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Research Article

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Mathematical Modelling to Analyse the Spread of Infectious Disease of Covid-19 and Aids

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Abstract

This study explores three fundamental epidemiological models, the Susceptible-Infected (SI), Susceptible-Infected-Susceptible (SIS), and Susceptible-Infected-Recovered (SIR) models of the disease of corona virus and aids. These models capture various aspects of disease transmission and recovery within population, offering insights into the dynamics infectious diseases across different scenarios. This SI, SIS, and SIR models, highlighting their significance in infectious disease modelling and their implications for public health.

1. Introduction

Much of our headway over the most recent couple of years has made it important to apply numerical strategies to genuine issues emerging from various fields be it Science, Money, executives and so forth. The utilization of math in tackling genuine issues has become broad, particularly because of the rising computational force of PCs and processing strategies. The World Health Organization (WHO) has named the novel coronavirus (CoV) "2019-nCoV",or "COVID-19" as the cause of the disease. There is a current pneumonia outbreak that started near Wuhan in December 2019 in China's Hubei Province. The COVID-19 virus is dangerous. Based on phylogenetic research using the entire available genome, bats are thought to be the reservoir of the COVID-19 virus, however the intermediate host or hosts have not yet been identified. The illness brought on by the SARSCoV-2 coronavirus is known as COVID-19. It is often spread through relationships and by touching. The COVID-19 vaccine is effective in preventing serious illness and death. Even after getting the vaccine, a person may have little or no symptoms of Covid-19. COVID-19 can infect anyone, and while most people recover without treatment, some can become seriously ill or die. Arzu ÇİLLİ and Kıvanç ERGEN analysis the number of infected people to present day for these diseases results showed that SI and SIS models, Rima Devi, Balendra Kumar Dev Choudhury work ona critical birth count of less than 1 between 9 and 10 days after infection indicates that the disease is under control for SIR Module [1,2]. R. Ross Analyzing epidemiological models to evaluate the effectiveness of bed nets as a preventive measure in malaria areas [3]. Constantinos analyse themodeling methods used for the surveillance and forecasting of infectious disease outbreaks [4].

The abbreviation of the AIDS is “Acquired Immune Deficiency Syndrome”, and HIV is “Human Immunodeficiency Virus”. Here in this disease the individual’s immune system fails to fight against the infection. The AIDS is caused by the retrovirus named as HIV. The individual come to know about this disease by undergoing a test i.e., “ELISA” “Enzyme-Linked Immunosorbent Assay” if that person has HIV-antibodies then he is called as HIV-Positive. P Affandi and Faisal studied A mathematical SIR model for successful malaria control in South Kalimantan [5]. According to reports from South Kalimantan, South Kalimantan is a province where malaria is prevalent due to the proximity of workplaces to the forest, such as miners and recruiters living on the edge of the forest.. Ashlynn R. Daughton, Nicholascontributed Develop mechanisms to enhance public health collaboration and community models to support positive disease detection during outbreaks [6]. Devi R & Choudhury BKD, given result as Chickenpox is a highly contagious disease [7]. The risk of complications depends on age and immunity. Again, Devi R & Choudhury BKD, analysedthe transmission of diseases in human population and their study of causes of existence is treat this as an infection. Mathematical models help predict the content of biological products in epidemiological studies and content that cannot be obtained directly from data [8]. Waleed M. Sweileh conclude that Mathematical models are becoming increasingly popular as tools for understanding the evolution of infectious diseases [9]. The use of mathematical models for infectious diseases seems to be the most important method. Collaborative research in mathematics with less developed countries is needed and should be prioritized and funded.. Wedajo AJ theresults of the mathematical analysis of the model are confirmed by the simulation study [10]. The mathematical analysis results of the model are confirmed by simulation studies. As a result,

it is concluded that the immigrant epidemic will cause disruption in the population and increase the number of diseases. It is concluded that the infected immigrants will contribute positively and increase the disease in the population.

1.1 Program Codefor Predicting Graphs

Python: Python is a famous significant level, broadly useful This programming language was created by Guido van Rossum in 1991 and was also developed by the Python Software Foundation. Programmers can express their ideas in fewer lines because the syntax is created primarily with readable code. Python is a programming language that allows faster and more efficient programming.The version used for below process is the Python version 3.8.10. The IDE used in our work is "SPYDER of version 5".

