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Analyzing pandemic dynamics through traveling waves: a mathematical model

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Abstract

Purpose of research. *Pandemic of 2019 has greatly altered human life and affected economies worldwide by increasing death rates. The relevance is understanding and controlling the spread of infections is vital to minimizing its effects. The purpose of the research investigation is to plug spatial dependence into the traditional SIR model to extend its usefulness in modeling the propagation process of the virus.*

Methods. *The methodology is to develop of a mathematical model to represent the pandemic spread as a traveling wave phenomenon. Analysis of the wave speed of the model is made as appropriate as well as the several numerical methods it applied in obtaining solutions. The new variable to the infected population equation is used along with variable transformation techniques and linearization in deriving analytical solutions and then computing and analyzing the wave speed associated with infection spread.*

Results *confirmed the previous outcomes generated by time-dependent models' analysis that the prime determinant of disease dissemination is the infection-to-recovery rate. It is shown that either transmission coefficient decreases or the recovery rate increases slows down the spread of the disease.*

Conclusion. *As a conclusion, the best possible way to curb its exposure is by minimizing interpersonal interaction (reduction of beta) or by expediting patient recovery and segregation (increase in alpha). It reduces the wave speed parameter q, which controls the rate of propagation of the disease.*

Keywords: *pandemic dynamics; traveling waves; mathematical modeling; SIR model; spatial dependence; wave speed; epidemic control strategies.*

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Анализ динамики пандемий через волны передвижения: математическая модель

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Резюме

Цель исследования. *Пандемия 2019 года значительно изменила жизнь людей и оказала влияние на мировую экономику, увеличив уровень смертности. Актуальность исследования заключается в том, что понимание и контроль за распространением инфекций имеют решающее значение для минимизации их последствий. Цель данного исследования — включить пространственную зависимость в традиционную модель SIR, чтобы расширить её применимость для моделирования процесса распространения вируса.*

Методы. *Методология исследования основана на разработке математической модели, описывающей распространение пандемии как явление бегущей волны. В работе проводится анализ скорости волны в модели, а также используются различные численные методы для получения решений. Новый переменный член добавляется в уравнение для инфицированного населения, и с помощью методов преобразования переменных и линеаризации выводятся аналитические решения. После этого вычисляется и анализируется скорость волны, связанная с распространением инфекции.*

Результаты *подтвердили предыдущие выводы, полученные из анализа временных моделей, что основным фактором, определяющим распространение болезни, является отношение скорости инфицирования к скорости выздоровления. Показано, что снижение коэффициента передачи или увеличение скорости выздоровления замедляет распространение заболевания.*

Заключение. *Наилучшим способом сдерживания распространения вируса является минимизация межличностных контактов или ускорение выздоровления и изоляции пациентов. Это приводит к снижению параметра скорости волны q, который управляет скоростью распространения болезни.*

Ключевые слова: *динамика пандемии; бегущие волны; математическое моделирование; модель SIR; пространственная зависимость; скорость волны; стратегии контроля эпидемий.*

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Introduction

The waves in the context of the pandemic are one of a wave of illness spreading and moving through a population. Mathematically, a wave is something that propagates with a constant shape and moves with a constant speed. The solution of this form is called a travelling wave solution. This traveling wave solution appears in our models by adding spatial dependence. In other words, we want to allow people to move around within our model and our epidemic scenario. In the SIR model, we only have time dependence for our three S, I and R variables, we can see this because we had only a time derivative. So, when we look at how those populations changed over time. We want to allow populations to also change in space because people might be moving around. What we're doing is creating a slightly more realistic model.

Pandemics have been defining moments throughout history, shaping human civilization and leaving indelible marks on societies, economies, and healthcare systems [1]. These global outbreaks of infectious diseases transcend borders and impact populations on a massive scale [2]. The dynamics of pandemics are complex, influenced by factors such as the virulence of the pathogen, speed of transmission, population density, healthcare infrastructure, and societal behaviors. Infectious diseases can spread rapidly through populations, fueled by global travel, urbanization, and interconnectedness [3].

Mathematical models have been widely used to study epidemics, including seminal works such as the SIR model introduced by Kermack and McKendrick. These models consider key concepts such as susceptibility, infectivity, and recovery rates to understand disease transmission dynamics [4]. They have been applied to real-world scenarios to make predictions and inform public health interventions. For example, mathematical modelling has been used to control the spread of diseases, manage resources, and make decisions in sports [5]. Deterministic and stochastic models have been employed, with computer simulation models being used for more complex scenarios [6]. Mathematical modelling systems aim to assess the effectiveness of epidemic control measures, analyze risks, and estimate economic damage [7].

