kiware 2020; Mizumoto et al. 2020) and whose infectious carriers often exhibit mild to no symptoms during this time (Dong et al. 2020; Du et al. 2020; Lai et al. 2020b; Li et al. 2020; Tang et al. 2020; Zhang et al. 2020b; Zhou et al. 2020). In fact, as of the timeline of this study, the estimated susceptible population is between 33.52% to 40.97% corresponding to the total infections of 8660 at 90% confidence interval as of June 30, 2020. The latter percentage of susceptible population can then be used as initial input to s(t=0). Relative to all of these, sudden spikes in the number of infections during this time may be associated to contamination in densely populated or highly congested areas such as slum areas and/or jails (Dave et al 2020; ICRC 2020; Franco-Paredes et al. 2020; Simpson and Butler 2020; Wang et al 2020; WHO 2020). We point out, however, that most reported outbreaks in Central Visayas were associated to infected individuals showing mild to no symptoms at all. In result, granular lock down was imposed in the highly congested areas of Cebu City as well as several extensions of ECQ (UPCCEI 2020).

To further improve the predictive power of the model, it is worth noting that granular lock down was to further control the viral spread (Basu et al. 2020; Mandal et al. 2020; Mishra et al. 2020; Santamaria et al. 2020; Srivastava 2020), and hence can be a good parameter to understand the dynamics of COVID-19 spreading. Possible inclusion of other parameters such as that of density–driven dynamics (Cardoso and Goncalves 2020; Munshi et al. 2020), exposure–weighted dynamics (e.g. subdivision of the parameter I(t) into asymptomatic, mild, severe, or critical) (Adhikari et al. 2020; Allen et al. 2020; Weitz et al. 2020) and/or age-dependent dynamics (Allen et al. 2020; Zhang et al. 2020b) may be seen to be a plausible direction to better understand the COVID-19 disease spread dynamics in Central Visayas or the country as a whole.

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