1.2 Spyder

Spyder is a powerful scientific environment written in python for the analyse and discuss of the diseases which are mentioned as before. Spyder is friendly IDE – "Integrated Development Environment" built specially for data science. Additionally, in case there is any syntax error then it shows a warning sign beside the line number and mentions the error in the code there by making easy for user to rectify the error.

2. Methodology

Here, we are going to discuss the three mathematical models of analysing the rate of spread of disease,

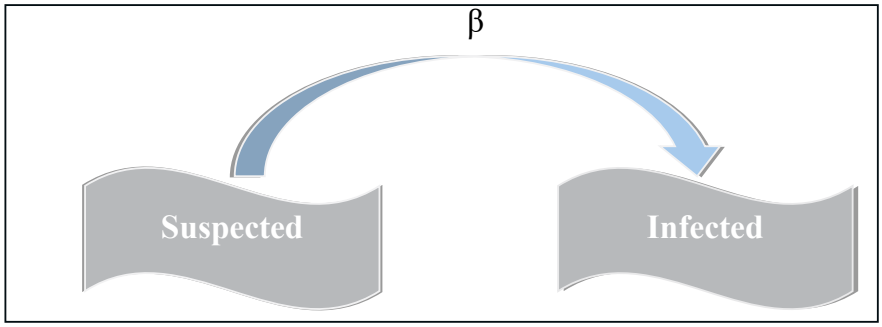
1. SI MODEL
2. SIS MODEL
3. SIR MODEL

2.1 SI Model

The SI Model is known as "SUSCEPTIBLE INFECTED MODEL". This is basic model used in epidemiology to understand the dynamics of infectious diseases.

Here, S stands for "SUSCEPTIBLE" and I stand for "INFECTED".

2.1.1 SI Model



In this model, there is no recovery stage or removal of infection i.e., once the person gets infected, he remains infected. This model doesn't capture the dynamics of improvement.

Mathematically, this model is described by using the differential equations I.e., to express the rate of change of individuals in each compartment with respect to time.

$$\frac{ds}{dt} = -\beta SI \quad \rightarrow ①$$

$$\frac{dI}{dt} = \beta SI \quad \rightarrow ②$$

Where, $\frac{ds}{dt}$: Rate of change of susceptible population over time t.

$\frac{dI}{dt}$: Rate of change of Infected population over time t.

β :Rate of Transmission from susceptible to infected.

2.2 Interpretation of Equations

The ① indicates susceptible population decrease due to increase in time as individual become infected.
The ② indicates increase of infected population i.e., the more infected individuals the faster the spread of disease.
β: Indicates how the transmission follows, the higher β leads to faster spread, emphasizing the measures of prevention.
To find the number of infected people after time 't'.
consider, $I = \frac{1}{x}$
Differentiate w.r.t time we get,

$$\frac{dI}{dt} = \frac{-1}{x^2}\frac{dx}{dt}$$

w.k.t.,

$$\boxed{\frac{dI}{dt} = \beta SI}$$

$$\frac{-1}{x^2}\frac{dx}{dt} = \beta \mathrm{SI}$$

$$\frac{-1}{x^2}\frac{dx}{dt} = \beta \mathrm{S}\frac{1}{x}$$

$$\frac{dx}{dt} = -x\beta \mathrm{S}$$

Eliminating 'S' from above equation we get,

$$\frac{dx}{dt} = -x\beta$$

By rearranging we get,

$$\frac{-dx}{x\beta} = dt$$

$$\int_{\frac{1}{I_0}}^{\frac{1}{I(t)}} \frac{-dx}{x\beta} = \int_0^t dt$$

$$-\left[\frac{\log\frac{1}{I(t)} - \log\frac{1}{I_0}}{\beta}\right] = t$$

$$-\left[\log\frac{1}{I(t)} - \log\frac{1}{I_0}\right] = t\beta$$

$$\log\frac{\frac{1}{I(t)}}{\frac{1}{I_0}} = -t\beta$$

$$\frac{\frac{1}{I(t)}}{\frac{1}{I_0}} = e^{-t\beta}$$

$$\frac{1}{I(t)} = \frac{e^{-t\beta}}{I_0}$$

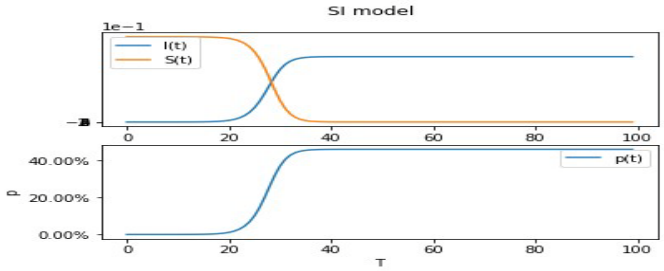
$$\boxed{I(t) = \frac{I_0}{e^{-t\beta}}}$$