Spatial dependence and traveling wave solutions have been explored in several studies to extend classical epidemic models and understand the spatial spread of diseases within populations. These studies have investigated the theoretical foundations of travelling wave models and their relevance in capturing the dynamics of epidemics. For instance, [8] investigated a nonlocal dispersal epidemic model with multiple nonlocal distributed delays and nonlinear incidence effects, defining the minimal wave speed and basic reproduction number to determine the existence of travelling wave solutions. Similarly, [9] used the method of travelling wave solution to transform partial differential equations into ordinary differential equations and derived solutions for infectious wave velocity and hypergeometric function in a spatial SIR model.

Mathematical models, including those incorporating travelling waves, have been utilized in public health research and policy-making. These models have been applied to inform interventions, vaccination strategies, and pandemic preparedness. For example, [10] discuss the frameworks and perspectives adopted for modelling infectious diseases using mathematical modelling. They highlight the methodology, tactics, and interconnections of these approaches. Review epidemiological network models, which have been used to explain COVID-19 and provide a sufficiently accurate approximation for policymakers to determine actions needed to curb the challenges and limitations associated with the mathematical modelling of epidemics including uncertainties in parameter estimation, simplifying assumptions, and the need for real-time data for accurate predictions. Future directions for research and development in the field of pandemic dynamics and mathematical modelling include exploring emerging technologies, interdisciplinary approaches, and novel methodologies to enhance our understanding of disease spread and inform public health responses [11]. Numerous lectures, hosted by the Oxford University Department for Continuing Education, have explored the dynamics of the SIR model, which researchers have utilized in this paper [12].

Materials and methods

Our starting point would be the same SIR model. We had three different equations, or we had three compartments of our population. We have S for susceptible, those who still catch the disease. We had I for infectives who are currently having the disease and spreading it through the populations, and R for the recovered category which are those who have caught the disease and either died or recovered and are now immune [13; 14; 15]. The model gave us three differential equations for each of the three population's parts:

$$\frac{dS}{dt} = -rSI, \tag{1}$$

$$\frac{dI}{dt} = rSI - aI, \tag{2}$$

$$\frac{dR}{dt} = aI. \tag{3}$$

Since we are introducing spatial dependence to our original SIR model, we need additional assumptions that explain how people interact with the space around them [16; 17]. Our first assumption is that these susceptible populations are not going to move, that is mean in the context of the current COVID-19 outbreak we can think of this assumption as saying that people susceptible to the disease stay at home [16]. The second assumption is going to be the movement of the infective migrate at a constant rate [18]. The third assumption is once people are in the removed population, they again don't move [19]. In summary, spatial dependence is focused on the infectives because the suspectable stay at home and don't move, and the removed population also doesn't move, we are interested in how the disease can infect others, who are going to migrate and spread the disease through the population. What this means for our equation is that we have an additional term in the second equation $\frac{dI}{dt}$ from the original SIR model. So, we add in term D which is the constant rate of diffusion, and then the way to model the diffusion mathematically is with a derivative, so we have a second derivative. So, equation (2) becomes

$$\frac{dI}{dt} = rSI - aI + D\frac{\partial^2 I}{\partial x^2}. \quad (4)$$

Because our population depends on both time and space, this is why we have partial derivatives. All derivatives have to be converted into curly letter ∂:

$$\frac{\partial S}{\partial t} = -rSI, \quad (5)$$

$$\frac{\partial I}{\partial t} = rSI - aI + D\frac{\partial^2 I}{\partial x^2}, \quad (6)$$

$$\frac{\partial R}{\partial t} = aI. \quad (7)$$

This is what signifies that it's a partial derivative of functions of our variables S, I and R, which are now depending on both time and space. To begin analyzing the equation, we have to do something called nondimensionalization to take all of the constants that are in our equations and combine them in such a way that we get one key parameter. And when we do this, we actually see that the parameter that appears is reproductive number R_o. The basic reproductive number gives the number of secondary infections that expect to happen in average in the population from a single primary infection. In other words, is the number of people that we expect one infected individual to pass the disease onto, and we define this mathematically as $R_o = S_o q$, $q = r/a$, where q is the fraction of the population that comes into contact with an infected individual during their period of infectiousness. As well as nondimensionalizing we can use a second mathematical trick which is to change variables. At the moment we have S, I, and R which all depend on time t and space x. What we would be going to do is to create a new variable called y, then we would convert these equations (5), (6) and (7) into differential equations just involving this one new variable which is given by

$$y = x - ct \quad (8)$$

Where c is t is a constant.

