Lockdown strategy worth lives: The SEIRD modelling in COVID-19 outbreak in Indonesia

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\textbf{Abstract.} Lockdowns, despite their conflicting restrictions and consequences they might offer when enforced as a national strategy, are deemed to be suggestive for a prompt conquer to the Coronavirus Disease-19 (COVID-19) outbreak. There have been some success stories such as in China, South Korea and our ASEAN member fellow, Vietnam, which exhibited extremely fallen numbers of COVID-19 cases post the enforcement of lockdown. Indonesia, however, remains in the crux of dispute whether or not the lockdown is opted to force COVID-19 transmission down under control. We, in this respect, employ the most popular model which has been broadly applied in the field of epidemiology, referred to as SEIRD (Susceptible, Exposed, Infectious, Recovered, and Death), the extension form of an age-structured SEIR, where the Death (D) is included to provide more factual situation. We modify the I (Infectious) fraction as symptomatic (Is) and asymptomatic (Ia) infectives. There are three lockdown scenarios simulated in our modified SEIRD with the starting date are 26 April 2020 when the immediate lockdown was enacted- and a-week and two-week-gaps, respectively. We figured out that by stipulating the lockdown without delay (26 April 2020), the new cases could be kept below 10,000. A week delay escalates case number to 5,000 and delay for one more week results in beyond 20,000 new cases. Furthermore, when the intervention is delayed following the delayed lockdown, normalization would demand a longer period within which dealing with more critical and dying patients is unavoidable and should be more anticipated.

\textbf{Keywords}: Contact matrices, COVID-19, Epidemiological modelling, Lockdown, SEIRD equation,
umbrella called Association of Southeast Asian Nations (ASEAN), they cope with the COVID-19 almost individually. Taking into account the nations under ASEAN share a lot of similarities in terms of natural resources and involved in such intense trading and political relationships, we presumed that the national intervention should reflect those similarities. Instead, we figured out that discrepancies among them were considerably huge. It is, simply, manifested through how as nations they strive to manage the impacts, which in majority are bad ones, and take a thorough control on the COVID-19 transmission and mitigation. Vietnam, for an instance, has lifted its lockdown since no more new cases surfaces [4] and being the first country in the ASEAN that officially ended the social distancing when another ASEAN’s members are still struggling [5]. Malaysia also showed an excellent performance in handling COVID-19 by successfully controlling its accumulative fatality rate to only 1.67% [6]. In contrary, Indonesia appeared to be far left behind by its most adjacent neighbor country, Malaysia. To date Indonesia exhibits no satisfying outcome neither post 14-day-nationwide self-quarantine nor post 2-week-large scale social-restriction (popular as PSBB, pembatasan sosial berskala besar) [7]. This big gap of inequality has left us thinking of substances that might be very key for either the success or the failure in respect with the COVID-19-impact managements. A mathematical model is deemed to serve a prominent assistance to grasp the interplay of lockdowns as the primary strategy in the outbreak handling and the COVID-19 itself. In addition, by plotting several plausible lockdown-scenarios we could as well produce a predictive model. In this study, we employed and modified the SEIRD (Susceptible, Exposed, Infectious Recovered, and Death) model. The model has been widely used for epidemiology studies [8]. Regarding COVID-19, the model was used in a study by Prem et al, to measure the progression of COVID-19 and resulted in it was a reduced median of infection numbers in Wuhan, China, by exceed 92% and 24% in mid-2020 and end-2020, respectively [9]. The model, however, did not take into account the demography features that might alter the increment of infection dissemination. We are keen to fulfil the gap and broaden scope of measurement to Indonesia. This is critical to avoid ineffectiveness in the strategy implementation during the pandemic that might cause unnecessary damages we could hardly afford.

