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A Mathematical Model of COVID-19 Transmission

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Abstract

Disease transmission is studied through disciplines like epidemiology, applied mathematics, and statistics. Mathematical simulation models for transmission have implications in solving public and personal health challenges. The SIR model uses a compartmental approach including dynamic and nonlinear behavior of transmission through three factors: susceptible, infected, and removed (recovered and deceased) individuals. Using the Lambert W Function, we propose a framework to study solutions of the SIR model. This demonstrates the applications of COVID-19 transmission data to model the spread of a real-world disease. Different models of disease including the SIR, SIRm and SEIR model are compared with respect to their ability to predict disease spread. Physical distancing impacts and personal protection equipment use will be discussed in relevance to the COVID-19 spread.

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Keywords: Lambert W function; SIR model; SEIR model; Nonlinear differential equations; Disease transmission.

1. Introduction

The First World War ravaged the world with death and destruction. A key contributor to the enormous death toll was not war, but a product of its chaotic environment; the 1918 “Spanish” Influenza. This H1N1 virus of avian origin spread throughout 1918-1919, infecting over 500 million individuals, and killing at least 40 million people worldwide [27, 18]. Lack of sanitation and resources during wartime, and no progress in the development of a vaccine, limited worldwide control efforts to non-pharmaceutical interventions such as isolation and use of informal disinfectants [12]. Due to the immense, rapid spread of disease, countries were unable to suitably prepare themselves to prevent or control the influenza.

Now, almost a century later, the world is rocked again by the emergence of the new strand of coronavirus disease (COVID-19). This novel virus was first reported in December 2019 in Wuhan, China and has since spread to pandemic proportions [24]. As this virus can be transmitted person to person [24], many protective measures such as masking and social distancing have been put in place to reduce human interactions.

COVID-19 targets the human respiratory system, resulting in clinical findings such as high fever, dyspnea and invasive multilobed lesions as seen in chest radiographs [23, 16]. It has been reported that the symptoms of this virus start about 5 days after contracting it [24]. These symptoms tend to get progressively worse as time goes on, some cases leading to death, while others successfully recover [16]. This is a major public threat since thousands of Canadians have been hospitalized due to respiratory issues along with other flu-like symptoms after being diagnosed with COVID-19 with no concrete vaccine yet developed [24].

While the world now has the advantage of more accessible resources and a better understanding of pandemics compared to 1918, there are still the problems of disease prevention and control. A way to combat this is to model the disease over time, to better understand the gravity of the situation [5]. Epidemics play a major role in understanding

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disease transmission by studying disease distribution, sources of diseases, causes of diseases, and methods of disease control [14]. Using data of epidemic curves, one can extrapolate disease data and trends to prepare for potential disease burden and determine public policies to mitigate risks of spread [5].

The Susceptible-Infected-Removed (SIR) model and its derivatives is one way to understand the transmission of diseases and predict future outcomes regarding COVID-19 cases. This study uses the SIR model, SIRM model, Susceptible-Exposed-Infected-Removed (SEIR) model, and the SEIRm to illustrate COVID-19 spread. This study also uses the Lambert W function to analyze the SIR and SEIR models to better understand disease spread.

Section 2 of this paper discusses data and methods used to illustrate COVID-19 trends through different models such as the SIR, SIRM, SEIR and the SEIRm models. By using Canadian data to model the current trend of COVID-19, it is possible to create graphs that depict where the individuals stand with respect to time during the spread of disease. Using a mixing factor m , it is possible to introduce a human-behaviour or social distancing factor into the situation. Section 3 presents the results of our paper and there will be simulations of Canadian COVID-19 data in context of the afore-mentioned models. In Section 4, the results obtained from our analysis will be discussed. Finally, Section 5 of this paper presents our conclusions.

2. Methods

In this study, open-source COVID-19 datasets provided by Public Health Agency of Canada's Public Health Infobase is used. The data ranges from January 22, 2020 to July 17, 2020, with each time series tracking an epidemiology statistic. The three-time series of focus are count of confirmed cases, deaths, and recovered cases nation-wide in Canada.

2.1. SIR Model

The SIR model is a representation that divides a population with respect to a disease's impact on an individual over time. An individual can be categorized as susceptible ($S(t)$), infected ($I(t)$), or removed ($R(t)$, dead or cured), denoted by S, I and R respectively, along an independent variable; time [25]. One of the most common SIR models is the classic Kermack–McKendrick Model for contagious diseases in a closed population over time. The model was created to illustrate the rapid changes in the number of infected patients during epidemics. It is assumed that there is a fixed homogeneous population size, random population mixing, instantaneous incubation period, and acute onset of disease [30, 31, 1]. The model variables can be represented as fractions:

$$s = \frac{S}{N} \quad (1)$$

where s is a fractional representation of the number of susceptible individuals (S) over a selected population (N) over time.

$$i = \frac{I}{N} \quad (2)$$

where i is a fractional representation of the number of infected individuals (I) over a selected population (N) over time.

$$r = \frac{R}{N} \quad (3)$$

and r is a fractional representation of the number of removed individuals (R) over a selected population (N) over time.

Overall, these equations must add to 1:

$$s + i + r = 1 \quad (4)$$

Using these equations, it is possible to extract three nonlinear differential equations that aid in tracking the illness progression. We present these equations below.

The Susceptible Equation:

$$\frac{ds}{dt} = -\beta si \quad (5)$$

where β represents the infection rate, the probability per day that an I-person can infect a S-person, assuming the absence of social distancing. The Infected Equation:

$$\frac{di}{dt} = \beta si - \gamma i \quad (6)$$

The Recovered Equation:

$$\frac{dr}{dt} = \gamma i \quad (7)$$

where γ represents the recovery rate, the probability per day that an I-person transitions into an R-person (becoming non-infectious permanently).

The ratio of S-persons transitioning into I-persons is the ratio of β to γ , referred to as the Reproduction Number; λ .

$$\lambda = \frac{\beta}{\gamma} \quad (8)$$

The higher the value of λ , the more transmittable the disease is; the infection rate eclipses the recovery rate.

While R_0 usually denotes the reproduction number, this paper uses R_0 to denote the initial value of the Recovered variable at time $t = t_0$.

There is always some natural immunity, so it is reasonable to assume that r_0 is greater than 0. If the population has been partly vaccinated, the value of r_0 might even be 0.40 or more. Similarly, even without vaccination, a prior asymptomatic spread of the disease in the population may have resulted in r_0 being perhaps 15 or 20 percent of the population [10].