This change would really simplify our set of equations:

$$0 = c\frac{dS}{dy} - IS, \quad (9)$$

$$0 = \frac{d^2 I}{dy^2} + c\frac{dI}{dy} + I\left(S - \frac{1}{R_o}\right) \quad (10)$$

Equations have changed quite dramatically, so we no longer have derivatives in terms of x and t with partial derivatives. We have gone back to full derivatives in terms of single variable y. As we need now to solve differential equations, we need some boundary or initial conditions. What I would do here is go backwards in time to before the start of the epidemic. So, we let time in equation (8) go to (–∞) which means going back into the past, then y in the same equation is going to go to plus infinity because of the minus sign between $x,\ t$.

The number of infections must go to zero because this is before the disease ever existed in the population. Also, the susceptible must go to its initial value where it is, but we've done a nondimensionalization, what we have actually done is convert our I and S from being full population numbers into being population ratios or a proportion of specific given population, so that S to go back to initial susptables population S_o in the nondimensional model, that's mean S must be go to 1:

$$As\ t \to -\infty \text{ (Past) } then\ y \to +\infty \text{ then } \mathrm{I} \to 0\,, \mathrm{S} \to 1. \tag{11}$$

We can also think about what we expect to happen in the future. So, the future here is when we let time *t* go to infinity and that would make y go to minus infinity, so if y goes to (+∞), then the outbreak must have passed so really far down in the future the disease has come in its spread through the population and now I's disappears once again, so infectives must go to zero.

$$As\ t \to +\infty \text{ (Future)} then\ y \to -\infty \text{ then } \mathrm{I} \to 0 \tag{12}$$

We don't know the value of *S* in the future yet.

The first question that we might want the answer is going to be how fast the disease is going to spread through the population. Because we are now picturing the disease as a wave propagating through the population and spreading the illness. We can calculate the speed of the spread of the disease in our outbreak. The question would be what is the wave speed? To answer the question, we would use a mathematical tool called linearization, in which we would use the value of S in the past as an approximation, so that $S = 1 - P$, where *P* is a small value (an approximation), and then because we are linearizing $S = 1 - P$ is telling us that we want to substitute it in our equations (9) and (10) and ignore any term which are *P* squared and higher, this will result a set of equations below:

$$0 = -c\frac{dP}{dy} - I, \tag{13}$$

$$0 = \frac{d^2I}{dy^2} + c\frac{dI}{dy} + I\left(1 - \frac{1}{R_o}\right). \tag{14}$$

These equations (13) and (14) might not look necessarily any simpler. It is now in a form that allows us to use another mathematical tool called Phase plane analysis. Applying phase plane analysis to equations (13) and (14) tells us that traveling wave solutions exist, then we must have

$$c \leq 2\sqrt{(1 - \frac{1}{R_o})}. \tag{15}$$

This expression is the minimum possible wave speed for there to be a travelling wave solution to exist.

The minimum required wave speed for traveling wave solutions to exist, but typically the wave speed itself is given by

$$c = 2\sqrt{(1 - \frac{1}{R_o})}. \tag{16}$$

So, the value of *C* in our change of variable formula (8) is actually the speed of the travelling wave, and therefore is the speed of the spread of the disease as it is propagated through our population.

In any epidemic, in particular for the current COVID-19, we want to make the speed (*C*) of the disease spread as small as possible, we want to slow down the propagation of the disease, and looking to the formula (16) we can make *C* small by making R_o also small. If *C* goes negative which would happen if R_o was small enough. This actually can't happen in the case of an epidemic which is what we are considering here, because in our first basic SIR, an epidemic will occur when R_o is greater than 1.

So, the absolute smaller value that R_o can be is one and when substituting $R_o = 1$ in equation (16) would give C_o. So, we should keep R_o as low as possible to lower the speed of the spread of the disease. The minimum value we can get it down to is just above one, to do that, we look at the formula $R_o = S_o q$ and see that the only thing we can control here is the contact ratio q since the number of susptables is fixed. To lower the contact ratio q we need to wash our hands all the time and stay at home as much as possible and if we have to go outside, we have to minimize the number of contacts through social distancing.