Up to date, in Indonesia COVID-19 is mainly reported as numbers: numbers of new positive cases, numbers of deaths and recovered rates. Mathematical model which incorporates aspects related to the case is barely presented rendering it arduous to orchestrate strategy or intervention which might fittest to control and manage the impacts. In the present study, we expand our horizon by striving measuring possible outcomes of COVID-19-handling strategies in Indonesia, mainly is lockdown. To do so we employed a modified SEIRD model with age structure and to allow our dataset which comprises susceptible, exposed, symptomatic and asymptomatic infectives, recovery rates and death toll, to be comprehensively measured. We found them to be important to evaluate to thoroughly weigh if consequences on the huge restriction system aimed at suppressing new incidences of COVID-19 is affordable.

2. Related Works
Given the situation where the global concerns are primarily concentrated on COVID-19, mathematical models are helpful tools for public health policy makers to formulate effective control strategies to manage the spread of the disease. Hitherto, SEIR model is considered to be the widely used mathematical model adopted to address queries in the epidemiology studies [10]. To the most recent was the work by Prem et al. that employed and modified SEIR model to simulate age-specific and location-specific transmission of COVID-19 at different stages in Wuhan as well as mitigation strategies [9]. Meanwhile, the use of age-structured SIR model with the same formulation of the social contact matrices was used to study the effect of social distancing and different lockdown scenarios affect the control strategies to combat the pandemic in India [11]. The age-specific contact matrices is important to reflect the vulnerability
characteristics for national mitigation policy as suggested by Kaban et al in their study for Indonesia population [12]. Separately in the same time, Gupta et al, were able to generate a prediction that from 31st March-13th April 2020 the new case of COVID-19 in India rose from 5,000-6,000 by employing both SEIR model and regression [10]. Both, however, were contradicted by the study of Grant where the SEIR model was observed to be underestimating peak infection rates and on the other hand overestimating epidemic persistence after the peak elapsed [13]. In addition, a extension of SEIR model called SIDARTHE (Susceptible, Infected, Diagnosed, Ailing, Recognised, Threatened, Healed, and Extinct (dead)) used to simulate the COVID-19 pandemic that differentiate between the diagnosed and non-diagnosed population as well as severity of the symptoms was proposed in Italian population by Giordano et al [14].

3. Methods

3.1. Data
The data of COVID-19 pandemic in Indonesia used in this work is publicly available from the official website of Indonesia COVID-19 task force [15]. The reporting period from 2 March 2020 to 26 April 2020. However, we only analyzed the data with the starting date of 9 March 2020 as the number of reported case became more consistent after that date for our model. The social contact matrices of 152 countries provided Prem et al. is also available from the supplementary in their paper [9]. The data of the age structure is obtained from PopulationPyramid.net website [16].

3.2. SEIRD Model
In this work, we assume that the number population is constant, since the number of births and deaths during the pandemic is much smaller than the number of total population. We studied the spread of an infectious disease within a population with a categorization into six states/compartments to: susceptibles ($S$), exposed ($E$), symptomatic infectives ($I_s$), asymptomatic infectives ($I_a$), recovered individuals ($R$), and deaths ($D$), which is depicted in figure 1. Susceptibles are the healthy subpopulation that are susceptible to the disease. The number of susceptible population decreases with the infection rate given by a time dependent quantity denoted as $\lambda(t)$. The exposed individuals are the infected population but not yet infectious and will eventually become infected either with clear symptoms/clinical or asymptomatic/subclinical. The incubation period denotes the period before the exposed individuals contracting with the disease become infectious. Our proposed model is a direct extension of an age-structured SEIR model developed by Singh et al. [11] in which we include the death compartment into the original model to provide a slightly more realistic situation. The population is categorized into 16 age groups with an age interval of 5 year, thus the total population can be written as $N = \sum_{i=1}^{16} N_i$. Our compartment model then can be written as the following system of ordinary differential equations (ODEs) for a particular age group $i$ as
\frac{dS_i}{dt} = -\lambda_i(t)S_i
\frac{dE_i}{dt} = \lambda_i(t)S_i - \gamma E_i
\frac{dI^A_i}{dt} = (1 - \alpha_i) \gamma E_i - \gamma I^A_i
\frac{dI^S_i}{dt} = \alpha_i \gamma E_i - (1 - p_i) \gamma s I^S - \gamma D p_i I^S_i
\frac{dR_i}{dt} = \gamma_A I^A_i + \gamma_S I^S_i
\frac{dD_i}{dt} = \gamma_D p_i I^S_i

