UNIVERSITI MALAYA

WID2002 Computing Mathematics 2

Following the Flow: Understanding Infectious Disease

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Contents

Glossary

λ Death & Birth rate.

δ Immunity weakened rate.

α Vaccination rate.

ϵ Vaccination effectiveness rate.

β Transmission rate.

σ Infectious rate.

γ Recovery rate.

N Total population size.

M Number of individuals with Maternally-derived immunity.

S Number of Susceptible individuals.

V Number of Vaccinated individuals.

E Number of Exposed individuals.

I Number of Infectious individuals.

D Number of Death.

R Number of Recovered individuals.

t Time.

1 Problem Statement

Over the past 30 years, World Health Organization, 2014 reported that more than 30 new infectious diseases have emerged, from severe acute respiratory syndrome (SARS) to Coronavirus disease (COVID-19). According to World Health Organization, 2004, infectious disease has accounted for a quarter to a third of all mortality. The impact of infectious diseases can be outrageous and detrimental. As reported by WHO, 2020, infectious diseases including lower respiratory infections, diarrheal diseases, malaria, tuberculosis and HIV/AIDS are among the leading causes of death globally in 2019. The most recent global spread of infectious disease, COVID-19 has resulted in over 6.94 million deaths as of June 7, 2023 (WHO, 2023b). Unfortunately, Malaysia has also suffered as a result of COVID-19 and has recorded 5.10 million COVID-19 cases and 37,100 deaths as of June 3, 2023 (Ministry of Health of Malaysia and Department of Statistics Malaysia, 2023).

The term ”infectious disease” has been frequently mentioned in the above paragraph but what does infectious disease mean exactly? Infectious diseases refer to medical conditions caused by microscopic organisms such as bacteria, viruses, fungi, or parasites passed from one person to another, directly or indirectly. Additionally, humans can also become infected when exposed to or in contact with an infected animal that carries a pathogenic organism capable of infecting humans (Baylor College of Medicine, 2023).

Moreover, the advent of advanced technology and globalization is a double-edged sword. On one hand, they enhance international interactions and connectivity among nations. However, on the other hand, they also contribute to the spread of infectious diseases from their country of origin to neighbouring countries. This has been clearly demonstrated by the COVID-19 pandemic that began in 2020. It is without a doubt that infections in one region can easily spread to another and until

the virus can be contained globally, a surge in cases in one area can definitely lead to resurgences of cases in other parts of the world (Baylor College of Medicine, 2023).

On top of that, the spread of infectious diseases is highly dependent on its transmission route. Transmission refers to how germs or viruses are spread to a susceptible individual to become infected. Viruses don't move independently. They highly depend on the presence of people and the surrounding environment for their dissemination (Centers for Disease Control and Prevention, 2016). Besides, according to the Ministry of Health – Manatū Hauora, 2021, the transmission of the virus can happen in 2 ways; directly (through close contact with an infected person) or indirectly (through the touch of contaminated objects like door handles). Thus, it is without a doubt, the dissemination of viruses is of no bounds.

What's more, it is often said that "Epidemiology is the basic science of preventive medicine" (Straif-Bourgeois et al., 2014). Undoubtedly, the first step in controlling and preventing disease is to understand it comprehensively. By understanding a particular disease, we are able to identify key factors such as vulnerable populations, transmission modes and rate, possible interventions and their effectiveness as well as to analyse the trend and the spreading of disease. This is far more important when it comes to infectious disease prevention and control as it allows the country's decision-makers to formulate effective measures and strategies in order to minimise the impact of infectious diseases on the societal and economic levels as much as possible.

Hence, we are intrigued to answer the following questions:

1. How do the susceptible rate, transmission rate, infectious rate, and recovery rate of disease affect society?

2. How effective are safety measures (i.e., social distancing, mask, lockdown and vaccination) in reducing disease transmission and controlling outbreaks?

3. What is the impact of maternally derived immunity on the dynamics of infectious diseases?

The following report explains our solution and method using compartmental models (Section 2). Then, we will analyse the results (Section 3), discuss the strengths and limitation of the proposed methods (Section 4), and suggest possible future works (Section 5). Lastly, we will conclude this report (Section 6).

2 Proposed Solution and Method

In this section, we will explain the compartmental model in Section 2.1. Subsequently, we will present our solution, starting with a simple SEIR model and then progressing to more complex models, MSEIRS and MSVEIRS, which will further be explained in Section 2.2, Section 2.3 and Section 2.4 respectively.

2.1 Compartmental Model

The most widely used techniques for comprehending disease dynamics are agent-based (ABM) and equation-based (EBM) models. ABM uses the means of algorithm to describe each agent's behaviour (Kasereka et al., 2023). On the other hand, EBM is the study of a system to determine the behaviour of an infectious disease by separating the overall population, N, into different compartments representing different health statuses.

In this report, we will primarily focus on the EBM because of its benefits as stated by Vodovotz and An, 2013 below:

- Able to provide a mathematical framework for an intuitive implementation of a causal mechanism
- Able to simulate numerically easily and inexpensively

- Able to provide both qualitative and quantitative predictions

EBM uses ordinary differential equations (ODE) w.r.t time, $\frac{\partial(\cdot)}{\partial t}$, where $\cdot$ is the compartmental state, to represent the population flows w.r.t time, t. Unlike partial differential equations that depend on partial derivatives of several variables, ordinary differential equations only consider derivatives w.r.t one variable. One of the simplest numerical solutions to solve ODE is the forward Euler method. The derivative is defined as:

$$\frac{\partial(K)}{\partial t}(t) = \lim_{\Delta t \to 0} \frac{K(t + \Delta t) - K(t)}{\Delta t} \tag{1}$$

where K represents an arbitrary compartmental state, and Δt is the time step, such as a day, hour, or month. For the remainder of this report, we will use a " day " time step unless specified otherwise.

By rewriting the ODE systems as a difference equation, we obtain:

$$K(t + \Delta t) = K(t) + \Delta t \frac{\partial(K)}{\partial t} \tag{2}$$

Choosing $\Delta t = 1$ (1 day), and substituting into Eq. 2, we can determine the number of individuals in a compartment for the next day, $K(t+1)$, by adding/subtracting the people moving in/out of the compartment per time step. Mathematically, this can be expressed as:

$$K(t + 1) = K(t) + \frac{\partial(K)}{\partial t} \tag{3}$$

To obtain the number of people in a compartment, we start with an initial value, $K(0)$, and repeat the Eq. 3 for the remaining time steps.

Further details and the introduction of the compartmental models will be explained in the latter section.

2.2 SEIR Model

Although there are many different types of equation-based models, the SEIR (Susceptible, Exposed, Infected, Recovered) compartmental model is widely recognized as the predominant equation-based model for describing epidemic dynamics (Hunter and Kelleher, 2022). To simplify the model, several assumptions are made:

1. There is no flow back to the Susceptible (S) compartment. Therefore, the equation can only decrease over time as more individuals become infected.