Some other variables can be introduced for the SIR model for convenience of comparison with information reported about the course of the epidemic. The total number of cases since the beginning of the epidemic is C . The initial value of the total number of cases, prior to time $t = t_0$, is C_0 . The number of new cases per day is J . The variable J is defined by:

$$J = \frac{dC}{dt} = \beta \frac{SI}{N} \quad (9a)$$

Therefore, considering a closed population ($N = 1$) this equation becomes:

$$j = \beta si \quad (9b)$$

where j is the number of cases per day in a closed population.

There is a possibility that some individuals may have been included in the R-group due to natural immunity or vaccination immunity, rather than as recovered cases. Therefore, by tracking the decline in S-persons, it is

possible to track the increase in total cases, c , while excluding the individuals with immunity [10]. This indicates that s can be used as an independent variable to find i as a function of s :

$$i(s) = 1 - s - r(s) \quad (10a)$$

where $r(s)$ can be written as $r_0 - \frac{1}{\lambda} \ln\left(\frac{s}{s_0}\right)$

$$i(s) = 1 - s - r_0 + \frac{1}{\lambda} \ln\left(\frac{s}{s_0}\right) \quad (10b)$$

Dividing equation (6) by equation (5) results in:

$$\frac{di}{ds} = \frac{\gamma - \beta s}{\beta s} \quad (11)$$

The solution of this equation for i gives a Lambert W Function as implicitly seen in the expression given in equation (10b). This remarkable function has created a renaissance in the solution of diverse problems in innumerable fields of knowledge [7]. The solution is as follows:

$$s = -\frac{1}{\lambda} W(-\lambda c \exp(\lambda i)) \quad (11a)$$

where $c = i_0 + s_0 - \frac{1}{\lambda} \ln(s_0)$ is the constant of integration to be determined from initial conditions by solving equation (11) with initial condition $i(s_0) = i_0$. Since equation (11a) has a Lambert W function with an exponential argument, this can also be expressed as an Omega Wright function [33].

To continue, it is possible to use r as an independent variable as well. The expressions of s can be found with respect to r :

$$s(r) = s_0 \exp[-\lambda(r - r_0)] \quad (12a)$$

If an R-curve graph shows a continued increase, it would indicate an increase in number of removed individuals [3].

Equation (12a) can then be substituted into the equation:

$$\frac{di}{dr} = \frac{\beta s - \gamma}{\gamma} = \lambda s - 1 \quad (12b)$$

to give:

$$\frac{di}{dr} = s_0 \exp[-\lambda(r - r_0)] \quad (12c)$$

This equation (12c) can be integrated to provide an equation that illustrates i as a function of r :

$$i(r) = i_0 + s_0\{1 - \exp[-\lambda(r - r_0)]\} - (r - r_0) \quad (13a)$$

$$i(r) = 1 - r - s_0 \exp[-\lambda(r - r_0)] \quad (13b)$$

If there are very few infectious people, the I-group becomes a very small fraction of the population, therefore $s + r \approx 1$. In addition, peak infections occur when $\frac{di}{dt} = 0$, the time when the I-group is the largest, assuming $t = t_1$ at I_{max} , it is possible to rework the Infection Equation as:

$$\beta s(t_1)i(t_1) = \gamma(t_1)i(t_1) \quad (14a)$$

$$\beta s(t_1) = \gamma \quad (14b)$$

$$s(t_1) = \frac{\gamma}{\beta} = \frac{1}{\lambda} \quad (14c)$$

Therefore, the lower the value of λ , the larger the number of people entering the R-group. This is as the recovery rate will overpower the rate of individuals entering the I-group.

When $\lambda < 1$; $\gamma > \beta$. This indicates that the $s(t)$ curve will decrease past $r(t)$ curve, which will increase. When $\lambda = 1$, the ratios of $s(t)$ and $r(t)$ are equal and will inverse after the point of equivalence. When $\lambda < 1$, the ratio of $s(t)$ was greater than $r(t)$. This demonstrates that the $i(t)$ value was increasing as the infection rate, β , is greater than the recovery rate, γ . A point of inflection occurs in the $i(t)$ curve at $I_{max} = t_1$ which illustrates that as the ratios inverse between the $s(t)$ and $r(t)$ curves. The λ value decreases, indicating a lower β value; implying a decrease in members in the I-group and a descending $i(t)$ curve.

The value of the inflection points can be found using the second derivative of s with respects to t :

$$\frac{d^2s}{dt^2} = -\beta \frac{d}{dt} [si] \quad (15)$$

As the epidemic dies out, the number of infectious people approaches zero, so an asymptotic limit is formed; $t \rightarrow \infty$, and therefore, $s + r = 1$. Inflection points will be discussed in greater detail in Section 4.2.

2.1.1 SIRm Model

The SIRm model, as derived from the SIR model, focuses on the relationship between disease transmission and the effect of public health measures. Consider a situation in which public health guidelines are introduced to slow the frequency, duration and - contact distance between S-people and I-people. This can be represented by making the value of the parameter β vary with time. However, a conceptually simpler way to describe such public health measures is to keep β constant and multiply it by a time-varying mixing factor m to reflect changes in social distancing. In the present section, we assume that β is constant, and develop the equations and approximations for the standard SIR model by setting all m values to 1.

As such, the differential equations in population fraction notation are:

$$\frac{ds}{dt} = -\beta msi \quad (16)$$

$$\frac{di}{dt} = \beta msi - \gamma i \quad (17)$$

$$\frac{dr}{dt} = \gamma i \quad (18)$$

$$s + i + r = 1 \quad (19)$$

Dividing equation (17) by equation (16) results in:

$$\frac{di}{ds} = \frac{-\beta ms + \gamma}{\beta ms} \quad (20a)$$

The solution of equation of (20a) is given as:

$$s = -\frac{1}{\lambda m} W(-\lambda mc \exp(\lambda mi)) \quad (20b)$$

where $c = i_0 + s_0 - \frac{1}{\lambda m} \ln(s_0)$ is the constant of integration to be determined from initial conditions by solving equation (20a), with initial condition $i(s_0) = i_0$.

This equation is in terms of the Lambert W function, which is defined after equation (27) below.