This is the infected rate after time 't'.

2.2.1 Python Code for SI Model with Graph

```
#Code from the IDE Spyder of 3.8 version Python
“import matplotlib.pyplot as pt
n = 1000000;
S = N - 1;
I = 1;
beta = 0.6 ;
suscept = [ ] #suspectible compartment;
infect = [ ] # infected compartment;
probab = [ ] # probability of infection at time t ;
def infection (S, I, n):
 t = 0
 while (t < 100):
 S = S - beta * ((S * I / n));
 I = I + beta * ((S * I) / n);
 p = beta * (I / n);
 suscept.Append(S);
 infect.append(I);
 probab.append(p) ;
 t = t + 1 ;
infection(S, I, n);
figure = pt.figure();
pt.suptitle('SImodel'); ax1=figure.add_subplot(211);
infect_line=pt.plot(infect,label='I(t)'); suscept_line = pt.plot(suscept,label='S(t)')
pt.legend(handles=[infect_line,suscept_line]) ;
pt.ticklabel_format(style='sci', axis='y', scilimits=(0,0)) # use scientific notation
ax2 = figure.add_subplot(212) ;
probab_line=pt.plot(probab,label='p(t)') ;
pt.legend(handles=probab_line) ;
# manipulate ;
vals = ax2.get_yticks() ax1.set_yticks(vals) ;
ax2.set_yticklabels(['{:3.2f}%'.format(x*100) for x in vals]) pt.xlabel('T') ;
pt.ylabel('p') ;
pt.show()”
```

• The plot (on the top) denotes the number of susceptible individuals (S) and infectious individuals (I) over time (t).



➢ The plot (on the top) denotes the number of

• Firstly, the number of susceptible individuals is rated high (nearer to the total size of the population, N), and the number of infectious individuals is rare (countable individual).
• As the time, the number of susceptible individuals diminishes while the number of infectious individuals gets more. This is why Because of the spread of disease from infected to suspected individual.
• Gradually, the number of susceptible individuals goes down to a low level, while the number of infectious individuals reaches a highest position and then begins to get vanished. This indicates that a sizeable portion of the population has been infected, and the epidemic starts to decline.
• The plot (to the bottom) shows the probability of infection (p) over time (t).
• Firstly, when the number of infectious individuals is less, the probability of infection is also less.
• As the number of infectious individuals goes higher, the probability of infection also gets higher. This is due to the spread going extremely fast from infected individuals, leading to a higher possibility of susceptible individuals getting infected.

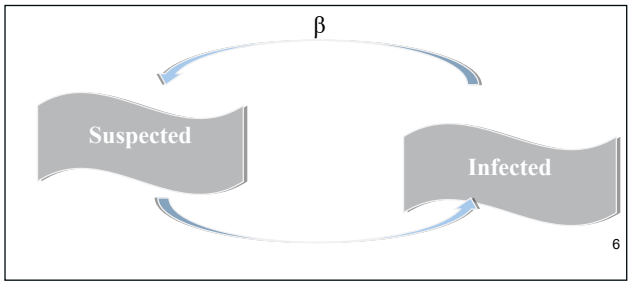
• The peak of the probability of infection depends on the epidemic where the disease spread rapidly.
• After reaching its peak, the probability of infection gradually goes down as the epidemic subsides and fewer individuals remain susceptible.

2.3 SIS Model

The SIS Model abbreviation is "SUSCEPTIBLE INFECTED SUSCEPTIBLE MODEL". This model also used in epidemiology to understand the dynamics of infectious diseases.
Here, S stands for "SUSCEPTIBLE" and I stand for "INFECTED" and again S stands for "SUSCEPTIBLE".