2. Population is perfectly mixed such that individuals come into contact with other individuals in the population.

3. Individuals can only be infected once.

4. Individuals cannot leave the Recovered (R) compartment.

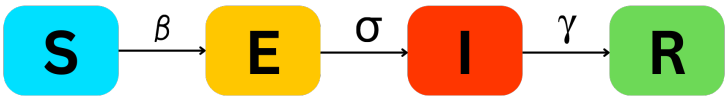


Figure 1: SEIR Compartments with rates β (contact rate), σ (latent-to-infectious rate), and γ (recovery rate) controlling the flow of individuals moving in/out of the compartments. S: Susceptible, E: Exposed, I: Infectious, R: Recovery.

As shown in Figure 1, this model categorizes individuals into four distinct health states or compartments, namely Susceptible (S), Exposed (E), Infected (I) and Recovered (R). The number of individuals in each compartment will be represented as a mathematical quantity, S(t), E(t), I(t) and R(t) respectively. To derive the model equation (Sundnes, 2023), we will first denote Δt as the time interval for the number of individuals moving between the compartments. The detailed explanation of the equation formulation for each compartment is as follows:

1. **Susceptible (S):**

   This compartment represents individuals who are yet to be exposed to the disease (susceptible individuals). However, if they are exposed to the disease due to coming into contact with an infectious individual, they will transit to the Exposed compartment, E (leaving compartment S into compartment E). The contact rate is represented by beta, β. Most of the population is in this compartment at the beginning of an outbreak.

   The proportion of infected individuals at any time step in the population is represented as $\Delta t\frac{I(t)}{N}$ where N is the total population size. The proportion of susceptible individuals is defined as $\frac{S(t)}{N}$. Assuming that individuals in the population are likely to come into contact with any other individual equally (perfect mixing), the probability of a contact occurring between an I and S individual is $\Delta t\frac{I(t)}{N} \times \frac{S(t)}{N}$.

   To determine the total number of contacts in the population, we multiply this probability by the number of contacts, which is determined by the transmission coefficient, β, multiplied by the population size, N, denoted as βN.

   Since there is no flow back to the Susceptible compartment, as those recovered will not be reinfected, the number of people in the Susceptible compartment can only decrease over time. Therefore, a negative sign is employed in the equation to indicate the decrement. By combining and simplifying all the factors, we can get the number of susceptible individuals at any time step with equation:

$$S(t + \Delta t) = S(t) - \Delta t\frac{\beta S(t)I(t)}{N} \tag{4}$$

2. **Exposed (E):**

   This compartment comprises individuals who have been exposed to the disease but are not yet infectious themselves. They are in the latent phase of

the infection and are not capable of transmitting the disease to others. After the latent period denoted as sigma, σ, the exposed individual will become infectious.

Individuals in the population can enter and exit the compartment E. The rate of individuals entering E will equal the rate of individuals leaving compartment S but in the opposite direction. Hence, the first part of the equation will be the negative value of the previous term:

$$-(-\Delta t\frac{\beta S(t)I(t)}{N}) = \Delta t\frac{\beta S(t)I(t)}{N} \tag{5}$$

The rate of exposed individuals becoming infected (leaving the compartment E and moving into the Infectious compartment (I)) at any time step is determined by 2 factors: (i) the infectious rate (σ), and (ii) the current number of exposed individuals (E(t)), denoted as $\Delta t\sigma$E(t). Leaving compartment E means a decrement in the number of exposed individuals; thus, a negative sign is employed. Therefore, by combining all the factors mentioned, we can get the number of exposed individuals at any time step with the following equation:

$$E(t+\Delta t) = E(t) + \Delta t\frac{\beta S(t)I(t)}{N} - \Delta t\sigma E(t) \tag{6}$$

3. **Infected (I):**

   This compartment represents individuals currently infected and capable of transmitting the disease to susceptible individuals. Infected individuals can experience symptoms and become severe cases requiring medical attention or remain asymptomatic carriers.

   Exposed individuals (E) who became infected at any time step enter the Infectious compartment (I) which is influenced by the infectious rate, σ and is

denoted as $\Delta t\sigma$E(t).

To leave compartment I, infected individuals who have recovered at any time step will transition to the Recovered compartment, R, at a rate determined by the recovery rate, γ and is denoted as $\Delta t\gamma$I(t). Leaving compartment I mean a decrement in the number of infected individuals; thus, a negative sign is employed. Therefore, by combining all the factors mentioned, we can get the number of infected individuals at any time step with the equation below:

$$I(t + \Delta t) = I(t) + \Delta t\sigma E(t) - \Delta t\gamma I(t) \tag{7}$$

4. **Recovered (R):**

   This compartment represents infected individuals who have recovered from the disease and have developed immunity (enter compartment R) at any time step. The recovery rate is represented by gamma, γ and is denoted as $\Delta t\gamma$I(t).

   In this model, we assume that no individuals can be reinfected and thus, no individuals will leave compartment R. Therefore, by combining all the factors mentioned, we can get the number of recovered individuals at any time step with the equation below:

$$R(t + \Delta t) = R(t) + \Delta t\gamma I(t) \tag{8}$$

To transform the above equations into ODEs, we begin by dividing all equations by Δt and rearrange them to get:

$$\frac{S(t + \Delta t) - S(t)}{\Delta t} = -\frac{\beta S(t)I(t)}{N} \tag{9}$$

$$\frac{E(t+\Delta t)-E(t)}{\Delta t} = \frac{\beta S(t)I(t)}{N} - \sigma E(t) \tag{10}$$

$$\frac{I(t+\Delta t)-I(t)}{\Delta t} = \sigma E(t) - \gamma I(t) \tag{11}$$

$$\frac{R(t+\Delta t)-R(t)}{\Delta t} = \gamma I(t) \tag{12}$$

As we let Δt approach 0, we can, therefore, formulate 4 differential equations representing the rate of change of each compartment as follows:

$$\frac{\partial S}{\partial t} = -\frac{\beta SI}{N} \tag{13}$$

$$\frac{\partial E}{\partial t} = \frac{\beta SI}{N} - \sigma E \tag{14}$$

$$\frac{\partial I}{\partial t} = \sigma E - \gamma I \tag{15}$$

$$\frac{\partial R}{\partial t} = \gamma I \tag{16}$$

We will follow the same approaches and steps employed in this model in formulating the ODEs for the following extended SEIR model (in Section 2.3 and Section 2.4) when formulating new equations for their respective newly added compartments.

