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Disease effects on individual exposure rates using Matlab tools for susceptibility-infection-recovery models

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Abstract

Infectious diseases with a viral origin are of significant worldwide concern. In recent times, pandemics are creating havoc across the entire globe. This paper presents a constructive analysis of a new mathematical concept that will help medical authorities to predict and to take controlling measures. In this work, we use ordinary first-order differential equations and compartmental model analysis for the calculation of the infection rate, transmission rate, and reproduction number of the patients. A new Advanced Susceptible-Exposed-Infectious-Recovered model has been introduced, which has greater accuracy of the reproduction number. The prediction of a model of disease transmission demonstrates the performance characteristics of the proposed model.

Keywords: Susceptible-Exposed-Infectious-Recovered model environmental compartment, Matlab.

Introduction

Introduction of a new mathematical model can be considered as one of the ways to fit the need of the hour. In the absence of a successful vaccine, mathematical model oriented interventions can be considered as an alternative strategy for reducing the infection burden. In recent years, several mathematical models have been proposed for infectious diseases. These models helped the medical authors have computed the crucial epidemiological model parameters for prediction of the spread of SARS outbreak. It was concluded that imposing social distancing can help minimize the spread of this pandemic as proposed in this paper.

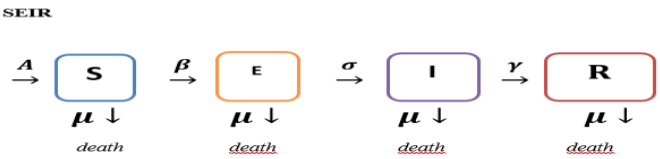
Materials and Methods:

The mathematical model formulated was modified to incorporate the rate at which the recovered return to susceptible because does not confer lifelong immunity (*1*). Also, the infectious rate (the rate at which the susceptible become infected) is a function of the number of infectious hosts in the population at time t, and thus it is a non-linear term. Other transitions were modeled as linear terms with a constant coefficient. Therefore, the dynamics model describe by a system of ODE which was solved to obtain the disease-free equilibrium (DFE) state and endemic state. The stability analysis of the DFE was carried out using the Jacobian matrix and the endemic stability using the R_0 Equ 2 (*2-5*).

Model equations

As shown in the compartmental model in next Figure, Figure and with the described variables and parameters, we have the following system of differential equations [1] to [4]:

SEIR model



$$\frac{dS}{dt} = A - \frac{\beta SI}{N} - \mu S \quad [1]$$

$$\frac{dE}{dt} = \frac{\beta SI}{N} - \sigma E - \mu E \quad [2]$$

$$\frac{dI}{dt} = \sigma E - \gamma I - \mu I \quad [3]$$

$$\frac{dR}{dt} = \gamma I - \mu R \quad [4]$$

Where

S: susceptible, individuals who have not been exposed to the virus.

E: exposed, individuals exposed to the virus, but not yet infection.

I: infected, exposed individuals who go on to become infections.

R: recovered, infectious individuals who recover and become immune to the virus.

A: birth rate.

μ: death rate.

N: the population size is taken as the sum.

β: is the transmission coefficient " A high value of β means the virus has more opportunity to spread".

σ: is the rate which exposed individuals become infectious think of it as the reciprocal of the average time it takes to become infectious. That is if an individual becomes infectious after 4 days on average." σ will be 0.25" .

γ: is the rate at which infectious individuals recover. The reciprocal of average time it takes to recover. That is, if it takes 10 days on average to recover, γ will be 0.1". Adding equations [1] to [4], this expression is given by:

$$\frac{dS}{dt}+\frac{dE}{dt}+\frac{dI}{dt}+\frac{dR}{dt}$$

$$= A-\frac{\beta SI}{N}-\mu S+\frac{\beta SI}{N}-\sigma E-\mu E+\sigma E-\gamma I-\mu I+\gamma I-\mu R$$

$$= A-\mu N$$

Where

$$N(t) = N_0\, e^{-\mu t} \quad + \frac{A}{\mu}\ (1 - e^{-\mu t})$$

N_0: is initial population.