If a person in his real gets caused by a viral disease and gets cured then again, he has possibility of getting affected by same disease in his future. In this SIS model we will study about the person getting infected again and again.

2.4 SIS Model



Mathematically, this model is described by using the differential equations I.e., to express the rate of change of individuals in each compartment with respect to time.

$$\frac{ds}{dt} = -\beta SI \quad \rightarrow ①$$

$$\frac{dI}{dt} = \beta SI \quad \rightarrow ②$$

Where, $\frac{ds}{dt}$:Rate of change of susceptible population over time t.

$\frac{dI}{dt}$: Rate of change of Infected population over time t.

β:Rate of Transmission from susceptible to infected.
γ: Transmission rate from infected to susceptible.

2.5 Interpretation of Equations

The ① indicates susceptible population decrease due to increase in time as individual become infected.
The ② indicates increase of infected population i.e., the more infected individuals the faster the spread of disease.
Now let, S(t) + I(t) = N

Where, N: Total population of the nation
Eliminating the S from equations we get

$$\frac{dI}{dt} = (\beta N - \gamma)I - \beta I^2$$

If initially there are no people who are infected, then the people of nation would have stayed healthy.

Hence, $I_0 \rightarrow$ at t = 0
$I_{(t)} \rightarrow$ at t = t

Where, I_0 is initial number of infected people in society.

To Find the number of infected people after time 't'.
consider, $I = \frac{1}{x}$

Differentiate w.r.t time we get,

$$\frac{dI}{dt} = \frac{-1}{x^2}\frac{dx}{dt}$$

w.k.t.,

$$\boxed{\frac{dI}{dt} = (\beta N - \gamma)I - \beta I^2}$$

$$\frac{-1}{x^2}\frac{dx}{dt} = (\beta N - \gamma)1/x - \beta(1)/\text{x}\text{\^{}}2$$

$$-\frac{dx}{dt} = (\beta N - \gamma)x - \beta$$

$$\frac{dx}{dt} = \beta - (\beta N - \gamma)x$$

Now by arranging and integrating we get,

$$\int_{\frac{1}{I_0}}^{\frac{1}{I(t)}} \frac{dx}{\beta - (\beta N - \gamma)x} = \int_0^t dt$$

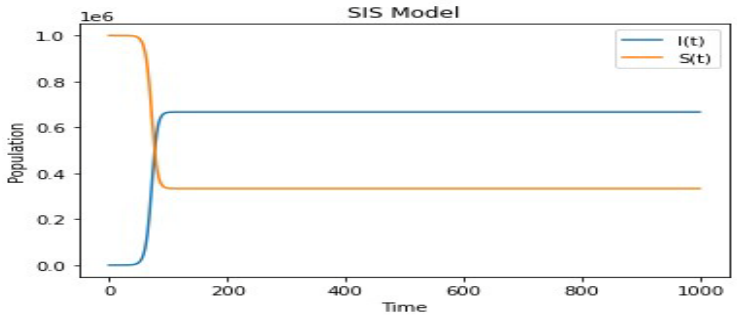
$$\log \frac{\beta - (\beta N - \gamma)x\,\frac{1}{I(t)}}{\beta - (\beta N - \gamma)x\,\frac{1}{I_0}} = -t(\beta N - \gamma)$$

$$\frac{\frac{\beta I(t) - (\beta N - \gamma)}{I(t)}}{\frac{\beta I_0 - (\beta N - \gamma)}{I_0}} = e^{-t(\beta N - \gamma)}$$

$$\frac{\beta I(t) - (\beta N - \gamma)}{I(t)} = \frac{\beta I_0 - (\beta N - \gamma)}{I_0} e^{-t(\beta N - \gamma)}$$

$$\boxed{I(t) = \frac{(\beta N - \gamma)}{\beta - \frac{\beta I_0 - (\beta N - \gamma)}{I_0} e^{-t(\beta N - \gamma)}}}$$

This is equation for the number of infected rates after the time ‘t’



