

Impact of Behavioral Changes on Disease Spread: A Nonlinear Analysis of the S_1S_2IR Model

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Abstract

We outline and discuss here an expanded epidemiological model, called the S_1S_2IR model, which incorporates behavioral heterogeneity in the susceptible class. The model distinguishes the susceptible class into two classes: those with average behavior (S_1) and those practicing protective behavior (S_2), to reflect more realistically disease transmission dynamics. The dynamics are modeled by a nonlinear system of differential equations capturing behavioral switching, infection saturation phenomena, and key dynamics. We derive two basic reproduction numbers R_{0_1} and R_{0_2} as threshold parameters for characterizing the stability of equilibria. Local stability and global stability of DFE and EE are studied by the Jacobian matrix, Routh–Hurwitz conditions, and Lyapunov functions. Analytical conditions are obtained for the

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persistence and asymptotic stability of all equilibrium states. Numerical simulations are presented to gain understanding of the dynamic behavior of the system in both the endemic and disease-free scenarios. The results confirm that behavioral responses are a determining factor in long-term disease spread outcomes. This work highlights the importance of incorporating behavior-modified transmission into epidemic modeling and provides a theoretical framework for evaluating public health interventions.

Keywords: *Epidemiological modeling, Nonlinear differential equations, Disease-free equilibrium, Endemic equilibrium, Basic reproduction number, Stability analysis, Lyapunov function. Behavioral response. Infectious disease dynamics.*

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1 Introduction

Mathematical modeling is a central element in infectious disease spread and control understanding. Classical compartmental models such as the SIR (Susceptible–Infected–Recovered) framework have succeeded in providing understanding of epidemic dynamics [4, 6]. However, real epidemics are not only driven by biological and demographic factors, but also by behavioral changes of individuals. In particular, individuals adapt their behavior according to disease prevalence, leading to heterogeneous susceptibility patterns [5]. To more accurately capture such dynamics, there is a growing need for incorporating behavioral heterogeneity into epidemic models [8].

Over the decades, the basic SIR model has been generalized along numerous dimensions to reflect more realistic biological, social, and environmental factors. The model was generalized by scientists to include latency periods (SEIR models), essential dynamics (births and deaths), vaccination campaigns, age-structured populations, and recently, the impact of human behavior in the context of disease risk. The COVID-19 pandemic also highlighted the need to include behavioral dynamics in disease models, since people’s reactions anything from mask-wearing to social distancing had a profound impact on transmission [9].

With this, recent epidemiological models have begun to incorporate behav-

ioral heterogeneity explicitly. One approach is to partition the susceptible population based on risk perception or level of precaution. This is what gives rise to models like the S_1S_2IR model, which introduces two types of susceptible individuals: the normally behaving ones (S_1) and the ones that have undergone protective behavior (S_2). This structure enables more precise simulation of population behavior, especially for long or repeated outbreaks where individuals modify their behavior over time. This approach has been studied in the form of the SIS model in [12] cases.

This paper adds to this school of development by working through the S_1S_2IR model in detail [10]. We extend the model with nonlinear incidence and demography, derive basic reproduction numbers, and discuss local and global stability of disease-free and endemic equilibria [10]. Our research employs the old favorites of the Jacobian matrix and Routh–Hurwitz conditions along with Lyapunov functions for global stability [5]. Finally, numerical simulations validate the theoretical findings and illustrate how dynamics of behaviors influence epidemic effects [7].

Through this work, we intend to make further progress in the historical development of epidemic modeling by further bridging the gap between classical compartmental models and behavior aware epidemiological models. This model can also be extended to travel between two regions [13].

The organization of this paper is the following. Section 2 explains the formulation of the S_1S_2IR model, with two distinct susceptible classes to include behavior heterogeneity in response to infection risk. The section provides the system of differential equations, all the parameters are defined, and provides the dimensionless version of the model for analysis. We analyze the endemic equilibrium of the system in Section 3. Analytical conditions for the existence and uniqueness of the endemic point are derived by solving the steady-state equations, and the local stability is examined in different regimes of the parameters. Section 4 considers the global stability of both the disease-free equilibrium (DFE) and the endemic equilibrium (EE). By applying Lyapunov functions and Routh–Hurwitz criteria, sufficient conditions are derived to guarantee that the DFE or EE is globally asymptotically stable. Section 5 introduces numerical simulations to confirm and demonstrate the theoretical results. Two distinct scenarios are studied: one with reproduction numbers $R_{0_1}, R_{0_2} > 1$ (endemic case), and another with $R_{0_1}, R_{0_2} < 1$ (disease-free case)[16]. Time evolution of the population compartments is plotted to confirm the stability behavior determined by the analysis. Finally, Section 6 provides a conclusion that summarizes the key findings, underscores

the value of including behavior-modified susceptibility in epidemic modeling, and suggests possible directions for future research.