Disease-Free Equilibrium state

An important in any epidemic model is known as the basic reproduction number, or R_0 . this is defined by

$$R_0 = \frac{\sigma\beta}{(\sigma+\mu)(\gamma+\mu)}$$

this number estimates the number of people who will be infected by the average infectious individual (*2*).

if $\mathrm{R}_0 > 1,$ then an outbreak of the virus is likely to become an epidemic.

if $\mathrm{R}_0 < 1,$ then an outbreak of the virus is likely to be contained.

when infection rate $\beta = 0.1$ consider the initial values

$\mathrm{S}(0) = 999,\ \mathrm{E}(0) = 1,\ \mathrm{I} = \mathrm{R} = 0,\ \mathrm{N} = 1000,$

$$\beta = 0.1,\ \ \mu = \gamma = 0.1,\ \ \ \sigma = 1,2,3.\ A = \mu N = \frac{1000}{10} = 100$$

we need study a relationship between infection rate and Exposed "σ exposed rate" , When

$$\sigma = 1 \Rightarrow R_0 = \frac{\sigma\beta}{(\sigma+\mu)(\gamma+\mu)} = \frac{1 * 0.1}{(1+0.1)(0.1+0.1)} = 0.45 < 1$$

$$\sigma = 2 \Rightarrow R_0 = \frac{\sigma\beta}{(\sigma+\mu)(\gamma+\mu)} = \frac{2 * 0.1}{(2+0.1)(0.1+0.1)} = 0.47 < 1$$

$$\sigma = 3 \Rightarrow R_0 = \frac{\sigma\beta}{(\sigma+\mu)(\gamma+\mu)} = \frac{3*0.1}{(3+0.1)(0.1+0.1)} = 0.48 < 1$$

the basic reproduction number R_0 in the case$R_0 < 1$, for different parameters values. the infection die out.

$$S(n+1) = S(n) + \bar{S}(n)\Delta t$$

$$E(n+1) = E(n) + \bar{E}(n)\Delta t$$

$$I(n+1) = I(n) + \bar{I}(n)\Delta t$$

$$R(n+1) = R(n) + \bar{R}(n)\Delta t$$

$$S(n+1) = S(n) + (A - \frac{\beta SI}{N} - \mu S)\Delta t$$

$$E(n+1) = E(n) + (\frac{\beta SI}{N} - \sigma E - \mu E)\Delta t$$

$$I(n+1) = I(n) + (\sigma E - \gamma I - \mu I)\Delta t$$

$$S(1) = S(0) + \bar{S}(0)(1)$$

$$= 999 + \left(100 - \frac{0.1*999*0}{1000} - 0.1*999\right)*(1) = 999.1$$

$$E(1) = E(0) + \bar{E}(0)\Delta t$$

$$E(1) = 1 + \left(\frac{0.1*999*0}{1000} - 1*1 - 0.1*1\right)*(1) = -0.1$$

$$I(1) = I(0) + \bar{I}(0)\Delta t$$

$$= 0 + (1*1 - 0.1*0 - 0.1*0)*(1) = 1$$

$$R(1) = R(0) + \bar{R}(0)\Delta t$$

$$= 0 + (0.1 * 0 - 0.1 * 0) * (1) = 0$$

$$N = S + E + I + R = 999.1 - 0.1 + 1 + 0 = 1000$$

Consider the reciprocal of the average time it takes to become infectious when calculating the rate at which exposed persons become contagious in Figure 1 that is, if a person spreads an infection after 4 days on average, it will affect those who are susceptible to people over time.
Similar to Figure 4, it has an impact on those who are exposed, hitting its peak at 0.3 before steadily dropping until, in the case of the rates we have, it closes to zero after 60 days.

However, we see that the susceptible and infected individuals are not impacted by rates, i.e., the rate of recovery of infected persons Figure 2 and Figure 3.