Another question we might want to answer is what the severity of the epidemic is, or what is the value of S_{end} which is in our boundary conditions in equation (9) $IS = c\frac{dS}{dy}$ and substitute it in equation (10). We would have all the terms have y derivatives, so we can integrate the whole equation resulting expression contain just I and S:

$$\frac{dI}{dy} + CI + C\left(S - \frac{1}{R_o} lnS\right) = \text{constant}. \quad (17)$$

To calculate the value of constant we have to use our initial boundary conditions in (11).

The number of susceptibles left at the end of the outbreak, therefore knowing the severity of the epidemic we need to let time go to infinity and therefore go to the future (12), this yield

$$S_{end} - \frac{1}{R_o}\ln(S_{end}) = 1. \quad (18)$$

Results and their discussion

As we have seen earlier, the best way to deal with equation (18) equation is to plot a graph. At first, we have to think about the range of values the S_{end} and R_o can take. So, because we were considering this non-dimensionalized model, this means that S is a proportion of the initial susceptible population, and so it can only vary between zero and one. Whereas R_o according to equation (16) depicts traveling wave speed that R_o should be greater than one for the epidemic to occur in the first place, and as we are modeling the spread of the epidemic, this means that R_o is also must be bounded by one.

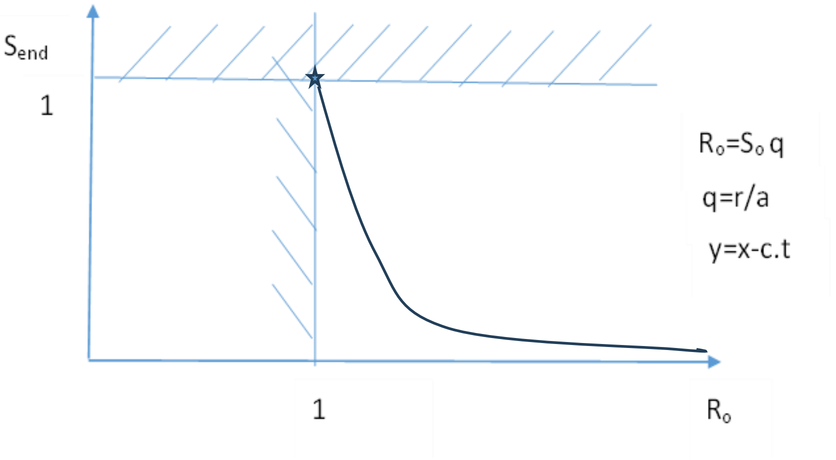

Fig. 1. Relation between Send and R_0

When plotting the graph for equation (18), what we see is a curve rapidly decreasing, so the maximum value when (S_{end}, R_o) equals (1,1). When send equals, one means that nobody caught the disease, we can also notice that the values of S_{end} are going to decrease as R_o goes bigger.

So, to go back to our question, what is the severity of the epidemic, the total number of people who catch the disease would be lower if the number of people unaffected or the number of susceptibles left at the end is as large as possible. So, we want to make S_{end} as big as possible by varying R_o, which means R_o would be close to one as much as possible which can be done by reducing the contact ratio q.

Conclusions

Using the traveling wave model for the spread of the disease, we've been able to derive an equation for the wave speed C in equation 16, which is the speed at which the disease would spread through the population. Also, we have been able to get an expression in equation (18) which determines the number of susceptible people left at the end of the outbreak. To minimize the severity and the impact of an outbreak such as COVID-19, we need to lower the wave speed as much as possible to make the disease spread as slowly as possible to give us more time to come up with solutions to combat it such as vaccines. To do this, we have to make R_o as small as we can where the lower bound for R_o is 1, to take R_o to one we have to remember the formula $R_o = q$. So, to make R_o small we need to minimize q to reduce the speed of the spread of disease. And for the second question about the severity of the epidemic equation (18) for the susceptible at the end, we want to make s_{end} as large as possible, because the number of the susceptible that remain after the outbreak tells us the number of people who have been unaffected by the disease so they haven't caught the disease, this can be done according to the figure 1 by reducing R_o approaches to one.

All the answers keep banging the same drum telling us we've got to lower contact ratio (q). But the fact that it keeps coming up in all of these models is good news because it gives us one specific parameter that we want to make as small as possible, and this is the power of mathematical modeling, because even in this work when we introduced the spatial dependence into the SIR model, we got different solutions, they now look like traveling waves. But all of the things we want to happen (a slower spread of the disease, fewer people getting the disease) have the same thing in common, they are all reduced by making the contact ratio as small as possible.

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