2 Diagram of model

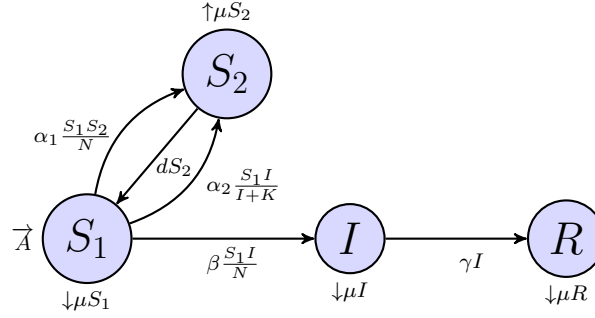


Figure 1: Diagram of model

Considering the diagram, the system of equations of the S_1S_2IR model is as follows:

$$\begin{cases} \frac{dS_1}{dt} = A - \alpha_1 \left(\frac{S_2}{N} \right) - \alpha_2 S_1 \left(\frac{I}{I+K} \right) + dS_2 - \mu S_1 - \beta S_1 \left(\frac{I}{N} \right) \\ \frac{dS_2}{dt} = \alpha_2 S_1 \left(\frac{I}{I+K} \right) + \alpha_1 \left(\frac{S_2}{N} \right) - dS_2 - \mu S_2 \\ \frac{dI}{dt} = \beta S_1 \left(\frac{I}{N} \right) - \gamma I - \mu I \\ \frac{dR}{dt} = \gamma I - \mu R \end{cases} \quad (2.1)$$

The initial values of $S_1(0)$, $S_2(0)$, $I(0)$, and $R(0)$ are all positive; also, all parameters of the above model are positive. The total population $N(t) = S_1(t) + S_2(t) + I(t) + R(t)$ holds in the equation $\frac{dN}{dt} = A - \mu N(t)$, so

$$\lim_{t \rightarrow \infty} N(t) = \frac{A}{\mu} = N_0,$$

Therefore, we study the behavior of the above system on the hyperplane $S_1 + S_2 + I + R = \frac{A}{\mu}$. We assume $s_1 = \frac{S_1}{N_0}$, $s_2 = \frac{S_2}{N_0}$, $i = \frac{I}{N_0}$ and $r = \frac{R}{N_0}$. Also,

since $R(t)$ has no effect in the first equation, we can temporarily remove it and examine the system in the 3×3 state and finally calculate $R(t)$ from the formula $N(t)$. Therefore, the system of equations (2.1) can be rewritten as follows:

$$\begin{cases} \frac{ds_1}{dt} = \mu - \alpha_1 s_1 s_2 - \alpha_2 s_1 \left(\frac{i}{i+k}\right) + ds_2 - \mu s_1 - \beta s_1 i \\ \frac{ds_2}{dt} = \alpha_2 s_1 \left(\frac{i}{i+k}\right) + \alpha_1 s_1 s_2 - ds_2 - \mu s_2 \\ \frac{di}{dt} = \beta s_1 i - \gamma i - \mu i \end{cases} \quad (2.2)$$

Where $k = \frac{K}{N_0}$. The system 2.2 has an obvious *DFE* equilibrium point $E_0 = (1, 0, 0)$ and a non-obvious *DFE* equilibrium point $E_1 = \left(\frac{d+\mu}{\alpha_1}, 1 - \frac{d+\mu}{\alpha_1}, 0\right)$. The Jacobian matrix of the 2.2 is as follows:

$$J(s_1, s_2, i) = \begin{bmatrix} -\alpha_2 s_2 - \alpha_2 \frac{i}{i+k} - \beta i - \mu & -\alpha_1 s_1 + d & \frac{-\alpha_2 s_1(i+k) + \alpha_2 s_1 i}{(i+k)^2} - \beta s_1 \\ \alpha_2 \frac{i}{i+k} + \alpha_1 s_2 & \alpha_1 s_1 - d - \mu & \frac{\alpha_2 s_1(i+k) - \alpha_2 s_1 i}{(i+k)^2} \\ \beta i & 0 & \beta s_1 - \gamma - \mu \end{bmatrix}$$

We place the equilibrium point of *DFE* in the Jacobian matrix

$$J_0 = J(E_0) = \begin{bmatrix} -\mu & -\alpha_1 + d & \frac{-\alpha_2}{k} - \beta \\ 0 & \alpha_1 - d - \mu & \frac{\alpha_2}{k} \\ 0 & 0 & \beta - \gamma - \mu \end{bmatrix}.$$

The matrix J_0 is an upper triangular matrix, so the eigenvalues of the elements are on the main diagonal, so

$$\begin{aligned} \lambda_1 &= -\mu, \\ \lambda_2 &= \alpha_1 - d - \mu, \\ \lambda_3 &= \beta - \gamma - \mu. \end{aligned}$$

According to the linearization theorem [?], λ_1 , λ_2 , and λ_3 must be negative for *DFE* to be a stable node; therefore

$$\begin{aligned} \lambda_1 &= -\mu < 0, \\ \lambda_2 &= \alpha_1 - d - \mu < 0 \rightarrow \alpha_1 < d + \mu \rightarrow \frac{\alpha_1}{d + \mu} < 1, \\ \lambda_3 &= \beta - \gamma - \mu < 0 \rightarrow \beta < \gamma + \mu \rightarrow \frac{\beta}{\gamma + \mu} < 1, \end{aligned}$$

Therefore, using the Jacobian matrix approximation method, the basic reproduction number in the S_1S_2IR model is obtained as follows:

$$R_{0_1} = \frac{\alpha_1}{d + \mu} \quad R_{0_2} = \frac{\beta}{\gamma + \mu}.$$

Clearly, if $R_{0_1} < 1$ and $R_{0_2} < 1$ the DFE is asymptotically stable, otherwise it is unstable. Now we analyze the equilibrium point E_1 . According to the previous calculations, the point E_1 can be rewritten as $E_1 = \left(\frac{1}{R_{0_1}}, 1 - \frac{1}{R_{0_1}}, 0\right)$. We also set $R_0^* = \frac{R_{0_2}}{R_{0_1}}$. By putting E_1 into the Jacobian matrix, we have

$$J_1 = J(E_1) = \begin{bmatrix} -\alpha_2 + \frac{\alpha_2}{R_{0_1}} - \mu & -\mu & -\frac{\alpha_2}{kR_{0_1}} - \frac{\beta}{R_{0_1}} \\ (d + \mu)(R_{0_1} - 1) & 0 & \frac{\alpha_2}{kR_{0_1}} \\ 0 & 0 & \frac{\beta}{R_{0_1}} - \gamma - \mu \end{bmatrix}$$