The infection rate for age \(i\), \(\lambda_i(t)\), with age-aggregated population is defined as

\lambda_i(t) = \beta \sum_{j=1}^{16} \left( C_{ij}(t) \frac{I^A_j}{N_j} + C_{ij}(t) \frac{I^S_j}{N_j} \right). \tag{2}

The public health interventions are encapsulated in the time dependent contact matrices \(C_{ij}(t)\). The matrices describe the structure of social mixing between different age groups. We employed location-specific contact social matrices denoted by \(C_{ij}^l\) computed by Prem et al.[17] for 152 countries, including Indonesia. The matrices describe the average number of interactions per day between an individual in age group \(i\) with an individual in age group \(j\) in a specific location. The matrices have been computed in home \((l = H)\), school \((l = S)\), workplace \((l = W)\), and other unspecified locations \((l = O)\). Therefore, the time dependent contact matrices can be written as a linear combination of \(C_{ij}^l\) as

\[ C_{ij}(t) = C_{ij}^H + f_S C_{ij}^S + f_W C_{ij}^W + f_O(t) C_{ij}^O. \tag{3} \]

Constant \(f_l\) describe the extent of the closure of the corresponding location to minimize social mixing and may be time-dependent functions. Meanwhile, other parameters in equation 1 except \(\alpha_i\) and \(p_i\): \(\beta, \gamma_E, \gamma_{I^A}, \gamma_{I^S}\), and \(\gamma_D\) are fit parameters describing the rate of progression into the corresponding states. The proportion of a case belongs to clinical/symptomatic case is denoted by \(\alpha_i\). Following the parameters used in [9], we utilized conservative proportions in different age groups: we put \(\alpha_i = 0.4\) for \(i \geq 4\) and \(\alpha_i = 0.8\) for \(i > 4\). Meanwhile, the fraction of mortality, \(p_i\), denote the proportions of critical cases to die due to the infection for a certain age group \(i\). As the proportions are not available publicly in Indonesia, as a rough estimate, we employed the death proportions used by website Worldometer from a report from New York City Health [18]. The proportions are multiplied by a common factor \(\gamma_D\) to represent death rate for age \(i\).

We define a rate \(\delta = d_D^{-1}\) where \(d_D\) is the number of days between the onset of symptoms and deaths that we assumed to be 14 days [18]. In addition, we utilized the formulation detailed by Diekmann et al.[19] and Singh et al. [11] to compute the basic reproduction number, \(R_0\), which is defined as the maximum eigenvalue of the next generation matrix (NGM).

We fitted the essential parameters in our model: \(\alpha_i, \beta, \gamma_E, \gamma_{I^A}, \gamma_{I^S}\), and \(\gamma_D\) by minimizing the following error function:

\[ \sum_{i=1}^{n} (I_{pred} - I_{data})^2 + \sum_{i=1}^{n} (D_{pred} - D_{data})^2 \]
Figure 1. A SEIRD model for a particular age group with both symptomatic and asymptomatic infectives are included.

Table 1. Best fit model parameters from the data.

| Parameters | Value |
|------------|-------|
| $\beta$    | 0.043 |
| $\gamma_E$ | 0.220 |
| $\gamma_{IA}$ | 0.118 |
| $\gamma_{IS}$ | 0.219 |
| $\gamma_D$  | 0.075 |

Quantities $I_{data}$, $I_{pred}$, $D_{pred}$, and $D_{data}$ are the number of reported positive cases, the number of simulated cases, number of reported deaths, and the number simulated death cases. We partially used utilities from PyRoss package for fitting the the parameters [20].