The equations for total cases per day, j , and the total cumulative cases, C are [29]:

$$j = \frac{dC}{dt} \quad (21a)$$

or

$$j = \beta msi \quad (21b)$$

and

$$C = C_0 + \int_0^t j(\tau) d\tau \quad (22a)$$

or

$$C = C_0 + \beta \int_0^t m(\tau)s(\tau)i(\tau) dt \quad (22b)$$

2.2. SEIR Model

The SIR model can be extended using the Susceptible-Exposed-Infected-Removed (SEIR) variant. This model also considers the susceptible, infected and removed populations but unlike the SIR model it also considers the exposed population; those who are incubating the virus but are not infectious or infected [19]. The SEIR model adds another layer of complexity to the SIR model, by allowing the analysis of conditions of susceptible and infected populations during an epidemic outbreak [9].

The SEIR model's governing equations are:

$$\frac{ds}{dt} = -\rho\beta si \quad (23)$$

$$\frac{de}{dt} = \rho\beta si - \alpha e \quad (24)$$

$$\frac{di}{dt} = \alpha e - \gamma i \quad (25)$$

$$\frac{dr}{dt} = \gamma i \quad (26)$$

where the parameters are defined as [4, 21]:

α : incubation rate from the exposed group to the infected group,

β : infection rate,

γ : removal rate from the infected group to removed group,

ρ : the reduced spread rate factor ($0 \leq \rho < 1$).

The equations have been modified to properly reflect a closed population.

This study examines the use of the Lambert W function in conjunction with the SIR and SEIR models, the multivalued inverse of the function $w \rightarrow we^w$ [7]. In the 18th century, scientist Johann Lambert gave a solution to a trinomial equation, upon which further work by Euler and Sir Edward Wright led to the now modern definition of Lambert's original work [28]. Their function, named to honour Lambert, is as follows:

$$W(z)e^{W(z)} = z \quad (27)$$

The Lambert W function is implicitly elementary in that it is defined by an equation composed of only elementary functions but is not an elementary function itself. It has applications in a variety of fields ranging from quantum physics, black holes to even the spread of disease [11].

Corless et al.'s article regarding the Lambert W function further studied the function's applicability in epidemics. Let us assume in a population of n people, everyone has the same contact with α random others [7]. If γ is the weak connectivity of this random net, and disease spreads through transitivity to those in close contact with the infected individual, the total infected population is approximated as γn for large n , where:

$$\gamma = 1 - e^{-\alpha\gamma} \quad (28)$$

This formula can also be applied for conditions where α is a fixed integer, as well as when α is an expected

value in that it is not fixed for all individuals and may not be an integer [26, 1]. Re-writing the above formula we obtain the following:

$$\alpha e^\alpha = \alpha(1 - \gamma)e^{\alpha(\gamma-1)} \quad (29a)$$

One can determine:

$$\gamma = 1 - T \frac{(\alpha e^{-\alpha})}{\alpha} = 1 - W \frac{(-\alpha e^{-\alpha})}{\alpha} \quad (29b)$$

where $\alpha \geq 1$, using the principal branch of T (of the Tree function) and W (of the Lambert W function) [7].

This epidemic problem is closely tied to a phenomenon described by Erdős and Rényi in which the epidemic problem is related to the size of the ‘giant component’ in a random graph [8]. Essentially, when a graph on n vertices with $m = \frac{1}{2}\alpha n$ edges is randomly chosen, it is almost certain it has a connected component with approximately γn vertices (for γ given by equation (2)) when $\alpha \geq 1$ [7].

2.2.1. SEIRm Model

The SEIRm model is a derivation of the SEIR model. The SEIRm model trials demonstrate various stabilities of the COVID-19 virus situation, based on an unpublished report and private communications by Ken Roberts [22]. By observing the value of m , the severity of the situation can be determined. A higher m value would indicate high infectivity which not only affects the volume of patients in the hospital, but various other aspects related to COVID-19 [20]. If the m value is lower, then that would demonstrate a more manageable situation [22]. This once again puts an emphasis on the importance of social distancing in order to maintain a lower m value. Two very important aspects that would be affected by the reported COVID-19 cases are the development of a vaccine for COVID-19 and medical equipment for patients and hospital staff. In SEIRm model trials, COVID-19 data for Ontario is used and $\alpha = 0.20$ and $\gamma = 0.20$, which gives $\beta = 0.81$ and $\lambda \approx 4$ [22].

2.3. Planck Blackbody Distribution

While analyzing several SIR models of disease, it was observed that some of the infection curves looked like Planck’s blackbody distribution curves due to the realistic asymmetry of the infection data curves [20]. Keeping this in perspective, it was decided this study would simulate infection curves using an asymmetric function rather than a purely symmetric one. Max Planck theorized that mode energies of the blackbody are not continuously distributed but are quantized. He devised a law for blackbody radiation as follows [2]:

$$B_\nu(T) = A \frac{(2 \cdot h \cdot \nu^\alpha / c^2)}{e^{h \cdot \nu / kT - 1}}, \alpha=3 \quad (30)$$

where the parameters are defined as:

B_ν : spectral radiance,

h : Planck’s constant,

c : speed of light in a vacuum,

k : Boltzmann constant,

ν : frequency of the electromagnetic radiation,

T : absolute temperature of the body,

α : any value other than 3 to run Planck-like simulations in other situations.

Therefore, this formula represents the spectral-energy distribution of radiation emitted by a blackbody.

The similarity of the SIR model infection curve suggests that it may be reasonable to model the infection curve for a few different values of α like in a Planck Blackbody Distribution function with an appropriate definition of the constants C_1 and C_2 [28].

In this paper, two adjusted formulas inspired from the Planck-like Blackbody Distribution are proposed to model infection as a function of time.

$$I(t) = \frac{(C_2 \cdot t^\alpha)}{e^{C_1 \cdot t} - 1} \quad (31)$$

where α can be any positive integer.

3. Results

The figures below display the results of the all models (SIR, SIRm, SEIR) fitted onto the given Canadian COVID-19 dataset by parametrically solving the system numerically using ParametricNDSolve from Wolfram Mathematica (version 12.3). The respective model parameters were derived by using NonlinearModelFit to fit the data to β and γ for the first 177 Days. The solid print lines refer to predicted trends, while the dotted lines refer to the Canadian data. During this study, it was found that none of the models were able to fully capture disease spread using one general approach—as such, it was found that parameters had to be fitted separately for two separate time windows for the SIR and SEIR models as recommended in [4] and varied for SIRm model in order to best capture disease spread. In the tables, the P-value signifies the probability of finding the modeled results least extreme to the observations under the assumption of the null hypothesis. Hence, the smaller the p-value is, the less likely it is to violate the null hypothesis and the result is deemed significant. The t-statistic is the ratio of the departure of the estimated value of a parameter from observations to its standard error. It is generally the case that when these values are greater than 2 or less than -2, the model fit is better.