The matrix J_1 has the eigenvalue $\lambda_3 = \frac{\beta}{R_{0_1}}\gamma\mu$, so we have

$$\lambda_3 = \frac{\beta}{R_{0_1}} - \gamma - \mu = \frac{\beta}{R_{0_1}} - \frac{\beta}{R_{0_2}} < 0 \Rightarrow R_{0_2} < R_{0_1} \Rightarrow R_0^* < 1,$$

Also, consider the following submatrix:

$$J_1^* = \begin{bmatrix} -\alpha_2 + \frac{\alpha_2}{R_{0_1}} - \mu & -\mu \\ (d + \mu)(R_{0_1} - 1) & 0 \end{bmatrix}.$$

In order to locally stabilize the point E_1 , we must show that $Trace(J_1^*) < 0$ and $Det(J_1^*) > 0$; therefore, we have

$$Trace(J_1^*) = -\alpha_2 + \frac{\alpha_2}{R_{0_1}} - \mu < 0 \Leftrightarrow R_{0_1} > 1, \quad Det(J_1^*) = (\mu)(d + \mu)(R_{0_1} - 1) > 0 \Leftrightarrow R_{0_1} > 1.$$

So if $R_0^* < 1$ and $R_{0_1} > 1$ then the point E_1 is locally stable.

3 Endemic equilibrium

In this section, we investigate the existence and dynamic properties of *ENDEMIC* equilibrium points and stable states. Suppose we denote the *ENDEMIC*

equilibrium point by (s_1^*, s_2^*, i^*) , such that $i^* \neq 0$. Therefore, from the third equation of the system 2.2 we have

$$s_1^* = \frac{\gamma + \mu}{\beta} = \frac{1}{R_{0_2}}.$$

Now we simplify the second equation of the system 2.2 and put s_1^* in it

$$\begin{aligned} & \alpha_2 s_1^* \left(\frac{i^*}{i^* + k} \right) + \alpha_1 s_1^* s_2^* - d s_2^* - \mu s_2^* = 0 \\ \Rightarrow & \alpha_2 s_1^* i^* + \alpha_1 s_1^* s_2^* (i^* + k) - d s_2^* (i^* + k) - \mu s_2^* (i^* + k) = 0 \\ = & \alpha_2 s_1^* i^* + \alpha_1 s_1^* s_2^* i^* + \alpha_1 s_1^* s_2^* k - d s_2^* i^* - \mu s_2^* i^* - s_2^* k \frac{\alpha_1}{R_{0_1}} = 0 \\ \Rightarrow & \alpha_1 s_2^* \left(\frac{i^*}{R_{0_2}} + \frac{k}{R_{0_2}} - \frac{k}{R_{0_1}} - \frac{i^*}{R_{0_1}} \right) + \frac{\alpha_2}{R_{0_2}} i^* = 0 \\ \Rightarrow & s_2^* \left(\frac{i^* + k}{R_{0_2}} - \frac{i^* + k}{R_{0_1}} \right) = -\frac{\alpha_2}{\alpha_1 R_{0_2}} i^* \\ \Rightarrow & s_2^* = \frac{-\alpha_2 R_{0_1}}{\alpha_1 (R_{0_1} - R_{0_2})} \times h(i^*) \end{aligned}$$

Where $h(i^*) = \frac{i^*}{i^* + k}$. Now we put s_1^* and s_2^* into the first equation of the system 2.2

$$\begin{aligned} & \mu - \alpha_1 s_1^* s_2^* - \alpha_2 s_1^* \left(\frac{i^*}{i^* + k} \right) + d s_2^* - \mu s_1^* - \beta s_1^* i^* = 0 \\ \Rightarrow & \mu + \frac{\alpha_2 R_{0_1} h(i^*)}{R_{0_2} (R_{0_1} - R_{0_2})} - \frac{\alpha_2 h(i^*)}{R_{0_2}} - \frac{d \alpha_2 R_{0_1} h(i^*)}{\alpha_1 (R_{0_1} - R_{0_2})} - \frac{\beta i^*}{R_{0_2}} - \frac{\mu}{R_{0_2}} = 0 \\ \Rightarrow & h(i^*) \left(\frac{\alpha_2 (\alpha_1 - d R_{0_1})}{\alpha_1 (R_{0_1} - R_{0_2})} \right) + \mu \left(\frac{R_{0_2} - 1}{R_{0_2}} \right) - \frac{\beta i^*}{R_{0_2}} = 0 \\ \Rightarrow & \left(\frac{R_{0_2} - 1}{R_{0_2}} \right) \mu = \frac{\beta i^*}{R_{0_2}} - \zeta h(i^*) = \frac{\beta i^* (i^* + k) - \zeta R_{0_2} i^*}{(i^* + k) (R_{0_2})} \\ \Rightarrow & (R_{0_2} - 1) (i^* + k) \mu = \beta i^* (i^* + k) - \zeta R_{0_2} i^* \\ \Rightarrow & \beta i^{*2} + (\mu - R_{0_2} \mu + \beta k - \zeta R_{0_2}) i^* + \mu k (1 - R_{0_2}) = 0 \end{aligned}$$