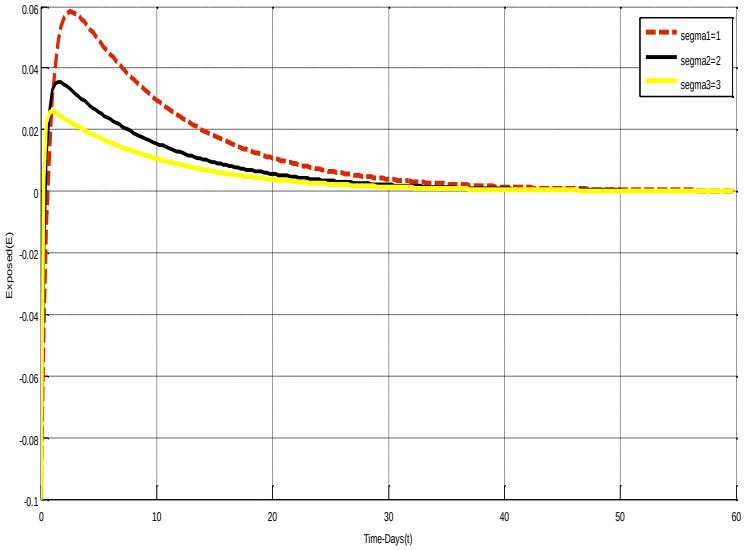


Figure 1: the Exposed individuals at
$\beta = 0.1, S(0) = 999, E(0) = 1, I = R = 0,$
$N = 1000, \mu = \gamma = 0.1, \sigma = 1,2,3$

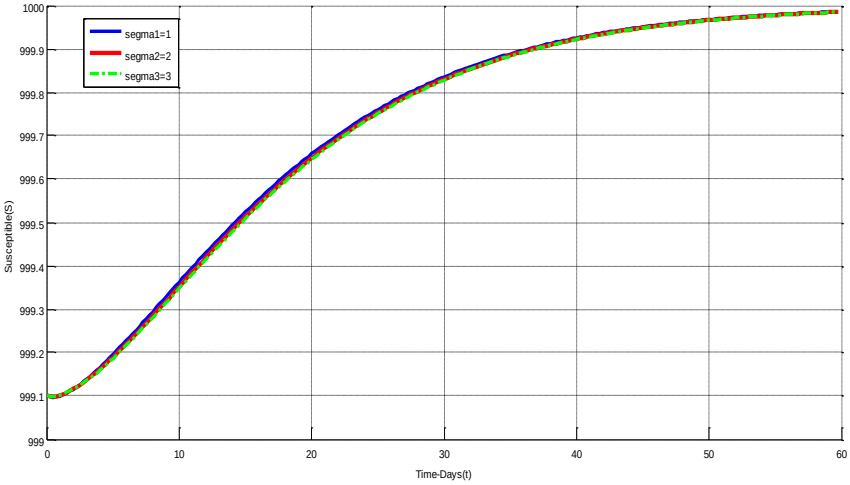


Figure 2: The Susceptible individuals at $\beta = 0.1, S(0) = 999, E(0) = 1, I = R = 0,\ N = 1000, \mu = \gamma = 0.1, \sigma = 1,2,3$.

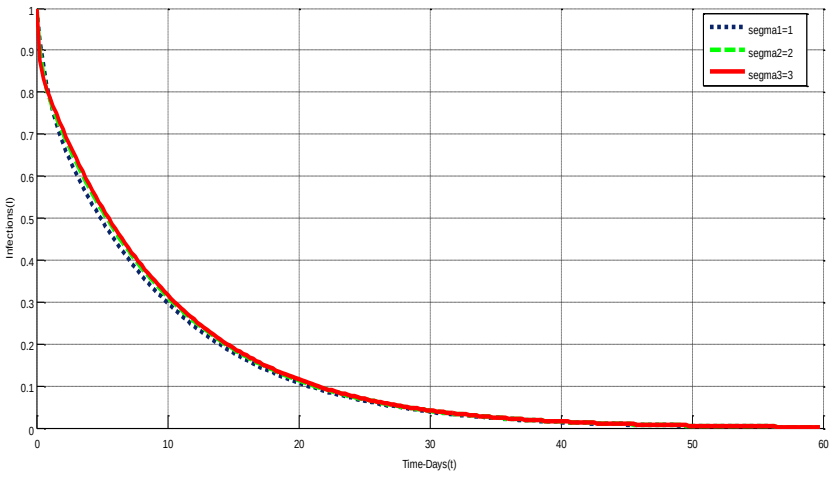


Figure 3: The Infective individuals at $\beta = 0.1, S(0) = 999, E(0) = 1, I = R = 0,\ N = 1000, \mu = \gamma = 0.1, \sigma = 1,2,3$.