3.1. SIR Model

For the SIR model, β is estimated to be 0.19626 and γ is estimated to be 0.08345 (refer to Table 1). The population (N) considered is 3,759,000, and initial infection, $i_0 = 1$. The SIR model predicted the infected and removed case counts accurately for the first 70 days. After which, the predicted trends fail to capture the rise of infected and removed case counts as fast as they had occurred (Figure 1). From days 101-177, the predicted trends linearly trace the infected and removed case counts. The predicted trend for removed cases do not accurately track the case data that was observed (Figure 2). In contrast, the predicted trend for infected cases faithfully tracks the actual infected cases from day 148 onwards (Figure 2).

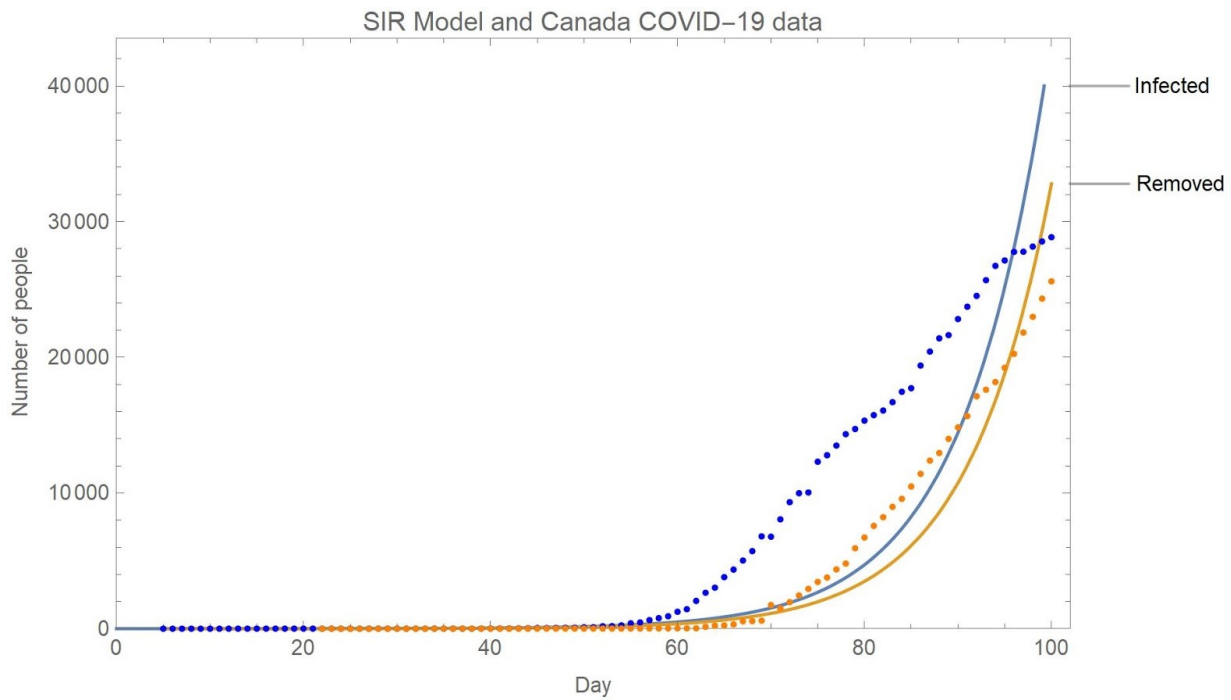


Fig.1. SIR model prediction of infected and removed cases with respect to data for Canada for days 1-100

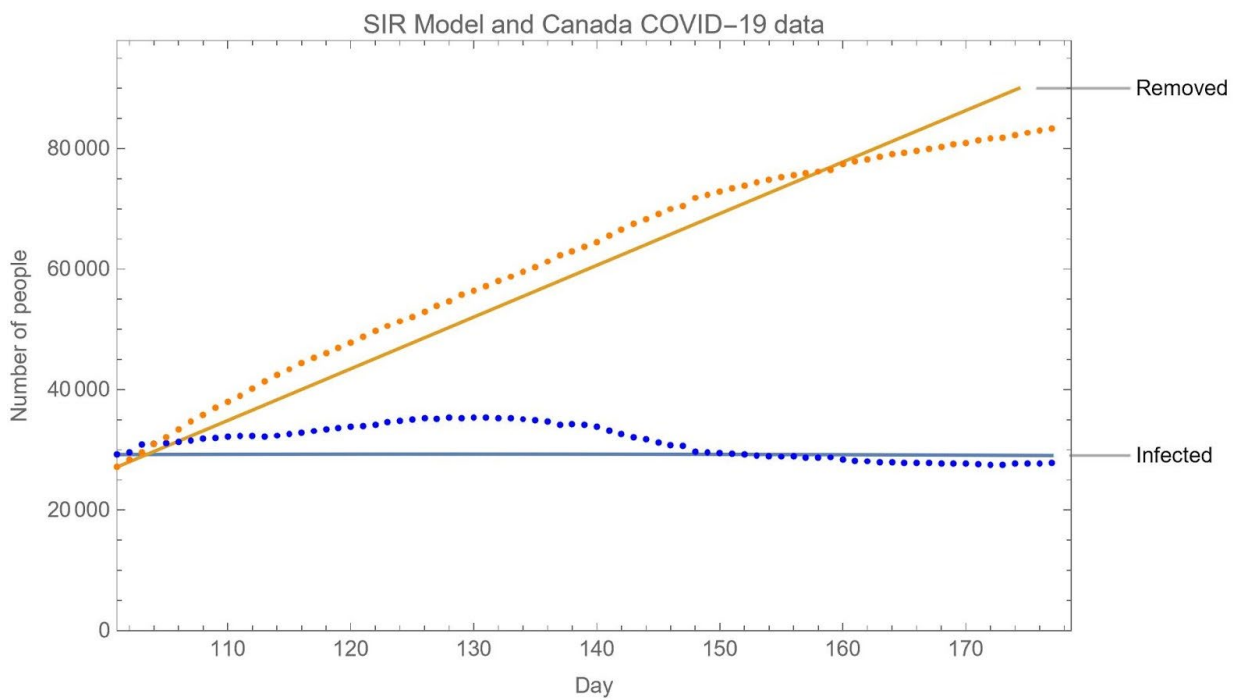


Fig. 2. SIR model prediction of infected and removed cases with respect to data for Canada for days 101-177