Where $\zeta = \left(\frac{\alpha_2 (\alpha_1 - d R_{0_1})}{\alpha_1 (R_{0_1} - R_{0_2})} \right)$. First, we determine the sign of ζ , so

$$\zeta = \left(\frac{\alpha_2 (\alpha_1 - d R_{0_1})}{\alpha_1 (R_{0_1} - R_{0_2})} \right) = \begin{cases} < 0, & R_0^* > 1 \\ > 0, & R_0^* < 1, \end{cases}$$

Since the inequality $\alpha_1 > dR_{0_1}$ always holds, we finally arrive at the following quadratic equation:

$$F(i^*) = Ai^{*2} + Bi^* + C = 0,$$

Where

$$\begin{aligned} A &= \beta > 0 \\ B &= \mu(1 - R_{0_2}) + \beta k - \zeta R_{0_2} \\ C &= \mu k(1 - R_{0_2}), \end{aligned}$$

It is clear that $C > 0 \Leftrightarrow R_{0_2} < 1$ and $C < 0 \Leftrightarrow R_{0_2} > 1$. So if $R_{0_2} > 1$, the curve $F(i^*)$ has two roots, which must be determined by their signs, so we have

$$\frac{C}{A} = \begin{cases} < 0, & R_{0_2} > 1, \\ > 0, & R_{0_2} < 1, \end{cases}$$

So in the case where $R_{0_2} > 1$, $F(i^*)$ has two different roots of the sign. Now we determine the sign of B ,

$$B = \mu(1 - R_{0_2}) + \beta k - \zeta R_{0_2} = \begin{cases} < 0, & R_{0_2} > 1, R_0^* > 1, \\ > 0, & R_{0_2} < 1, R_0^* > 1, \end{cases}$$

So as long as $B^2 > 4AC$ in all cases $F(i^*)$ has the following two roots:

$$i^* = \frac{-B + \sqrt{\Delta}}{2A} > 0 \quad \text{and} \quad i^* = \frac{-B - \sqrt{\Delta}}{2A} < 0.$$

Consequently, if $R_{0_2} > 1$ and $R_0^* > 1$ the system has a unique *ENDEMIC* point

$$E_2 = (s_1^*, s_2^*, i^*) = \left(\frac{1}{R_{0_2}}, \frac{-\alpha_2 R_{0_1}}{\alpha_1(R_{0_1} - R_{0_2})} \times h(i^*), \frac{-B + \sqrt{\Delta}}{2A} \right).$$

Theorem 3.1. *If $R_{0_1} > 1$, $R_{0_2} > 1$, $\alpha_2 > \alpha_1$ and $R_{0_2} > R_{0_1}(R_0^* > 1)$, then the point $E_2 = (s_1^*, s_2^*, i^*)$ is locally asymptotically stable*

Proof. In order to prove the asymptotic local stability in E_2 , we use the Routh-Hurwitz criterion. Therefore, by calculating the characteristic equation of the matrix J , we have

$$P(\lambda) = \lambda^3 + a_1\lambda^2 + a_2 + a_3 = 0,$$

Where

$$\begin{aligned} a_1 &= \alpha_2 s_2^* - (d + \mu)(R_{0_1} s_1^* - 1) + \alpha_2 h(i^*) + \beta i^* + \mu, \\ a_2 &= \alpha_1^2 s_1^* s_2^* + \alpha_1 \alpha_2 s_1^* h(i^*) - \alpha_1 d s_2^* - \alpha_2 h(i^*) d - \chi \beta i^* + \beta^2 i^* s^* \\ &\quad - (d + \mu)(R_{0_1} s_1^* - 1)(\alpha_2 s_2^* + \alpha_2 h(i^*) + \beta i^* + \mu), \\ a_3 &= \beta d \chi i^* - \alpha_1 \beta \chi s_1^* i^* + \chi \beta i^* (d + \mu)(R_{0_1} s_1^* - 1) - \beta^2 i^* s_1^* (d + \mu)(R_{0_1} s_1^* - 1), \end{aligned}$$

Where $\chi = -\frac{\alpha_2 s_1^* k}{(i^* + k)^2}$. We need to show that $a_1 > 0$, $a_2 > 0$, $a_3 > 0$ and $a_1 a_2 > a_3$. As a result, we have

$$a_1 > 0 \Leftrightarrow (d + \mu)(R_{0_1} s_1^* - 1) < 0 \Leftrightarrow \frac{R_{0_1}}{R_{0_2}} - 1 < 0 \Leftrightarrow R_{0_2} > R_{0_1},$$

To prove $a_2 > 0$ we need to analyze the following expressions:

$$-(d + \mu)(R_{0_1} s_1^* - 1)(\beta i^* + \mu) > 0 \Leftrightarrow R_{0_2} > R_{0_1},$$

and

$$\begin{aligned} &\alpha_1 \alpha_2 s_1^* h(i^*) - \alpha_2 h(i^*) d - \alpha_2 h(i^*) (d + \mu)(R_{0_1} s_1^* - 1) \\ &= \alpha_2 h(i^*) \left(\frac{\alpha_1}{R_{0_2}} - d - \frac{\alpha_1}{R_{0_1}} \left(\frac{R_{0_1}}{R_{0_2}} - 1 \right) \right) \\ &= \alpha_2 h(i^*) \left(\frac{\alpha_1}{R_{0_1}} - d \right) \\ &= \alpha_2 h(i^*) (d + \mu - d) \\ &= \alpha_2 h(i^*) \mu > 0, \end{aligned}$$