2.3 MSEIRS Model

The SEIR model is expanded to become the MSEIRS (Maternally-derived immunity, Susceptible, Exposed, Infectious, Recovered) model. The additional compartment, **Maternally-derived immunity (M)**, represents the immunity naturally acquired in newborns. Unlike the SEIR model, where an individual can be infected

only once, in this model, the recovered patients lose their immunity at the rate of delta (δ) and return to the Susceptible compartment. Additionally, this model incorporates the death rate, lambda (λ) since most infectious diseases can be fatal. Figure 2 illustrates the compartments and the respective rates in the MSEIRS model.

In order to maintain a constant population (i.e., $N(0) \equiv N(t)$) as well as to simplify our modelling, the following assumptions are made in addition to those mentioned in Section 2.2:

1. The birth and death rates of the population are equal.
2. Maternally-derived immunity and recovery-acquired immunity have the same rate of weakening.
3. The probability of babies born with maternally-derived immunity equals the fraction of recovered individuals in the population.

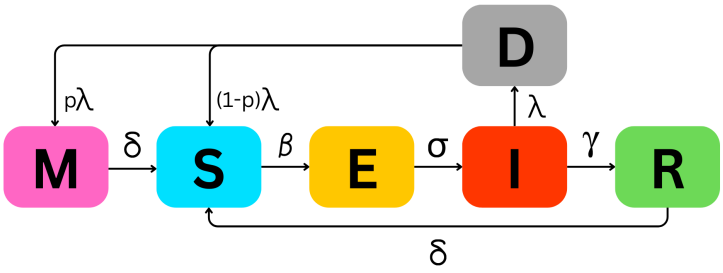


Figure 2: MSEIRS Compartments with rates $\lambda, \delta, \beta, \sigma, \gamma$ controlling the flow of individuals moving in/out of the compartments and p is the probability of newborns with immunity. M: Maternally-derived immunity, S: Susceptible, E: Exposed, I: Infectious, R: Recovery, D: Death.

Since the birth and death rates are equal, the number of newborn babies increases by λI for every time step. Therefore, the rate of change of death, $\frac{\partial D}{\partial t} = \lambda$I. Among the newborns, a fraction $p = \frac{R}{N}$ enters the Maternally-derived immunity (M) compartment. Combining this with the δM individuals leaving compartment M, we have

the equation below, where M represents the number of individuals with maternally-derived immunity.

$$\frac{\partial M}{\partial t} = -\delta M + \frac{R}{N}\lambda I \tag{17}$$

In the Susceptible (S) compartment, in addition to individuals leaving for the Exposed (E) compartment as described in Eq. 13, its rate of change incorporates: (i) the loss of immunity in newborns δM, (ii) the remaining $1 - p$ fraction of the newborns without immunity, $1 - \frac{R}{N}$ and (iii) the number of recovered individuals entering the compartment after the immunity weakened, δR, forming the equation below:

$$\frac{\partial S}{\partial t} = -\frac{\beta SI}{N} + \delta M + \frac{N - R}{N}\lambda I + \delta R \tag{18}$$

The rate of change of the Exposed (E) compartment remains unchanged as in Eq. 14. While for the Infected (I) compartment, the individuals can leave the compartment either by recovering or dying from the disease, which is represented by the Recovered and Death compartments, respectively, forming $-\gamma I$ and $-\frac{\partial D}{\partial t}$ and ultimately:

$$\frac{\partial I}{\partial t} = \sigma E - \gamma I - \lambda I \tag{19}$$

For the Recovered (R) compartment, in addition to the individuals leaving E for R, the individuals in compartment R will leave and join compartment S after a weakening period, forming:

$$\frac{\partial R}{\partial t} = \gamma I - \delta R \tag{20}$$

2.4 MSVEIRS

On top of the MSEIRS model, a new compartment, **Vaccination (V)** has been added as shown in Figure 3. This addition introduces two additional parameters: the vaccination rate (α) and the effectiveness of vaccines (ϵ), representing the recipro-

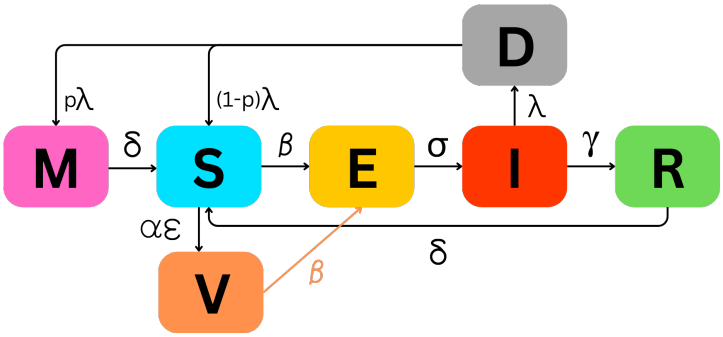


Figure 3: MSVEIRS Compartments with rates $\lambda, \delta, \alpha, \epsilon, \beta, \sigma, \gamma$ controlling the flow of individuals moving in/out of the compartments and p is the probability of newborns with immunity. M: Maternally-derived immunity, S: Susceptible, V: Vaccination, E: Exposed, I: Infectious, R: Recovery, D: Death.

cal number of people vaccinated per day and the percentage of effective vaccines, respectively.

In addition to Eq. 18, the transition of susceptible individuals from compartment S to the Vaccinated compartment (V) due to receiving effective vaccination determined by α and ϵ, is given by the following equation:

$$\frac{\partial S}{\partial t} = -\frac{\beta SI}{N} + \delta M + \frac{N-R}{N}\lambda I + \delta R - \alpha\epsilon S \tag{21}$$

Despite the fact that individuals have been vaccinated, there remains a possibility of them getting exposed to and eventually infected with the disease. The number of vaccinated individuals transitioning to the Exposed compartment (E) due to having contact with infectious individuals is determined by the transmission rate (β) and the proportion of vaccinated individuals becoming exposed at any time step in the population, denoted as $\frac{\beta VI}{N}$, where V and I denote the number of vaccinated individuals and infected individuals, respectively. Combining Eq. 14 with this consideration, the updated formulation for $\frac{\partial E}{\partial t}$ is as follows:

$$\frac{\partial E}{\partial t} = \frac{\beta SI}{N} - \sigma E + \frac{\beta VI}{N} \tag{22}$$

Given that the individuals can enter (via vaccination) and exit (by becoming exposed) compartment V, specified by the rate of individuals entering compartment V, $\alpha \epsilon S$, and the rate of individuals exiting compartment V, $\frac{\beta VI}{N}$ are considered. Thus, the following equation is derived:

$$\frac{\partial V}{\partial t} = \alpha \epsilon S - \frac{\beta VI}{N} \tag{23}$$

3 Results and Discussion

Unless stated otherwise, the experiment environment and parameters of the compartmental models are as stated in Experiment Setting 1 and Table 1.