Table 1. SIR and SIRm model parameters used in Figures 1-4

Days	Parameter	Estimate	Standard Error	t-Statistic	P-Value
1-100	β	0.19626	0.0052631	37.2899	1.28271×10^{-84}
	γ	0.0834452	0.00549364	15.1894	1.16729×10^{-33}
101-177	β	0.0297597	0.000343304	86.6863	2.54249×10^{-131}
	γ	0.0293381	0.000431199	68.0386	9.82261×10^{-116}

3.1.1. SIRm Model

For the SIRm model, the m value used is 1.05 to modify β and $p(t) = 1 - 0.004t$ as a variation in γ (refer to Table 1). The variation of the SIR model parameters as a function of time was recently recommended in [34] as well. The SIRm model faithfully predicts the infected and removed case counts for the first 70 days. The predicted trends then rise faster in case counts when compared to the actual numbers of infected and removed cases seen (Figure 3). From days 101-177, the predicted trend for infected cases is generalized as a plateau, underestimating case counts until day 141, after which the trend overestimates case count. From days 101-177, the predicted trend for removed cases underestimate actual case counts until 154, after which they overestimate cases.

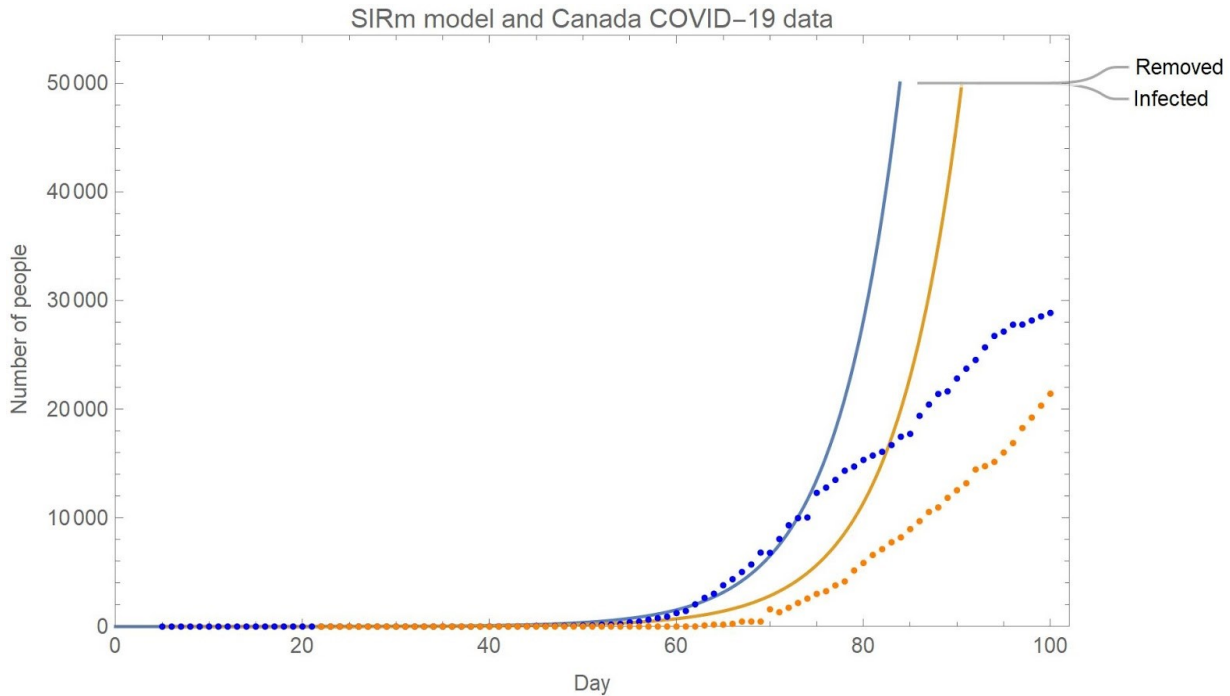


Fig. 3. SIRm model prediction of infected and removed cases with respect to data for Canada for days 1-100
 (The orange curve and datapoints refer to the removed cases while, the blue refer to the infected)