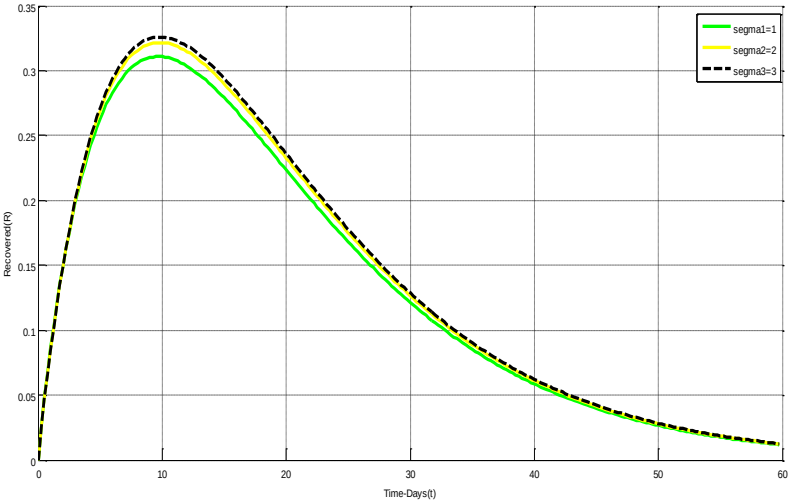


Figure 4: The Recovered individuals at
$\beta = 0.1, S(0) = 999, E(0) = 1, I = R = 0$
$N = 1000, \mu = \gamma = 0.1, \sigma = 1,2,3$.

Conclusion:

In this paper, the SEIR compartmental model for the prediction of the cumulative infectious cases of diseases is formulated. In the mathematical formulation, the following features are included: a new environmental component in the transmission dynamics; variations in the transmission rates for reflecting the impact of coronaviruses; and the evaluation of individual reproduction number to know the model of transmission of the disease are taken into consideration. Further, the quantification of the severity of the disease is reflected by calculating the basic reproduction with Ro qual to the proposed model with the model of the cumulative confirmed cases of diseases is verified through graphical interpretation, which leads to greater accuracy and minimal error.

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آثار المرض على معدلات التعرض الفردي باستخدام أدوات الماتلاب القابلية للإصابة بالعدوى والتعافي

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المستخلص العربي

تشكل الأمراض المعدية ذات الأصل الفيروسي مصدر قلق كبير في جميع أنحاء العالم. في الآونة الأخيرة ، تسببت الأوبئة في إحداث الفوضى في جميع أنحاء العالم. تقدم هذه الورقة تحليلاً بناءً لمفهوم رياضي جديد من شأنه أن يساعد السلطات الطبية على التنبؤ واتخاذ تدابير التحكم. في هذا العمل ، نستخدم المعادلات التفاضلية العادية من الدرجة الأولى وتحليل النموذج الجزئي لحساب معدل الإصابة ومعدل الانتقال وعدد التكاثر للمرضى. تم تقديم نموذج جديد متقدم يتميز بدقة أكبر في عدد التكاثر. يوضح التنبؤ بنموذج انتقال المرض.
يمكن اعتبار تقديم نموذج رياضي جديد كإحدى الطرق لتلبية حاجة الساعة. في حالة عدم وجود لقاح ناجح ، يمكن اعتبار التدخلات الموجهة نحو النموذج الرياضي كاستراتيجية بديلة لتقليل عبء العدوى. في السنوات الأخيرة ، تم اقتراح العديد من النماذج الرياضية للأمراض المعدية. ساعدت هذه النماذج المؤلفين الطبيين في حساب النماذج الوبائية الحاسمة للنموذج الوبائي للتنبؤ بانتشار تفشي فيروس سارس .استنتج أن فرض التباعد الاجتماعي يمكن أن يساعد في تقليل انتشار هذا الوباء. كما هو مقترح في هذه الورقة.
الكلمات المفتاحية: التعرض الفردي، ادزات الماتلاب، القابيلية للإصابة