Experiment Settings 1
Population, N = 1,000,000; Simulation period = 365 days

M	**S**	**V**	**E**	**I**	**R**	**D**
0	999,999	0	1	0	0	0

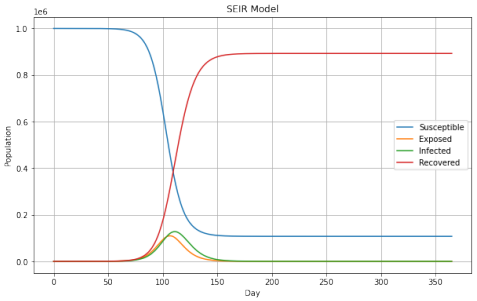
(a)

$\lambda \downarrow$	$\delta \downarrow$	$\alpha \uparrow$	$\epsilon \uparrow$	$\beta \downarrow$	$\sigma \downarrow$	$\gamma \uparrow$
0.050	0.100	0.006	0.800	0.500	0.250	0.200

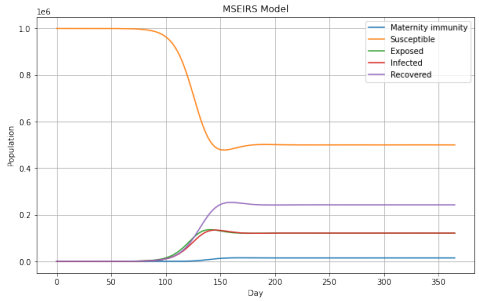
(b)

Table 1: Initial population and parameter values for the model. (a) shows the distribution of individuals among different compartments: M (Maternally-derived immunity), S (Susceptible), V (Vaccinated), E (Exposed), I (Infectious), R (Recovered), D (Death). (b) displays the default values of the model parameters: λ (Death rate), δ (Immunity weakened rate), α (Vaccination rate), ϵ (Vaccination effectiveness rate), β (Transmission rate), σ (Infectious rate), γ (Recovery rate). Up arrows (↑) and down arrows (↓) represent the best direction in changing the rates to control the disease.

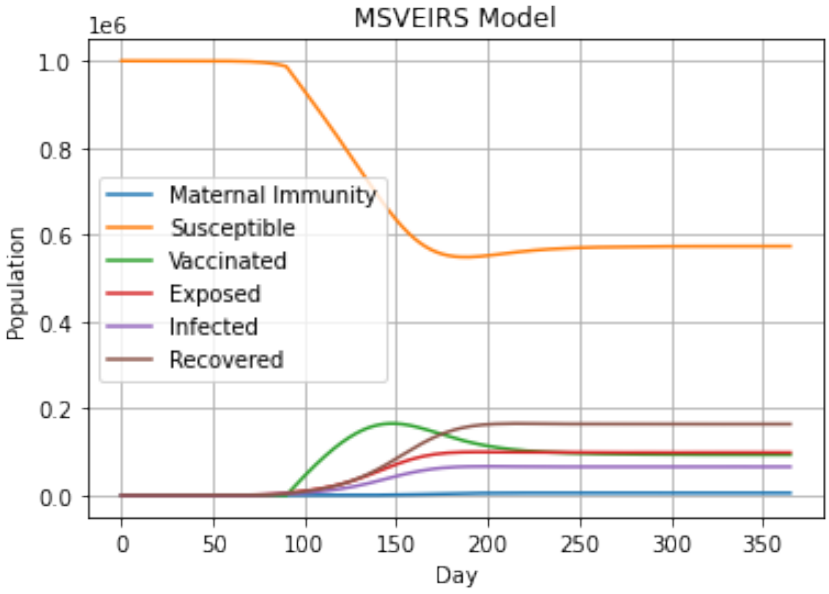
3.1 Graph of SEIR, MSEIRS and MSVEIRS



(a)



(b)



(c)

Figure 4: Graphs of populations over time with different epidemic models: (a) SEIR, (b) MSEIRS, and (c) MSVEIRS.

Based on Figure 4, the susceptible population remains high in the beginning as the disease has yet to spread widely. As time progresses, the susceptibility will decrease approximately on Day 60, Day 75, and Day 90 respectively for each model as the number of infected people starts to increase with their peak infectious of 127,749 people, 134,301 people, and 66,596 people infected on Day 111, Day 146 and Day 199 respectively. This peak indicates the highest number of active cases during the

outbreak, demonstrating the transmission of disease in the population.

Following the peak of infection, the number of infected people starts to decrease gradually as more people recover and gain immunity. Simultaneously, the number of exposed people increases, reaching its peak of 109,689 people, 136,110 people, and 99,871 people exposed on Day 107, Day 140, and Day 196 respectively. Subsequently, the number declines as more people enter the Infectious compartment (I).

As time progresses, the number of people who recovered increases and stabilises as more people successfully recovered from the disease. In the SEIR model, it is assumed that recovered individuals will acquire immunity from the disease and are no longer susceptible to the infection. On the other hand, in the MSEIRS and MSVEIRS models, those recovered can be infected again. Hence, allowing them to transit back to the susceptible compartment. This explains why the recovery curve on the SEIR model appears to be higher than both the MSEIRS and MSVEIRS models whereas the susceptible curve for both the MSEIRS and MSVEIRS models appears to be higher than the SEIR model.

Upon comparing the susceptible populations in all models, it is evident that the MSVEIRS model demonstrates a higher number of plateaued values and requires a longer time frame to reach the peak, followed by the MSEIRS and SEIR models. This observation suggests that the presence of immunity, regardless of, whether acquired maternally or through vaccination, serves as a protective factor for society, leading to an increased proportion of individuals who have yet to be infected with the disease.

3.2 Effects of Changing Rates in Reducing Mortality

Production of a vaccine takes time. It may take months, years or even decades. While waiting for the vaccine, reducing the number of death should be the focus as

all would be pointless if there is no survivors. Death instils fears, thus, highlighting the importance of reducing mortality as one of the primary objectives in outbreak control. Using the **Death (D)** compartment in the MSEIRS model, by manipulating specific parameters, we can observe the pattern and identify which rate is the most effective in reducing the number of deaths, leading to making more informed decisions based on the results obtained, ultimately contributing to better management strategies. With the control set obtaining 1,511,541 death (Figure 5), each parameter is adjusted by varying the parameters by 0.05 as shown in Table 2 to observe the changes and patterns further.