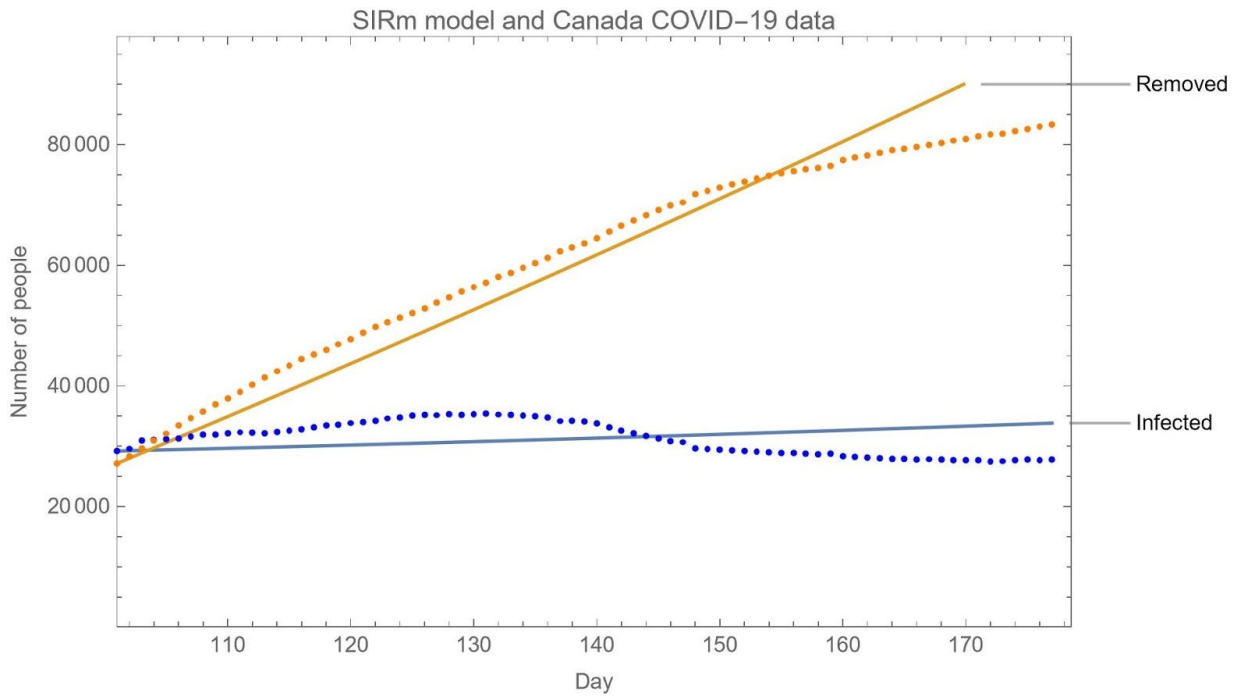


Fig. 4. SIRm model prediction of infected and removed cases with respect to data for Canada for days 101-177

3.2. SEIR Model

For the SEIR model, it is assumed that $\rho = 1$ to produce the classic SEIR model results. In this model, α is estimated to be 0.0267402, θ is estimated to be 0.309797 and γ is estimated to be 0.039089 (refer to Table 2). Note that $\rho = 0$ implies everyone in the society is quarantined, while $\rho = 1$ implies no social distancing. The SEIR model is able to follow the general trend of the actual case counts for the first 100 days. It is important to note that for the first 100 days, the predicted trend for the infected underestimated the actual case counts until day 95 and then breaks away from the real data. The predicted trend for removed cases overestimates the actual cases observed for the first 100 days (Figure 5). From days 101-177, the predicted trends for both infected and removed follow the general linear trends. However, it is important to note that from day 145 onwards the infected real data very accurately follows the predicted trend but, from day 158 onwards the removed real data underestimates the predicted trend (Figure 6).

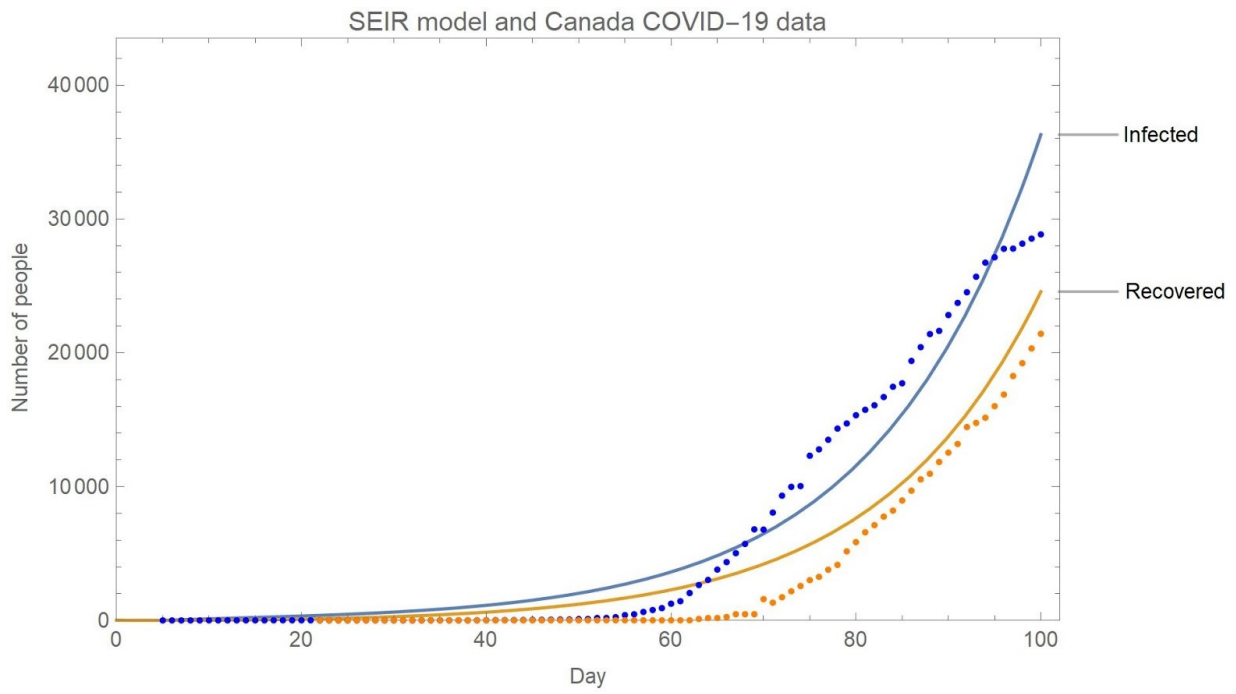


Fig.5. SEIR model prediction of infected and removed cases with respect to data for Canada for days 1-100