and

$$\begin{aligned} &\alpha_1^2 s_1^* s_2^* - \alpha_1 d s_2^* - \alpha_2 s_2^* (d + \mu)(R_{0_1} s_1^* - 1) = \frac{\alpha_1^2 s_2^*}{R_{0_1}} - \alpha_1 d s_2^* - \frac{\alpha_1 \alpha_2 s_2^*}{R_{0_2}} + \frac{\alpha_1 \alpha_2 s_2^*}{R_{0_1}} \\ &= \alpha_1 s_2^* \left(\frac{R_{0_1}(\alpha_1 - \alpha_2) + R_{0_2}(\alpha_2 - d R_{0_1})}{R_{0_1} R_{0_2}} \right) > 0 \Leftrightarrow R_{0_1}(\alpha_1 - \alpha_2) + R_{0_2}(\alpha_2 - d R_{0_1}) > 0 \\ &\Leftrightarrow (R_{0_2} - R_{0_1})(\alpha_2 - d R_{0_1}) + R_{0_1}^2 \mu > 0 \Leftrightarrow \alpha_2 - d R_{0_1} > 0, R_{0_2} - R_{0_1} > 0. \end{aligned}$$

It is clear $\alpha_2 - dR_{0_1} = \frac{d(\alpha_2 - \alpha_1) + \alpha_2 \mu}{d + \mu} > 0 \Leftrightarrow \alpha_2 > \alpha_1$ and $R_{0_2} > R_{0_1}$ and $\beta^2 i^* s^* - \chi \beta i^* > 0$ because $\chi < 0$, so if $R_{0_2} > R_{0_1}$ and $\alpha_2 > \alpha_1$ then $a_2 > 0$. To prove $a_3 > 0$ we need to analyze the following expressions:

$$\begin{aligned} \beta d \chi i^* - \alpha_1 \beta \chi s_1^* i^* + \chi \beta i^* (d + \mu) (R_{0_1} s_1^* - 1) &= -\chi \beta i^* \left(-d + \alpha_1 s_1^* - \frac{\alpha_1}{R_{0_2}} + \frac{\alpha_1}{R_{0_1}} \right) \\ &= -\chi \beta i^* \left(\frac{\alpha_1}{R_{0_1}} - d \right) \end{aligned}$$

Since $\chi < 0$, then it is only sufficient to

$$\frac{\alpha_1}{R_{0_1}} d > 0 \Leftrightarrow d + \mu > d \Rightarrow \mu > 0,$$

for the above inequality to always hold. We also have

$$\beta^2 i^* s_1^* (d + \mu) (R_{0_1} s_1^* - 1) < 0 \Leftrightarrow R_{0_2} > R_{0_1},$$

So if $R_{0_2} > R_{0_1}$ then $a_3 > 0$.

Finally, we need to show that if $R_{0_2} > R_{0_1}$ then $a_1 a_2 > a_3$. We know that

$$a_3 = \beta d \chi i^* - \alpha_1 \beta \chi s_1^* i^* + \chi \beta i^* (d + \mu) (R_{0_1} s_1^* - 1) - \beta^2 i^* s_1^* (d + \mu) (R_{0_1} s_1^* - 1).$$

The expressions $\chi \beta i^* (d + \mu) (R_{0_1} s_1^* - 1)$ and $\beta^2 i^* s_1^* (d + \mu) (R_{0_1} s_1^* - 1)$ repeat exactly in the product $a_1 a_2$, so we only need to compare

$$\beta d \chi i^* - \alpha_1 \beta \chi s_1^* i^* = \beta \chi i^* \left(d - \frac{\alpha_1}{R_{0_2}} \right),$$

The similar expression on the side $a_1 a_2$ is as

$$\beta \chi i^* (-\alpha_2 s_2^* - \alpha_2 h(i^*) - \beta i^* - \mu),$$

Since $\chi < 0$, it is clear that if $R_{0_2} > R_{0_1}$ the inequality

$$\beta \chi i^* (-\alpha_2 s_2^* - \alpha_2 h(i^*) - \beta i^* - \mu) > \beta \chi i^* \left(d - \frac{\alpha_1}{R_{0_2}} \right),$$

holds and therefore $a_1 a_2 > a_3$. □

4 Global stability of DFE and ENDEMIC points

Theorem 4.1. *The equilibrium point $E_0 = (1, 0, 0)$ is globally stable if $R_{0_2} < 1$ and $R_{0_1} < 1$.*

Proof. We use the Lyabanov function to prove global asymptotic stability. Consider the following Lyabanov function:

$$V(s_1, s_2, i) = k_1 \left(s_1 - s_1^* - s_1^* \ln \frac{s_1}{s_1^*} \right) + \frac{1}{\gamma + \mu} i,$$

Where $k_1 > 0$. By deriving it, we have

$$\frac{dV}{dt} = k_1 \left(1 - \frac{s_1^*}{s_1} \right) \frac{ds_1}{dt} + \frac{1}{\gamma + \mu} \frac{di}{dt},$$

We put $k_1 = 1$, so

$$\begin{aligned} \frac{dV}{dt} &= -\alpha_1 s_1 s_2 + \alpha_1 s_2 - \alpha_2 h(i) s_1 + \alpha_2 h(i) + ds_2 - d \frac{s_2}{s_1} + \beta i - \beta s_1 i \\ &\quad + 2\mu - \mu s_1 - \frac{\mu}{s_1} + R_{0_2} s_1 i - i. \end{aligned}$$