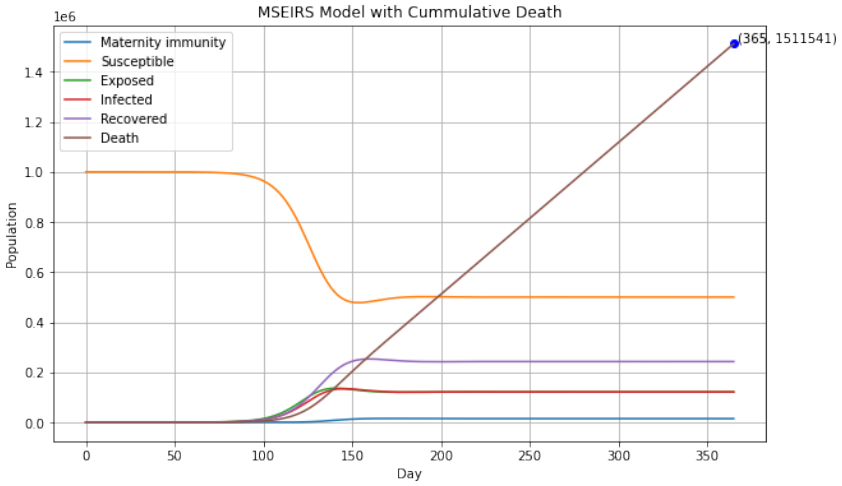


Figure 5: Graph of controlled MSEIRS model with recorded deaths. On Day 365, the number of deaths recorded is 1,511,541 individuals.

Based on the results in Table 2, the number of deaths can be sorted in ascending order. The ascending order of deaths would be: increased γ (902,859 deaths), decreased δ (1,036,742 deaths), decreased β (1,217,903 deaths), decreased σ (1,336,456 deaths), increased σ (1,642,023 deaths), increased β (1,752,636 deaths), increased δ (1,800,412 deaths) and lastly, decreased γ (2,364,798 deaths).

From Figure 6, it is clear that increasing the recovery rate (γ) is associated with a delayed onset of the mortality peak. This suggests that implementing measures or interventions that enhance the recovery rate, such as improved medical treatments

Parameter	Rate Change	Number of Death
$\delta \downarrow$	0.05	1,036,742
	0.15	1,800,412
$\beta \downarrow$	0.45	1,217,903
	0.55	1,752,636
$\sigma \downarrow$	0.20	1,336,456
	0.30	1,642,023
$\gamma \uparrow$	0.15	2,364,798
	0.25	902,859

Table 2: Table showing the number of deaths for different rates (± 5 of the control set). Up arrows ($\uparrow$) and down arrows ($\downarrow$) represent the best direction in changing the rates to control the disease.

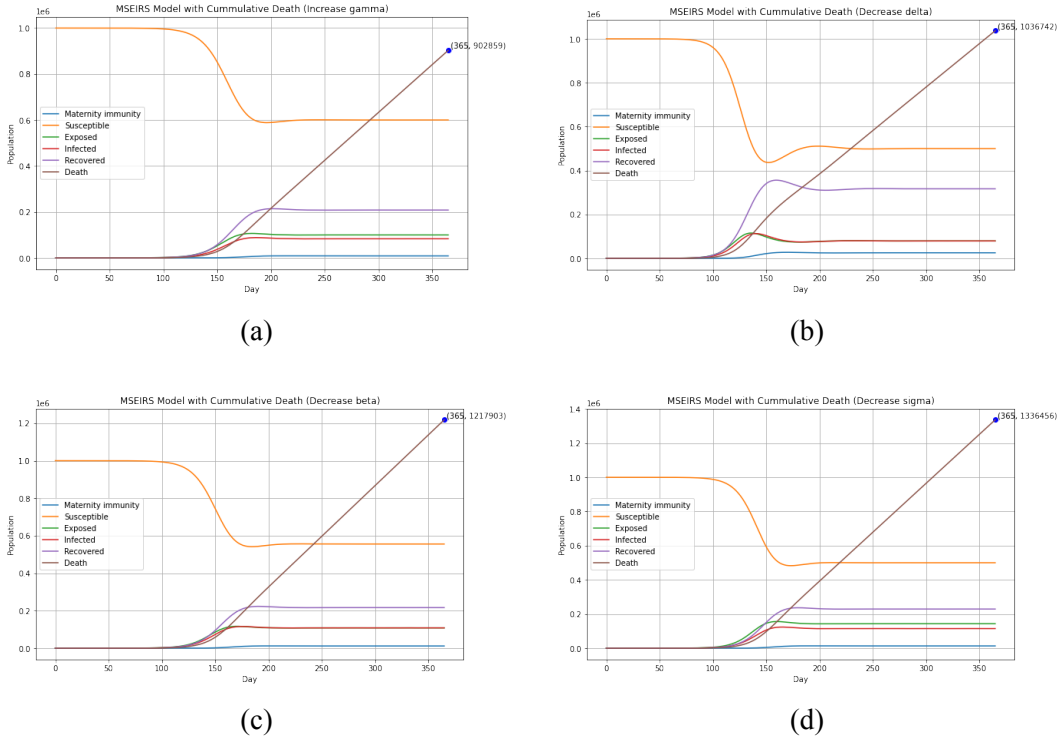
or access to healthcare, can help delay a surge in deaths.

Similarly, decreasing the transmission rate (β) and infectious rate (σ) also contribute to a delay in the day when the sudden increase in deaths happens. These findings emphasize the importance of implementing preventive measures to reduce the spread of the disease, such as vaccination campaigns, social distancing, and hygiene practices. Reducing the transmission and infectious rates can postpone the peak in mortality, providing more time for healthcare systems to prepare and respond effectively.

Therefore, it can be concluded that the most effective rate in reducing the number of deaths is increasing the recovery rate (γ). Following closely behind is decreasing the immunity weakened rate (δ), transmission rate (β), and finally, infectious rate (σ). Hence, decision-makers can prioritize implementation strategies based on the results.

3.3 Effects of Maternally Derived Immunity

To understand the influence of maternally derived immunity on the spread of infectious diseases and its societal impact, we conducted experiments with the MSEIRS model where we varied the probability of babies acquiring immunity from their



(a) (b)

(c) (d)

Figure 6: Graphs of the mortality rate of MSEIRS by varying parameters $\gamma(\uparrow)$, $\delta(\downarrow)$, $\beta(\downarrow)$, and $\sigma(\downarrow)$ by 0.5 towards the best direction of changing the rates to control the disease. (a) Increasing γ, (b - d) Decreasing δ, β, and σ respectively.

mothers (p) as stated in Experiment Setting 2. All other variables are kept constant.

Experiment Settings 2
$p \in \{0.0, 0.2, 0.4, 0.6, 0.8, 1.0\}$

From the graph of the Infectious compartment over time (Figure 7), we observed that increasing the probability of babies acquiring maternal immunity led to a decrease in the peak infectious population. This finding suggests that maternally derived immunity results in fewer infectious individuals. This is because the immunity provides increased protection against the disease. Hence, emphasising the importance of incorporating this factor into the epidemiological modelling.

Furthermore, from the detailed statistics in Table 3, we can see that the mater-

nally derived immunity affects Susceptible the most (+13.77%), followed by Exposed (-5.98%), Infected (-5.93%) and Recovered (-4.20%).