4. Results and Discussion

During our analysis, we employed the calculation of the cumulative cases with the initial date 9 March 2020 because the result of the tests from the previous days became more available (we observed that the reported cases at that date tripled from the previous day). The progress of the reported case went relatively smooth from that day forward that might be partially due to the improved procedures for the tests. By varying the number of days to be included for fitting the parameters, we found that the daily data from the period 9 March, 2020 to 7 April, 2020 (30 days) produce the best fit parameters. The resulting fit is given in table 1. From the simulation, we also obtained that the basic reproduction number in the early days of the pandemic in Indonesia $R_0 = 3.6192$. This result excludes the dynamics of the early pandemic as the data is not available.

As a concrete example, we considered a lockdown scenario that mimics the data of the infected cases in Indonesia. First of all, from 9 March 2020 until 16 March 2020, without any interventions, all social mixing across ages in public places still took place, which means $f_S = f_W = f_O = 1$. Afterward, Indonesia’s government started to implement a public intervention at 16 March 2020 by prompting a total school closure, which could be assumed to be implemented immediately across country, and also only suggested workplace closure and maintaining physical distance in public spaces. Formulating in our case, this means $f_S = 0$ and we assumed that only 50% of the workplaces were shut down, $f_W = 0.75$, and the public suggestion only closed 80% of public spaces, $f_O = 0.8$. As the pandemics worsened, the government took a more strict measure called PSSB (large scale physical distancing) to stop the
viruses spread in public spaces and ordered the workplaces to be closed. We assume that 75% working from home \((f_W = 0.25)\) and 50% of other public places were closed \((f_O = 0.5)\). We invent the last stage, a so-called “total lockdown”, which is essential to decrease the number of infected cases that was implemented in Hubei province, and currently being implemented by half European countries, including Italy and Spain. This stage ideally closes public spaces \((f_O = 0)\) and only allows for 10% workplaces opened such as hospitals and markets/supermarkets/shops for essential needs \((f_W = 0.1)\).

We simulated three lockdown scenarios based on three different starting date of the lockdown with a period of 45 days. The bold dashed black line shown in the figure indicates the curve when no interventions were introduced since the beginning of the day until today, which is untrue but it provides a baseline information. The first scenario (green line) is the immediate lockdown taken by the government at 26 April 2020 (the last data point in our data). On the other hand, the second (blue line) and the third (red line) lockdown scenario take place one week and two weeks after the first scenario, respectively, corresponding to the delayed interventions. Our results can be seen in Figure 2. Visually, the data points follow the infection curve until the last date of the data because we adjusted the magnitude of the contact matrices via \(f\)-value as described above in such way that the choice of percentages leads to the expected trajectory. The first scenario (green line) is able to keep the number of cases below ten thousands. However, a one-week delay in the second scenario increases the number by 5,000 cases and further, a two-week delay results in more than devastating 20,000 infected cases. The delayed interventions clearly imply a longer lockdown period needed to normalize the situation while the medical system is fully overwhelmed and thousands more of critical patients die.

We must emphasize that the results from the toy simulation do not reflect the correct dynamics of COVID-19 pandemic in Indonesia as the number of cases may be underreported and we mostly estimate the parameters from the preliminary data from another countries. The result, however, once again resonates the widely existing suggestion made by countless scientific
reports involving more advanced and realistic simulations that strict lockdown scenarios are needed now. The period duration must be adjusted by the government by considering a lot of multi-aspect constraints.

Our model can be extended to include another compartment/state to provide a more realistic simulation (i.e predicting hospitalizations, triage, unobserved cases, region-specified cases, and more) as more data available as developed by Giordano et al [14]. However, the main difficulty of simulating the data-driven SEIRD model is the lack of clinical and non-clinical information that may provide clear initial bounds for the parameters since the accurate SEIRD modelling relies on correct initial values. Nevertheless, aggregating the age groups and social contract matrices as well as other information such as gender, geospatial location, detailed characters of the cities, and more may provide a first step for the public health policy maker to plan a decision mitigating the disease.