The expressions

$$2\mu - \mu s_1 - \frac{\mu}{s_1} = \mu \left(2 - s_1 - \frac{1}{s_1} \right) = -\mu \left(\frac{(s_1 - 1)^2}{s_1} \right),$$

and

$$\begin{aligned} \beta i(1 - s_1) + i(R_{0_2} s_1 - 1) &= i(R_{0_2}(\gamma + \mu)(1 - s_1) + R_{0_2} s_1 - 1) \\ &= i(R_{0_2}(\gamma + \mu) - 1 - ((R_{0_2}(\gamma + \mu)s_1 - R_{0_2} s_1)) \end{aligned}$$

Are negative if and only if

$$R_{0_2}(\gamma + \mu) - 1 < 0 \Rightarrow \beta < 1.$$

and

$$R_{0_2}(\gamma + \mu)s_1 - R_{0_2} s_1 > 0 \Rightarrow (\gamma + \mu) > 1.$$

As a result $R_{0_2} = \frac{\beta}{\gamma + \mu} < 1$.

On the other hand, if

$$\alpha_2 h(i) - \alpha_2 h(i) s_1 = \alpha_2 h(i)(1 - s_1) \Rightarrow \alpha_2 h(i) - \alpha_2 h(i) s_1 < 0 \Leftrightarrow s_1 > 1,$$

and

$$\begin{aligned}\alpha_1 s_2 - \alpha_1 s_1 s_2 + ds_2 - d \frac{s_2}{s_1} &= \alpha_1 s_2 (1 - s_1) - \frac{ds_2}{s_1} (1 - s_1) \\ &= (1 - s_1) \left(\alpha_1 s_2 - \frac{ds_2}{s_1} \right),\end{aligned}$$

To establish $\alpha_1 s_2 - \alpha_1 s_1 s_2 + ds_2 - d \frac{s_2}{s_1} < 0$ with respect to $s_1 > 1$, we have

$$\alpha_1 s_2 - \frac{ds_2}{s_1} > 0 \Rightarrow s_1 > \frac{d}{\alpha_1},$$

Therefore, the two inequalities $s_1 > 1$ and $s_1 > \frac{d}{\alpha_1}$ require that $d > \alpha_1$ which leads to the inequality $R_{0_1} < 1$. $\square$

The phase portrait illustrated in Figure 2 demonstrates the global stability of the disease-free equilibrium of the model under the condition of theorem 4.1.

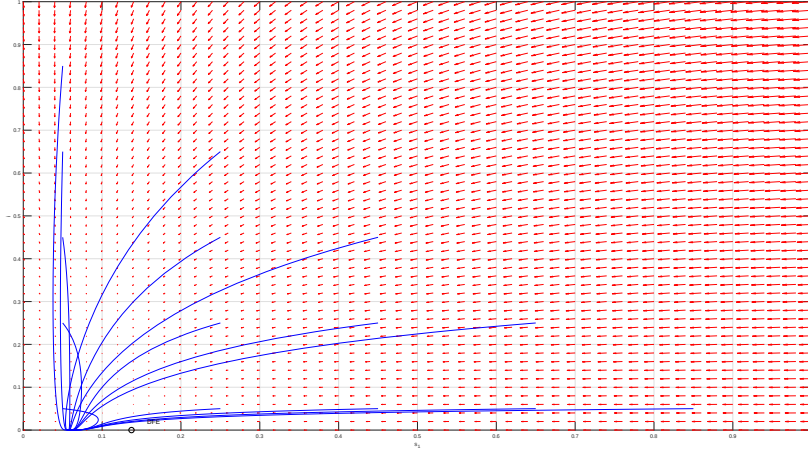


Figure 2: Phase portrait near the Disease-Free Equilibrium.

Theorem 4.2. Suppose $R_0^* > 1$ and $R_{0_2} > 1$, then the steady state EN-DEMIC is globally stable, when $s_1 > 2$, $\frac{R_{0_1} + R_{0_2} - R_{0_1} R_{0_2} s_1}{R_{0_2} - R_{0_1}} < \frac{s_2}{s_2^*} < \frac{R_{0_2} s_1}{R_{0_2} s_1 - 1}$ and $\frac{h(i)}{h(i^*)} < \frac{s_2}{R_{0_2} s_1 s_2^* - s_2}$, where $h(i) = \frac{i}{i+k}$

Proof. We use the Lyabanov function to prove global asymptotic stability. For this purpose, we define the Lyabanov function $V(s_1, s_2, i) : \mathbb{R}^3 \rightarrow \mathbb{R}$ as follows:

$$V(s_1, s_2, i) = k_1 \left(s_1 - s_1^* - s_1^* \ln \frac{s_1}{s_1^*} \right) + k_2 \left(s_2 - s_2^* - s_2^* \ln \frac{s_2}{s_2^*} \right) + k_3 \left(i - i^* - i^* \ln \frac{i}{i^*} \right),$$