These observations provide valuable insights into the challenges of modelling complex infectious diseases using simple compartmental models such as SEIR. The SEIR models do not include maternal immunity, thus, may result in an overestimation of the number of infectious individuals. This highlights the need to include relevant and realistic factors, such as maternal immunity, in disease modelling to understand disease dynamics better and to ensure that the disease modelled can be as similar as it would be in reality.

Moreover, these insights are crucial for health authorities and decision-makers in determining appropriate vaccine timing and dosing strategies. Understanding the influence of maternal immunity on disease transmission and population vulnerability can guide decisions regarding the optimal administration of vaccines, particularly in situations where maternal immunity plays a significant role in protecting vulnerable populations such as infants. By considering these insights, health authorities can devise more effective vaccination strategies, potentially leading to better control and mitigation of infectious diseases.

State, p	0.0	0.2	0.4	0.6	0.8	1.0	Change (%)
M	0.00	7.54	14.90	22.07	29.07	35.91	100.00
S	231.92	238.75	245.39	251.84	258.04	263.86	13.77
E	89.87	88.72	87.65	86.59	85.54	84.52	-5.95
I	87.07	86.02	84.98	83.94	82.92	81.91	-5.93
R	768.08	761.25	754.61	748.16	741.90	735.83	-4.20

Table 3: Maximum population for each state (except Susceptible with the minimum population) in thousands (K) when varying the probabilities of babies acquiring immunity. The "Change (%)" column represents the percentage change in the population of each state between $p = 0$ and $p = 1$, calculated using the formula $\% = \frac{N_1 - N_0}{N_0} \times 100\%$, where N_p is the population in a state with a probability p of babies acquiring immunity.

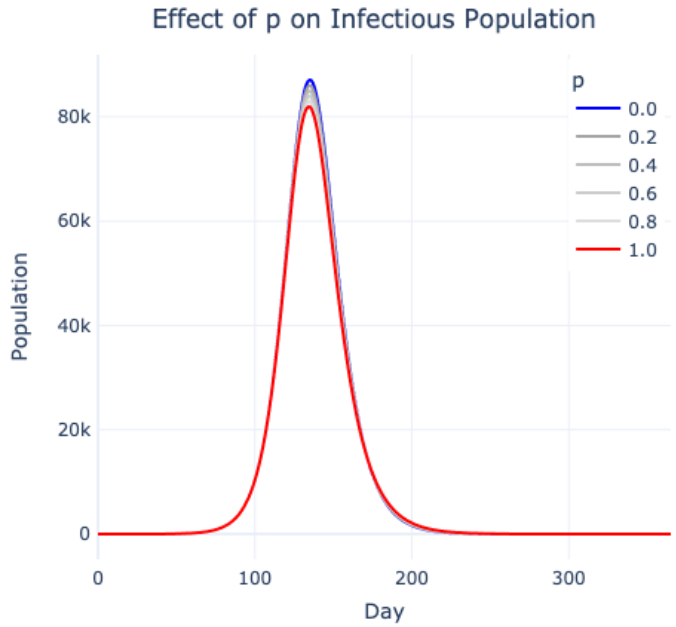


Figure 7: Graph of the effect of p on Infectious population

3.4 Effects of Intervention Methods

It is extremely important to control the spread of diseases especially those infectious to prevent them from escalating, leading to a pandemic. The impact of a pandemic can be catastrophic and thus, several intervention methods have been proposed as a plan of action. However, are the proposed interventions for infectious disease outbreaks truly effective? What are the impacts associated with each of these proposed interventions in reducing the number of people getting infected? By understanding the effectiveness of different interventions, decision-makers can prioritise the implementation of intervention methods to reduce the impact of infectious disease effectively. To investigate the impacts of each proposed intervention, we have developed a comprehensive model from MSEIRS and MSVEIRS (for vaccination). The study is set according to Experiment Setting 3 and parameters outlined in Table 4a.

Experiment Settings 3
All interventions are conducted over a period of 6 months, beginning on Day-90 and ending on Day-270.

The interventions considered in our study are as follows:

1. **No Intervention:**

   No intervention will act as a control. Parameters are initialised as in Table 1.

2. **Social Distancing:**

   Social distancing increases the physical distance between people to minimize close contact and reduce transmission. The further you are from people, the lesser contact you have with people, the less likely you are exposed to and contract the virus. In line with the goal of reducing transmission and infection rates, we have updated the parameter values to reflect the impact of social distancing. The new values are $\beta = 0.375$ and $\sigma = 0.1875$.

3. **Mask:**

   Most infectious diseases are spread through the air, primarily through talking, sneezing and coughing. Masks protect an individual from direct exposure to the virus (NCIRD, 2023). Likewise, for an infected person, masks can prevent the disease from spreading through the air. Thus, wearing masks can reduce transmission and infection rates. Based on a study by Max Planck-Gessellschaft, 2021, wearing masks is more effective than social distancing. Thus, β and σ are updated as 0.125 and 0.0625, respectively to reflect the impact of wearing masks.

4. **Lockdown:**

   Lockdown is one of the most extreme methods whereby the people are ordered

to stay home and most of the economic activities are halted. As a result, there is a significant reduction in interpersonal contact among individuals. With minimal social interactions and reduced mobility, the opportunities for the virus to spread from person to person are greatly reduced. Thus, β and σ are updated as 0.10 and 0.05 respectively to reflect the impact of lockdown.

5. **Vaccination:**

   Vaccines play a crucial role in safeguarding global health. Vaccination reduces transmission and infectious rates (Tan et al., 2023). Vaccine-induced antibodies lead to milder symptoms, thereby contributing to an elevated recovery rate (WHO, 2023a). Thus, β, σ and γ are updated as 0.45, 0.2 and 0.25, respectively, to reflect the impact of vaccination. Since vaccination is a life-long process, the end time for vaccination is not initialised. Whereas the vaccination rate, α, and effectiveness of vaccines, ϵ, were initialised as 0.006 (6,000 of the population are vaccinated per day) and 0.8 (of all people vaccinated, 80% will be immune to the disease while 20% are not).

By substituting the updated parameter values, we can calculate the number of people infected and not infected, as well as the percentage change compared to the **No Intervention** scenario using Equation 24. These percentage changes allow us to assess the effectiveness of each intervention method. The results are presented in Table 4b and Figure 8.

$$\text{Percentage change (\%)} = \frac{\text{Intervention X} - \text{Intervention Control}}{\text{Intervention Control}} \times 100\% \quad (24)$$

Based on the findings in Table 4b, we conclude that lockdown is the most effective measure in increasing the number of people not contracting the disease (+20.83%). On the other hand, vaccination has the highest impact on reducing the infectious patient, with a large decrement of 50.41%.