• At the very first stage, there are small number of infected individuals (initial_I) and a vast number of suscepted individuals (initial_S). This is stage before fully spread.
• As the progress, the number of infected individuals (I(t)) increases initial stage. This is due to infected individuals spread the disease to suscepted individuals
• Further, the number of suscepted individuals (S(t)) goes down as soon as individuals become infected.
• The rate of increase in the infected population is governed by the transmission rate (β) and the proportion of suscepted and infected individuals, while the decrease in the infected population is governed by the recovery rate (γ).
• The suscepted population continues to decline until it reaches a certain level, while the infected population stabilizes around an equilibrium point.
• Gradually, the epidemic reaches a dynamic equilibrium where the number of infectious individuals stabilizes. This equilibrium

represents a balance between the rate of new infections and the rate of recoveries.
• At equilibrium state, the suscepted population also stabilizes at a lower level compared to its initial value.
• In the SIS model, individuals can become infected multiple times since there is no immunity conferred after recovery. This leads to oscillations in the infectious population around the equilibrium point.
• These oscillations represent the ongoing transmission of the disease within the population, where individuals alternate between being suscepted and infected multiple times.
• The steady state reached by the system indicates a stability present in between suscepted and infected individuals. This suggests that the disease persists within the population without being eradicated completely.

2.5.1 SIR Model

The SIR Model abbreviation is "SUSCEPTIBLE INFECTED RECOVERED MODEL". This model also used in epidemiology to understand the dynamics of infectious diseases.
Here, S stands for "SUSCEPTIBLE" and I stand for "INFECTED" and R stand for "RECOVERED".
The "SIR" model is a mathematical model used to understand the spread of infectious diseases within a population. It divides the population into three parts: Susceptible (S), Infected (I), and Recovered (R).

In this model, there is recovery stage or removal of infection, and this model captures the dynamics of improvement.
Mathematically, this model is decent using the differential equations i.e., to express the rate of change of individuals in each compartment with respect to time.

$$\frac{dS}{dt} = -\beta SI \quad \rightarrow ①$$
$$\frac{dI}{dt} = \beta SI - \gamma I \quad \rightarrow ②$$
$$\frac{dR}{dt} = \gamma I \quad \rightarrow ③$$

Where, $\frac{dS}{dt}$:Rate of change of susceptible population over time t.
$\frac{dI}{dt}$: Rate of change of Infected population over time t.
$\frac{dR}{dt}$: Rate of change of Recovered population over time t.
β :Transmission rate from susceptible to infected.
γ : Transmission rate from infected to recovered.

2.6 Interpretation of Equations

• The ① denotes that the number of Susceptible individual's decrease over the time as they encounter infected person and become infected.
• The ② denotes that the first term (βSI) is rate at which susceptible individuals become infected. This rate is presented by the transmission rate (β) and the number of susceptible (S) and infected individuals(I).
• The second term (γI) denotes the rate at which infected individuals recover. This rate is influenced by the recovered rate (γ).
• The ③ denotes the number of recovered individuals increases over time as infected individuals recover from the disease.

Now let, S(t)+I(t)+R(t) =N
Where N = Total population of the nation.
Eliminating the S from equations we get,

$$\frac{dI}{dt} = I(\beta N - \beta R - \gamma) - \beta I^2$$

Hence, $I_0 \rightarrow$ at t = 0
$I(t) \rightarrow$ at t = t
Where, I0 is initial number of infected people in society.
To find the number of infected people after time 't'.

Solution: Let us consider $x = \frac{1}{I}$

$$\frac{dI}{dt} = \frac{-1}{x^2}\frac{dx}{dt}$$

$$\frac{-1}{x^2}\frac{dx}{dt} = (\beta N - \beta R - \gamma)\frac{I}{x} - \frac{\beta}{x^2}$$

$$\frac{-dx}{dt} = (\beta N - \beta R - \gamma)x - \beta$$

$$\frac{dx}{dt} = \beta - (\beta N - \beta R - \gamma)x$$

$$\int_{\frac{1}{I_0}}^{\frac{1}{I(t)}} \frac{dx}{\beta - (\beta N - \beta R - \gamma)x} = \int_0^t dt$$

$$\left|\log \beta - (\beta N - \beta R - \gamma)x\right|_{\frac{1}{I_0}}^{\frac{1}{I(t)}} = -t(\beta N - \beta R - \gamma)$$

$$\left[\log \beta - (\beta N - \beta R - \gamma)\frac{1}{I(t)} - \log \beta - (\beta N - \beta R - \gamma)\frac{1}{I_0}\right] = -t(\beta N - \beta R - \gamma)$$

$$\log \frac{\beta - (\beta N - \beta R - \gamma)\frac{1}{I(t)}}{\beta - (\beta N - \beta R - \gamma)\frac{1}{I_0}} = -t(\beta N - \beta R - \gamma)$$

$$\frac{\beta - (\beta N - \beta R - \gamma)\frac{1}{I(t)}}{\beta - (\beta N - \beta R - \gamma)\frac{1}{I_0}} = e^{-t(\beta N - \beta R - \gamma)}$$