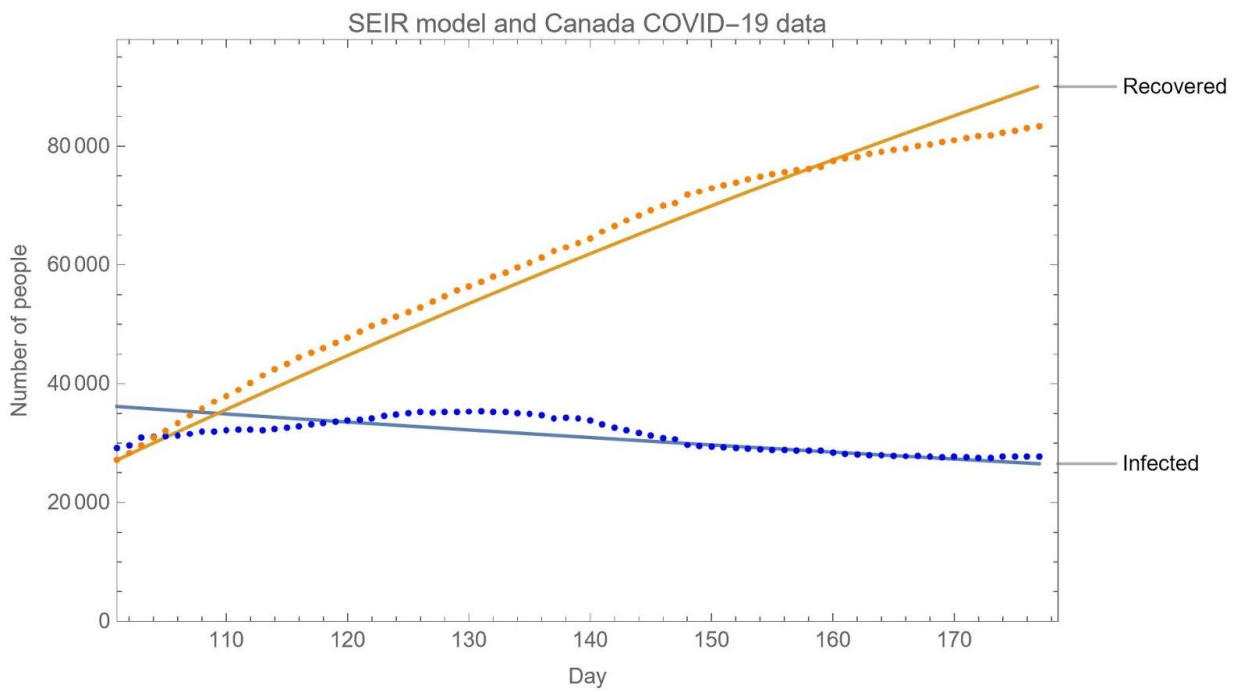


Fig. 6. SEIR model prediction of infected and removed cases with respect to data for Canada for days 101-177

Table 2. SEIR model parameters used in [Figures 5-6]

Days	Parameters	Estimate	Standard Error	t-Statistic	P-value
1-100	α	0.0267402	0.00396713	6.74045	2.2902×10^{-10}
	β	0.309797	0.0470421	6.58553	5.29441×10^{-10}
	γ	0.039089	0.00159929	24.4415	7.67106×10^{-58}
101-177	α	0.820113	0.0102798	79.7794	2.37222×10^{-125}
	β	0.022746	0.000620057	36.6837	4.21413×10^{-77}
	γ	0.0265887	0.000348606	76.2714	1.79093×10^{-122}

3.3. Planck-Like Blackbody Function

Figure 7 displays the results of the predicted infected curves after conducting a non-linear fit of the parameters C_1 and C_2 . The parameters C_1 and C_2 were estimated to be 0.0693891 and 2.7832×10^{-11} respectively (see Table 3). Several trials of different α values were run, and it was determined that an α value of 9 yielded the best fit for modelling COVID-19 data (Figure 7) getting a good estimation of the peak number of infected cases.

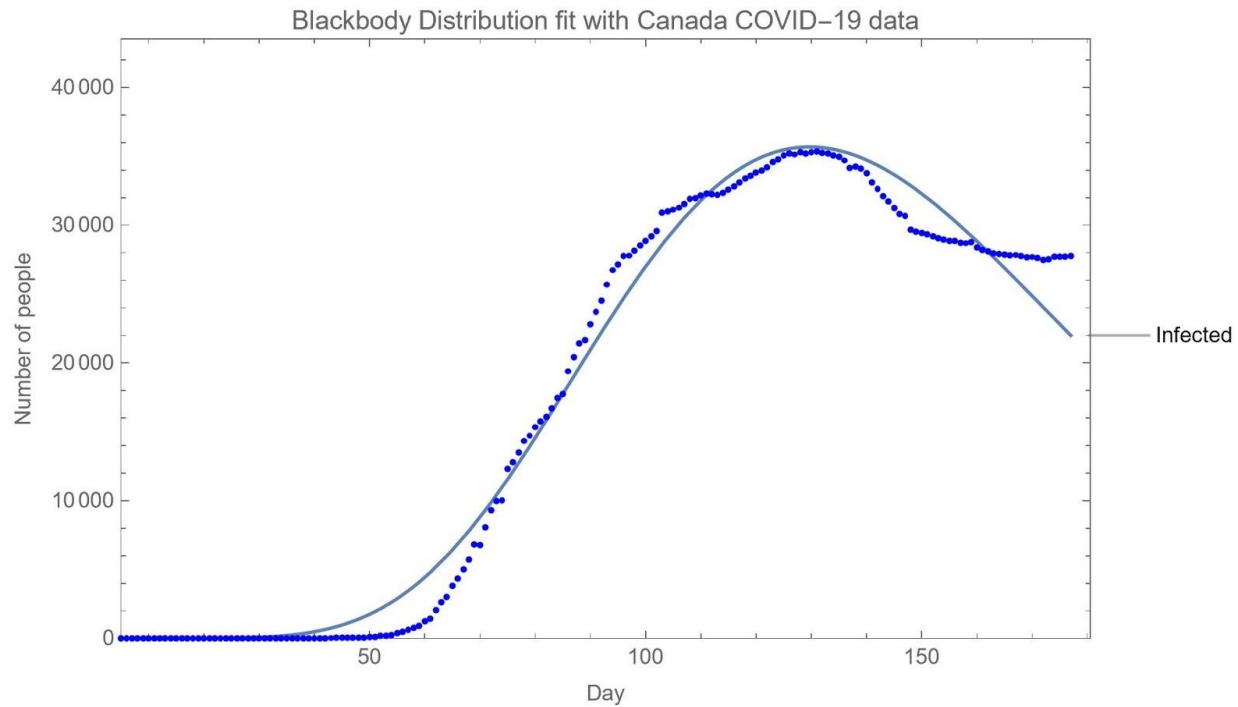


Fig..7 Blackbody distribution fit of infected cases using a Planck Function ($\alpha=9$) with respect to data in Canada from days 0-177

Table 3. Parameters for Planck Blackbody.

Parameter	Estimate	Standard Error	t-Statistic	P-Value
C_1	0.0693891	0.00024041	288.628	8.17177×10^{-232}
C_2	2.7832×10^{-11}	8.85294×10^{-13}	31.4382	5.61764×10^{-73}

4. Discussion

4.1. Model Interpretations

Social distancing is the practice of reducing physical contact to reduce opportunity for spread of transmissible diseases [6]. Common practices include social isolation, self-quarantine and cancellation of mass gatherings. Matrajt and Leung used a mathematical model to illustrate how implementing social distancing measures earlier in an epidemic will delay the epidemic curve while interventions started later will flatten the curve. The model also illustrated that the epidemic would rebound when interventions are suspended, indicating the importance of maintaining social distancing practices for the safety of the population [17].