Method	$\lambda \downarrow$	$\beta \downarrow$	$\sigma \downarrow$	$\delta \downarrow$	$\gamma \uparrow$
No Intervention	0.05	0.500	0.2500	0.1	0.20
Social Distancing	0.05	0.375	0.1875	0.1	0.20
Mask	0.05	0.125	0.0625	0.1	0.20
Lockdown	0.05	0.100	0.0500	0.1	0.20
Vaccination	0.05	0.450	0.2000	0.1	0.25

(a)

Intervention	Susceptible		Infected	
	# Individuals	Change (%)	# Individuals	Change (%)
No intervention	477,812	0	134,301	0
Social Distancing	486,395	1.80	129,090	-3.89
Mask	564,029	18.04	122,767	-8.59
Lockdown	577,355	20.83	119,691	-10.88
Vaccination	548,357	14.76	66,596	-50.41

(b)

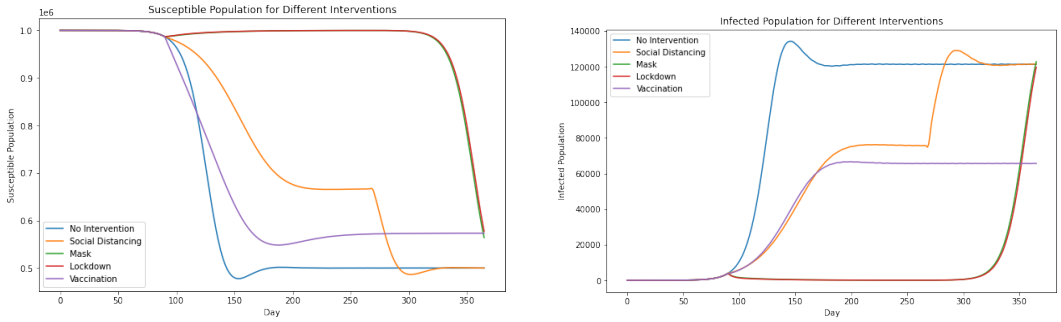
Table 4: Rates of each intervention method and the respective results. (a) Overview of rates used for each intervention method. No Intervention is the control set where the settings are constant throughout the experiment. Up arrows (↑) and down arrows (↓) represent the best direction in changing the rates to control the disease. (b) Results of different interventions on the Susceptible and Infected compartments where # Individual represents the number of individuals in the respective compartments and the ”Change (%)” column represents the percentage change compared to No Intervention.

As a matter of fact, the impact of the disease can be reduced significantly if both measures are implemented simultaneously. Therefore, these findings suggest that there is a need to combine multiple interventions in combating infectious disease.

4 Strengths and Limitations

4.1 Strengths

Compartmental models have been widely used for nearly a century to predict the spread of infectious diseases due to their applicability and flexibility. The following strengths of compartmental models are noteworthy:



(a) (b)

Figure 8: Population over time of different interventions for the compartments: (a) Not Infected (Susceptible) and (b) Infectious. The graphs depict the population dynamics under various intervention methods.

1. **Flexible Model Structure**:

   Compartmental models offer a flexible framework that allows for easy modification of the model structure. This adaptability enables researchers to incorporate new compartments or split existing compartments, facilitating more accurate infection predictions. For example, separate compartments can be created to represent undetected or asymptomatic cases, improving the model's ability to capture the dynamics of the epidemic.

2. **Benefit from Established Approaches**:

   Compartmental models can benefit from well-established approaches such as Bayesian inference, mixed-effects modeling, and stochastic walk. These approaches enhance parameter estimation and contribute to the accuracy of the model predictions.

3. **Tailoring to Research Requirements**:

   By employing novel approaches and efficiently modifying compartmental models, researchers can tailor the models to meet specific research requirements and address the challenges posed by evolving pandemics.

4.2 Limitations

Despite their strengths, compartmental models have certain limitations:

1. **Single Peak Prediction**:

   When used independently, compartmental models can only predict a single peak in the epidemic curve. They may not accurately capture complex scenarios that exhibit multiple peaks or diverse shapes and timings of infection trends.

2. **Over-Parameterization**:

   Estimating numerous parameters in compartmental models can present challenges in model fitting. Over-parameterization can lead to increased computational complexity and the risk of overfitting the model to the data.

3. **Time-Invariant Formulation**:

   The time-invariant formulation of hyperparameters restricts the model from accurately capturing the evolving nature of the epidemiological phenomenon under investigation. The fixed values may not adequately represent the dynamic changes occurring during the course of the epidemic.

To overcome these limitations and enhance the prediction accuracy for complex scenarios, it is often necessary to combine compartmental modeling with other methods or techniques.

5 Future Work

The SEIR model is the most basic yet widely used model in the field of epidemiology to study and forecast the trend of epidemics. It provides a valuable framework

for understanding how infectious diseases spread and enables the evaluation of different interventions such as face masks, social distancing and lockdowns which are all implemented during disease outbreaks. However, the SEIR model overestimates the trend of epidemics (Feng et al., 2021). Thus, it is necessary to add more compartments (features) to the SEIR model to depict a more realistic epidemic model allowing for a more detailed analysis of disease spread, resulting in a better understanding of the disease. Subsequently, allowing decision-makers to better strategise and plan intervention methods.

Although we did expand the SEIR model into the MSEIRS model as well as into the MSVEIRS model in this report, it is still inadequate as we have not covered several aspects from various perspectives. For example, stages of infections, medium of transmission and transmission rate based on age groups. Therefore, we aim to increase the complexity of the model in our future work by incorporating more compartments to simulate a more realistic infectious disease outbreak.

These models could be a good extension for a machine learning algorithm, leading to the second future work we aim to conduct which is an integration of the neural network with the epidemic models. Machine learning is a machine that uses data and algorithms to mimic closely human learning towards a subject and learn over time (IBM, 2022). It can help us classify and predict the outcomes based on the data given. The use of machine learning models, particularly neural networks, can be valuable in extending and enhancing epidemic models. Neural networks can be integrated with epidemic models to add flexibility and adaptability, allowing for various modifications and functions to be incorporated. For example, if we want to extend the SEIR model, we can remodel it into a more complicated model such as SEIER, SEIRE, SEIRI and add death outcomes for each compartment. In fact, there are so much more combinations we can do. Applying a recurrent neural network or a similar approach can effectively handle compartments that have back-

and-forth interactions by utilising its backpropagation property (Zisad et al., 2021). This enables the model to revisit and update previous states, leading to improved estimations. With that, more effective strategies and interventions can be taken in safeguarding countries from an outbreak.

Looking ahead, it would be beneficial for the medical field to collaborate with technology companies such as Google to develop epidemiologic model extensions using popular machine learning frameworks such as TensorFlow and Keras. By making these tools available to the public, researchers are able to experiment, reproduce results and contribute to advancements in healthcare research. This will also foster collaboration and knowledge sharing within the healthcare research community, ultimately leading to better preparedness and understanding of various disease outbreaks.