5. Conclusion
In our modified SEIRD model, we simulated three different scenarios of lockdown and evaluated what would be plausible consequences for each option. Our first scenario is when the lockdown is effectively activated on 26 April 2020. This assists the super limited new case emergences. A week- and two-week delays cause 5,000 and 20,000 new cases, respectively. Although the model would not be able to offer an absolute number, it worth a deeper thought especially in the perspectives of socio-economic consequences which might be unaffordable for a nation given the damages COVID-19 has caused by far. Therefore, modification in the enacted lockdowns should have been prior-anticipated with the focus on the mitigation by which normalization could be feasible within a relatively short time.

References
[1] Li Q, Guan X, Wu P, Wang X et al. 2020 New England Journal of Medicine 382 1199–1207 pMID: 31995857 URL https://doi.org/10.1056/NEJMoa2001316
[2] Khafaie M A and Rahim F 2020 Osong Public Health and Research Perspectives 11 74
[3] International Labour Organization 2020 Covid-19 and the world of work. third edition: Updated estimates and analysis
[4] Reuters Vietnam to ease nationwide coronavirus lockdown URL https://www.bangkokpost.com/world/1905235/vietnam-to-ease-nationwide-coronavirus-lockdown
[5] La V P, Pham T H, Ho M T, Nguyen M H et al. 2020 Sustainability 12 2391 URL https://www.mdpi.com/2071-1050/12/7/2391
[6] Salim N, Chan W H, Mansor B, Bazar N E N, Amarasi N, Mohd Fauzi A A, Huspi S H, Khoo E J H and Shithil S M 2020 medRxiv URL https://www.medrxiv.org/content/early/2020/04/11/2020.04.08.20057463
[7] Media informasi resmi terkini penyakit infeksi emerging. covid 19 2020 URL https://covid19.kemkes.go.id/
[8] Li M Y and Muldowney J S 1995 Mathematical biosciences 125 155–164
[9] Prem K, Liu Y, Russel T W, Kucharski A J, Eggo R M, Davies N, for the Mathematical Modelling of Infectious Diseases COVID-19 Working Group C, Jit M and Klepac P 2020 Lancet: Public Health URL https://www.thelancet.com/journals/lanpub/article/PIIS2468-2667(20)30073-6/fulltext
[10] Vynnycky E and White R 2010 An Introduction to Infectious Disease Modelling (Oxford University Press)
[11] Singh R and Adhikari R 2020 Age-structured impact of social distancing on the covid-19 epidemic in india (Preprint 2020.12055)
[12] Kaban P A, Kurniawan R, Caraka R E, Pardamean B, Yunianto B and Sukin 2019 Procedia Computer Science 157 31 – 37 ISSN 1877-0509 the 4th International Conference on Computer Science and Computational Intelligence (ICCSSCI 2019) : Enabling Collaboration to Escalate Impact of Research Results for Society URL http://www.sciencedirect.com/science/article/pii/S1877050919310567
[13] Grant A 2020 medRxiv URL https://www.medrxiv.org/content/early/2020/04/12/2020.04.02.20050674
[14] Giordano G, Blanchini F, Bruno R and Colaneri P a c 2020 Nature Medicine 157 31 – 37 ISSN 1877-0509 URL https://www.nature.com/articles/s41591-020-0883-7
[15] Gugus tugas pencepatan penangan covid-19 2020 URL https://covid19.go.id/
[16] PopulationPyramidNet 2020 URL https://www.populationpyramid.net/
[17] Prem K, Cook A R and Jit M 2017 Plos Computational Biology 13(9)
[18] Worldometer 2020 Age, sex, existing conditions of covid-19 cases and deaths URL https://www.worldometers.info/coronavirus/coronavirus-age-sex-demographics/
[19] Diekmann O, Heesterbeek J A P and Roberts M G 2009 J. Royal Soc. Interface 7(47) 873–885 URL https://royalsocietypublishing.org/doi/10.1098/rsif.2009.0386
[20] PyRoss 2020 Mathematical modelling of infectious disease in python URL https://github.com/rajeshrinet/pyross