In this study, the SIR and SIRm models demonstrate that while initially a good fit for modelling disease spread, it veers away from actual data as time passes since it fails to account for several anthropological factors such as adherence to prevention methods. The implication that β and γ values vary in the model to best fit the results suggest that models that vary these parameters would better fit the actual data, and therefore be able to better predict the disease spread. Overall, the SEIR model was able to predict disease trends better, but it also fails to fully capture the impact of anthropological factors. One way to combat this problem would be to focus on models that incorporate the addition of other factors such as public compliance and mixing factor. In recent work, the SEIRm model results displayed that the mixing factor, m , decreased rapidly to 0.2 levels over approximately the first 150 days since April 10, 2020 [22]. The m factor then proceeds to increase to 0.3779 by September 16, 2020 [22].

The m factor in the SEIRm model plays a crucial part in the significance of this model. The values of the m factor indicate the severity of the situation regarding COVID-19 case numbers. As indicated earlier, the greater the value of m , the more severe the situation. Regarding COVID-19, if a greater m value was seen, this would indicate that numbers are rising which then puts greater pressure on hospitals due to a rapid increase in patients. A higher m value would not only affect hospitals but would also impact equipment manufacturing companies and companies that are working to develop a vaccine for COVID-19. Alternatively, a lower m value would indicate a more controlled or lower number of COVID-19 cases. This lessens the strain on hospitals, personal protection equipment manufacturers, and labs working on vaccine development. Moreover, the m value also allows for a hypothetical timeline to be developed. A timeline would be a very useful aid in creating a plan for various areas in order to properly control the spread of COVID-19.

This study's results on various modified disease spread models illustrate the importance of social distancing and its effects on the rise of infections during a pandemic. The ability of a population to adhere to social parameters set by the government can greatly influence and control the spread of an infection. The m factor presents a good representation of adherence to social parameters however, it is important to note that many other factors can be introduced to better reflect these anthropological variables which are subject to change.

4.2. SIR Model Inflection Points

An important aspect of disease modelling is understanding the peak of infection. An inflection point in the curve would suggest the peak of infection has been reached which may not be visible using the variable, time (t), in the earlier stages of the spread. For this reason, it is important to be able to use the s , i , and r variables independently to derive the inflection point without depending on time (t) as a variable.

In this case, the condition to determine an inflection point are as follows, recalling that equation (5) states $\frac{ds}{dt} = -\beta si$:

$$s'' = \frac{d^2s}{dt^2} \quad (32a)$$

For an inflection point to occur, $s'' = 0$ and si are constant

$$\frac{ds}{dt}i + \frac{di}{dt}s = 0 \quad (32b)$$

$$\frac{di}{dt} = \beta si - \gamma i \quad (32c)$$

Equation (32c) can be rewritten as:

$$\frac{ds}{dt} i = -s \frac{di}{dt} = -si(\beta s - \gamma) \quad (32d)$$

Factoring out i , we have a simplification,

$$\frac{ds}{s} = -(\beta s - \gamma) dt \quad (32e)$$

or

$$\frac{ds}{s(\beta s - \gamma)} = -dt \rightarrow \int \left(\frac{1}{s} - \frac{\beta}{\beta s - \gamma} \right) ds = \gamma \int dt \quad (32f)$$

$$\log(s) - \log(\beta s - \gamma) = \gamma t \rightarrow \log\left(\frac{s}{\beta s - \gamma}\right) = \gamma t \quad (32g)$$

$$t_{inflection} = \frac{\log(s) - \log(\beta s - \gamma)}{\gamma} \quad (32h)$$

4.3. Planck-Like Blackbody Distribution and Infectivity

When analyzing several SIR models of disease, it was observed that the infection curve can resemble the Planck-like Blackbody function curves. The Planck's Blackbody Distribution is known to have two dependents: wavelength and temperature. While the SIR models illustrate singular dependence, the SIRm model introduces a second anthropological factor that, much like how the temperature factor in a blackbody affects the peak of the intensity, can affect the rise of infections according to time and change the peak's position on the graph.

A blackbody is a physical phenomenon that absorbs all incidence of radiation while emitting a continuous spectrum dependent on its thermal conditions. The higher the temperature of the blackbody, the higher the peak of re-emission intensity at a lower wavelength [35].

This can be compared to the infection curve in the SIRm model. The mixing factor, referred to as the m factor, is much like the temperature factor of the blackbody. If the population of a country is akin to the blackbody, a high m factor value of a population will allow for a maximum peak of infection to occur earlier during the pandemic. This is similar to the temperature variable in a blackbody, which can induce a maximum peak of the intensity at a lower wavelength. This allows the m factor to present a measure of how much a population obeys social distancing measures provided by the government.

This comparison presents a good approach as to how the infection rate of a virus can depend on both time and compliance attributes of a population.

5. Conclusions

The equations used in the SIR model were time dependent [1]. This study examined not only the time dependent equations but also derived the different variable relationships to one another. Specifically, this study derived the equation for the number of infected cases depending on the number of susceptible individuals, which in turn was found with respect to removed individuals. These equations allow for the study of infection in relation to transmission. That is, using these models, one can now mathematically study the relationship between infected, susceptible and removed individuals in epidemic models.

With the SEIR model, this study wanted to examine the impact of protective procedures on reducing disease spread. The equations were modelled to account for the effect of social distancing on the SEIR model - particularly, the exposed and infected groups by the variable ρ [32]. While the feasibility of complete adherence is difficult, these results support ideas of protective measures in reducing exposure - therefore, infection - of disease. The models discussed in this study have a good range of variability and applicability - but they are not perfect. It is important to note that these models assume ideal conditions so they may not truly reflect the actual situations when

anthropological factors such as interventions are considered.

To our knowledge, no other study has examined COVID-19 transmission with respect to the SIR model using specific variable related derivations, the SEIR model with focus on impact of social distancing and the similarities of the infection curves to Planck-like blackbody functions. This study presented several mathematical approaches for the modelling of disease transmission using methodologies ranging from the SIR model to the SEIR model, and simulations by the Planck blackbody function. Specifically, it demonstrated practical applications of these models by comparing their results fitted onto the Canadian COVID-19 cases data. Through the predicted values from each model, meaningful inferences about the behaviour and trajectory of the COVID-19 pandemic were drawn.

The results of this study can be used to better understand - or help confirm - the trends of COVID-19 transmission in a Canadian context. Further studies can use this data to further investigate the efficacy of using these mathematical models in extrapolating COVID-19 transmission trends.

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