6 Conclusion

Infectious diseases can spread like wildfire if it is not well controlled. In this era of globalisation, the world is smaller than ever, leading to a higher vulnerability in humans as the spreading of infectious diseases is boundless and limitless. The key to controlling an infectious disease is to understand the nature of it first. Without understanding the disease, the presumed best plan may not be the right plan after all.

Thus, mathematical models play a major role in comprehending and analysing the dynamics of infectious diseases as the models are capable of simulating an outbreak. In this report, we mainly focus on the utilisation of the SEIR, MSEIRS and MSVEIRS models to explain the dynamics of infectious diseases by incorporating different conditions and manipulating the parameters of the models. Through these models, we can observe the potential changes and patterns in disease dynamics and

gain valuable insights from them.

For how changing the susceptible rate, transmission rate, infectious rate, and recovery rate of the disease affect mortality, the MSEIRS model is used to observe patterns and identify the most effective rate in reducing death. Our findings (refer Section 3.2) prove that it is vital to enhance treatment effectiveness aimed at helping infected individuals to recover in order to minimise fatality.

For the impact of maternally derived immunity on the dynamics of infectious diseases, our findings (refer Section 3.3) highlight the importance of considering maternally derived immunity in the population. Using this finding as an example, it shows that it is necessary to consider various factors in epidemiological modelling to reflect and represent more realistic disease dynamics.

By analysing the MSVEIRS model, our findings (refer Section 3.4) reveal that lockdown is the most effective measure in reducing transmission rate. Lockdown involves movement restriction which aims to limit contact between individuals, hence, reducing the transmission rate and resulting in a decline in new infections. On the other hand, vaccination is the most effective measure in reducing the infectious rate. Vaccination aims to provide immunity against disease to individuals. Thus, vaccinated individuals are less likely to be infected with the disease. These findings highlight the importance of combining various measures in combating infectious diseases effectively.

It is in fact undeniable that, in reality, it is far more complex to understand an infectious disease especially if the disease is new and therefore, unknown. The world is constantly evolving and so do diseases. With this report, we hope that the proposed models and solutions in the report can provide sufficient and new insights into understanding infectious diseases as well as improving the existing epidemiological modelling. We also hope that this report is able to pique your interest to start experimenting with different factors in order to create a more accurate and reliable

model in the future. With a more accurate model, humans can better understand a disease's nature, allowing us to prepare and formulate better measures whenever an outbreak strikes.

7 Members' Contributions

Member	Contributions
Nah Wan Jun	- Topic brainstorming - Tasks distribution - Discussion - Propose solution - Writing report - Writing code
Jasmine Chong See Yan	- Topic brainstorming - Discussion - Propose solution - Writing report - Writing code
Janice Chong See Wai	- Topic brainstorming - Discussion - Propose solution - Writing report - Writing code
Cheok Xin Yu	- Topic brainstorming - Discussion - Propose solution - Writing report - Writing code
Muhammad Ikram Bin Jaafar	- Topic brainstorming - Discussion - Propose solution - Writing report - Writing code

References

Baylor College of Medicine. (2023). Introduction to infectious diseases. https://www.bcm.edu/departments/molecular-virology-and-microbiology/emerging-infections-and-biodefense/introduction-to-infectious-diseases

Centers for Disease Control and Prevention. (2016). How infections spread. https://www.cdc.gov/infectioncontrol/spread/index.html

Feng, S., Feng, Z., Ling, C., Chang, C., & Feng, Z. (2021). Prediction of the COVID-19 epidemic trends based on SEIR and AI models (J. Zhang, Ed.). *PLOS ONE*, *16*(1), e0245101. https://doi.org/10.1371/journal.pone.0245101

Hunter, E., & Kelleher, J. D. (2022). Understanding the assumptions of an seir compartmental model using agentization and a complexity hierarchy. *Journal of Computational Mathematics and Data Science*, *4*, 100056. https://doi.org/https://doi.org/10.1016/j.jcmds.2022.100056

IBM. (2022). What is machine learning? https://www.ibm.com/topics/machine-learning

Kasereka, S., Zohinga, G., Kiketa, V., Ngoie, R.-B., Mputu, E., Kasoro, N., & Kyandoghere, K. (2023). Equation-based modeling vs. agent-based modeling with applications to the spread of COVID-19 outbreak. *Mathematics*, *11*(1), 253. https://doi.org/10.3390/math11010253

Max Planck-Gessellschaft. (2021). Masks protect better than distancing, study finds. https://as.cornell.edu/news/masks-protect-better-distancing-study-finds

Ministry of Health – Manatū Hauora. (2021). How infectious diseases spread. https://www.health.govt.nz/your-health/healthy-living/environmental-health/infectious-disease-prevention-and-control/how-infectious-diseases-spread

Ministry of Health of Malaysia and Department of Statistics Malaysia. (2023). Covid-19: The latest data on the pandemic in malaysia. https://data.moh.gov.my/covid

NCIRD. (2023). How to protect yourself and others. https://www.cdc.gov/coronavirus/2019-ncov/prevent-getting-sick/prevention.html

Straif-Bourgeois, S., Ratard, R., & Kretzschmar, M. (2014). Infectious disease epidemiology. In *Handbook of epidemiology* (pp. 2041–2119). Springer New York. https://doi.org/10.1007/978-0-387-09834-0_34

Sundnes, J. (Ed.). (2023). *Solving ordinary differential equations in python*. Simula Research Laboratory. https://sundnes.github.io/solving_odes_in_python/ode_book.pdf

Tan, S. T., Kwan, A. T., Rodríguez-Barraquer, I., Singer, B. J., Park, H. J., Lewnard, J. A., Sears, D., & Lo, N. C. (2023). Infectiousness of SARS-CoV-2 breakthrough infections and reinfections during the omicron wave. *Nature Medicine*, *29*(2), 358–365. https://doi.org/10.1038/s41591-022-02138-x

Vodovotz, Y., & An, G. (Eds.). (2013). *Complex systems and computational biology approaches to acute inflammation*. Springer New York. https://doi.org/10.1007/978-1-4614-8008-2

WHO. (2020). The top 10 causes of death. https://www.who.int/news-room/fact-sheets/detail/the-top-10-causes-of-death

WHO. (2023a). Vaccines and immunization. https://www.who.int/health-topics/vaccines-and-immunization#tab=tab_2

WHO. (2023b). Who coronavirus (covid-19) dashboard. https://covid19.who.int/

World Health Organization. (2004). *The world health report: 2004: Changing history*.

World Health Organization. (2014). A brief guide to emerging infectious diseases and zoonoses.

Zisad, S. N., Hossain, M. S., Hossain, M. S., & Andersson, K. (2021). An integrated neural network and SEIR model to predict COVID-19. *Algorithms*, *14*(3), 94. https://doi.org/10.3390/a14030094