Where $k_1 > 0$ $k_2 > 0$ and $k_3 > 0$. As a result

$$\begin{aligned} \frac{dV}{dt} &= k_1 \left(1 - \frac{s_1^*}{s_1} \right) s_1' + k_2 \left(1 - \frac{s_2^*}{s_2} \right) s_2' + k_3 \left(1 - \frac{i^*}{i} \right) i' \\ &= k_1 \left(1 - \frac{s_1^*}{s_1} \right) \left(\mu - \alpha_1 s_1 s_2 - \alpha_2 s_1 \left(\frac{i}{i+k} \right) + ds_2 - \mu s_1 - \beta s_1 i \right) \\ &\quad + k_2 \left(1 - \frac{s_2^*}{s_2} \right) \left(\alpha_2 s_1 \left(\frac{i}{i+k} \right) + \alpha_1 s_1 s_2 - ds_2 - \mu s_2 \right) + k_3 \left(1 - \frac{i^*}{i} \right) (\beta s_1 i - \gamma i - \mu i) \\ &= k_1 \left(1 - \frac{s_1^*}{s_1} \right) \left(\mu - \alpha_1 s_1 s_2 - \alpha_2 s_1 \left(\frac{i}{i+k} \right) + ds_2 - \mu s_1 - \beta s_1 i \right) \\ &\quad + k_2 \left(\frac{(s_2 - s_2^*)}{s_2} \alpha_2 s_1 h(i) + s_2 \frac{\alpha_1}{R_{0_1}} (R_{0_1} s_1 - 1) - s_2^* \frac{\alpha_1}{R_{0_1}} (R_{0_1} s_1 - 1) \right) \\ &\quad + k_3 \left(\beta(i - i^*)(s_1 - \frac{1}{R_{0_2}}) \right), \end{aligned}$$

We set $\mu = \alpha_1 s_1^* s_2^* \alpha_2 s_1^* h(i^*) - ds_2^* \mu s_1^* \beta s_1^* i^*$ So we have

$$\begin{aligned} \frac{dV}{dt} &= k_1 \alpha_1 s_1^* s_2^* - k_1 \alpha_1 s_1 s_2 + k_1 \alpha_1 s_1^* s_2 + k_2 \alpha_1 s_1 s_2 - k_2 s_2 \frac{\alpha_1}{R_{0_1}} - k_2 \alpha_1 s_1 s_2^* + k_2 s_2^* \frac{\alpha_1}{R_{0_1}} \\ &\quad + k_1 \alpha_2 s_1^* h(i^*) - k_1 \alpha_2 h(i) s_1 + k_1 \alpha_2 h(i) s_1^* + k_2 \frac{(s_2 - s_2^*)}{s_2} \alpha_2 s_1 h(i) + k_1 \beta s_1^* i + k_1 \beta s_1^* i^* - k_1 \beta s_1 i \\ &\quad + k_3 \beta s_1 i - k_3 \beta s_1 i^* - k_3 \beta s_1 \frac{i}{R_{0_2}} + k_3 \beta s_1 \frac{i}{R_{0_2}} + k_1 ds_2 - k_1 ds_2^* - k_1 ds_2 \frac{s_1^*}{s_1} + 2k_1 \mu s_1^* - k_1 \mu s_1 \\ &\quad - k_1 \mu \frac{s_1^*}{s_1} \end{aligned}$$

By substituting $k_1 = k_2 = k_3 = 1$, we analyze the expressions as follows:

$$\begin{aligned}
& \alpha_1 s_1^* s_2^* \left(1 + \frac{s_2}{s_2^*} - \frac{s_1}{s_1^*} - \frac{s_2}{R_{0_1} s_1^* s_2^*} + \frac{1}{R_{0_1} s_1^*} \right) \\
&= \alpha_1 s_1^* s_2^* \left(1 + \frac{s_2}{s_2^*} - R_{0_2} s_1 - R_0^* \frac{s_2}{s_2^*} + R_0^* \right) \\
&\Rightarrow 1 + \frac{s_2}{s_2^*} - R_{0_2} s_1 - R_0^* \frac{s_2}{s_2^*} + R_0^* < 0 \Leftrightarrow \frac{R_{0_1} + R_{0_2} - R_{0_1} R_{0_2} s_1}{R_{0_2} - R_{0_1}} < \frac{s_2}{s_2^*},
\end{aligned}$$

and

$$\begin{aligned}
& \beta s_1^* i^* \left(1 + \frac{i}{i^*} - \frac{s_1}{s_1^*} - \frac{i}{R_{0_2} s_1^* i^*} + \frac{1}{R_{0_2} s_1^*} \right) \\
&= \beta s_1^* i^* (2 - R_{0_2} s_1) \\
&\Rightarrow 2 - R_{0_2} s_1 < 0 \Leftrightarrow s_1 > 2, R_{0_2} > 1,
\end{aligned}$$

and

$$\begin{aligned}
& \alpha_2 s_1^* h(i^*) - \alpha_2 h(i) s_1^* - \alpha_2 \frac{s_2^* s_1}{s_2} h(i) \\
&= \alpha_2 s_1^* s_2^* h(i^*) \left(\frac{1}{s_2^*} + \frac{h(i)}{h(i^*) s_2^*} - \frac{s_1 h(i)}{s_1^* s_2 h(i^*)} \right) \\
&\Rightarrow \frac{1}{s_2^*} + \frac{h(i)}{h(i^*) s_2^*} - \frac{s_1 h(i)}{s_1^* s_2 h(i^*)} > 0 \Leftrightarrow \frac{h(i)}{h(i^*)} < \frac{s_2}{R_{0_2} s_1 s_2^* - s_2},
\end{aligned}$$

and

$$\begin{aligned}
& ds_2 - ds_2^* - ds_2 \frac{s_1^*}{s_1} \\
&= ds_1^* s_2^* \left(\frac{s_2}{s_1^* s_2^*} - \frac{1}{s_1^*} - \frac{s_2}{s_2^* s_1} \right) \\
&= ds_1^* s_2^* \left(R_{0_2} \frac{s_2}{s_2^*} - R_{0_2} - \frac{s_2}{s_2^* s_1} \right) \\
&\Rightarrow R_{0_2} \frac{s_2}{s_2^*} - R_{0_2} - \frac{s_2}{s_2^* s_1} < 0 \Leftrightarrow \frac{s_2}{s_2^*} < \frac{R_{0_2} s_1}{R_{0_2} s_1 - 1},
\end{aligned}$$