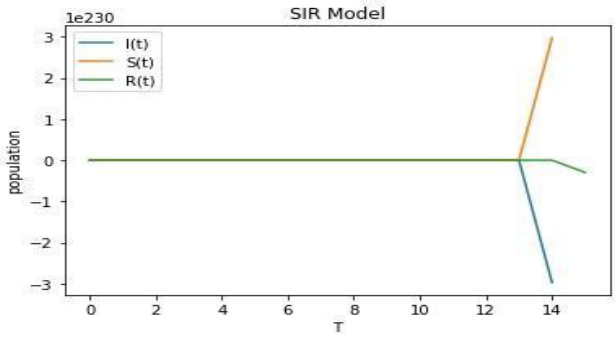
$$\frac{1}{I(t)} = \frac{\beta - (\beta N - \beta R - \gamma)\frac{1}{I_0}e^{-t(\beta N - \beta R - \gamma)}}{\beta - (\beta N - \beta R - \gamma)}$$

$$\boxed{I(t) = \frac{\beta - (\beta N - \beta R - \gamma)}{\beta - (\beta N - \beta R - \gamma)\frac{1}{I_0}e^{-t(\beta N - \beta R - \gamma)}}}$$

This is the required rate of infected individuals.

2.6.1 Python Code for SIR Model with Graph

#Code from the Spyder of 3.8 version of python
"import matplotlib.pylab as pt N = 1000000;
S = N – 1;
I = 1;
R = 0;
beta = 0.5;
mu = 0.1;
suspect = [];




```
infect = [];
recover = [];
def infection(S, I, R, N):;
for t in range (1, 100):;
dS = S –(beta * S * I)/N ;
dI = I + ((beta * S * I)/R) – R;
dR = mu * i ;
S=S+dS ;
I=I+dI ;
R=R+Dr;
suscept.append(S);
infect.append(I);
recover.append(R);
infection (S, I, R, N);
pt.plot(infect,label='I(t)');
pt.plot(suscept,label='S(t)');
pt.plot(recover,label='R(t)');
pt.legend();
pt.xlabel('t');
pt.ylabel('population');
pt.title('SIR MODEL')"
pt.show()
```

• The total population `N` is set at 1,000,000.
• Initial values are set for the number of infected (`I = 1`) and recovered (`R = 0`) individuals. The number of suscepted individuals `S` is calculated as the total population minus the number of infectious and recovered individuals.
• β represents the transmission rate, determining how easily the infection spreads from infected to suscepted individuals.
• γ represents the recovered rate, indicating the rate at which infected individuals recover and become immune.
• The `infection` function simulates the spread of the infection over time using Euler's method for numerical integration. It iterates over a range of time steps (from 1 to 100) and calculates the changes in the number of suscepted, infected, and recovered individuals based on the SIR model equations.
• Within each iteration, the changes (`dS`, `dI`, and `dR`) are calculated using the differential equations of the SIR model. Then, the suscepted (`S`), infected (`I`), and recovered (`R`) populations are updated accordingly. - The values of `S`, `I`, and `R` at each time step are appended to their respective lists (`suspect`, `infect`, `recover`).
• The number of infectious individuals (`I(t)`), susceptible individuals (`S(t)`) and recovered individuals (`R(t)`) are plotted against time (`T`).
• The legend indicates which curve corresponds to each population category.
• Axes labels and a title are added to the plot to provide context.

3. Conclusion

In conclusion, the Susceptible-Infected (SI), Susceptible-Infected Susceptible (SIS), and Susceptible-Infected-recovered (SIR) models represent indispensable tools in understanding the dynamics of infectious disease such as HIV and COVID-19. These models have provided valuable insights into the transmission dynamics, endemic equilibrium, and the impact of invention strategies on diseases.

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