and

$$\begin{aligned}
& 2\mu s_1^* - k\mu s_1 - \mu \frac{s_1^*}{s_1} \\
&= \mu s_1^* \left(2 - \frac{s_1}{s_1^*} - \frac{1}{s_1} \right) \\
&= \mu s_1^* \left(2 - R_{0_2} s_1 - \frac{1}{s_1} \right) \\
&\Rightarrow 2 - R_{0_2} s_1 - \frac{1}{s_1} < 0 \Leftrightarrow s_1 > 2, R_{0_2} > 1.
\end{aligned}$$

As a result, we have shown that if $R_{0_2} > 1$ and $R_0^* > 1$, $s_1 > 2$, $\frac{R_{0_1} + R_{0_2} R_{0_1} R_{0_2} s_1}{R_{0_2} R_{0_1}} < \frac{s_2}{s_2^*} < \frac{R_{0_2} s_1}{R_{0_2} s_1 1}$ and $\frac{h(i)}{h(i^*)} < \frac{s_2}{R_{0_2} s_1 s_2^* s_2}$ then $\frac{dV}{dt} < 0$ $\square$

The phase portrait illustrated in Figure 3 demonstrates the global stability of the ENDEMIC equilibrium of the model under the condition of theorem 4.2.

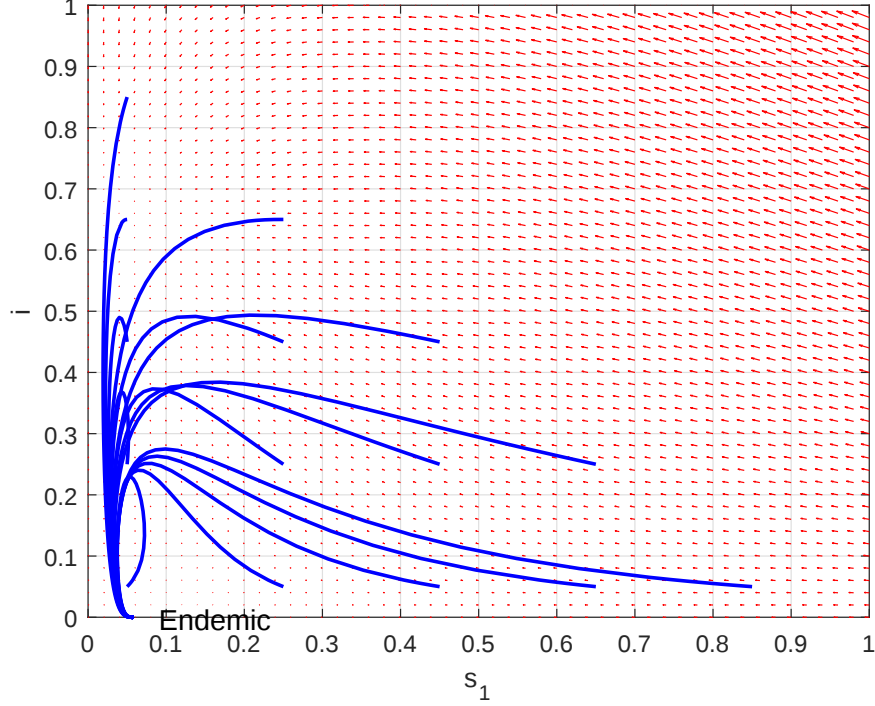


Figure 3: Phase portrait near the ENDEMIC Equilibrium.

5 Numerical Simulations

We consider two following states:

Simulation is for the ENDEMIC equilibrium case. To better understand the dynamic behavior of the S_1S_2IR epidemiological model, we perform numerical simulations using realistic parameter values. These simulations confirm the theoretical results of the previous sections regarding local and global stability.

The goals of this simulation are to show the path of each component $s_1(t)$, $s_2(t)$, and $i(t)$ over time, to confirm the stability of the endemic equilibrium point, and to show the evolution of the susceptible and infected populations of the model under nonlinear dynamics. The following parameter values were chosen to simulate a realistic endemic scenario with $R_{0_1} > 1$ and $R_{0_2} > 1$. Initial conditions are $s_1(0) = 0.9$, $s_2(0) = 0.05$ and $i(0) = 0.05$. Figure 4 presents the time series of the three state variables $s_1(t)$, $s_2(t)$, and $i(t)$ over

Table 1: Parameter values for simulation.

<i>Parameter</i>	<i>Value</i>	<i>Description</i>
μ	0.01	<i>Natural birth/death rate</i>
α_1	0.2	<i>Interaction rate between s_1 and s_2</i>
α_2	0.3	<i>Infection pressure due to behavior – modified transmission</i>
β	0.5	<i>Transmission rate</i>
γ	0.1	<i>Recovery rate</i>
d	0.05	<i>Transferrate from s_1 to s_2</i>
k	0.1	<i>Saturation constant for incidence function</i>

the interval $t \in [0, 200]$, based on the numerical solution of the normalized S_1S_2IR model. Each curve corresponds to the evolution of one compartment in the population, under the parameter regime where the basic reproduction numbers R_{0_1} and R_{0_2} are both greater than 1. This ensures the existence and stability of an endemic equilibrium.

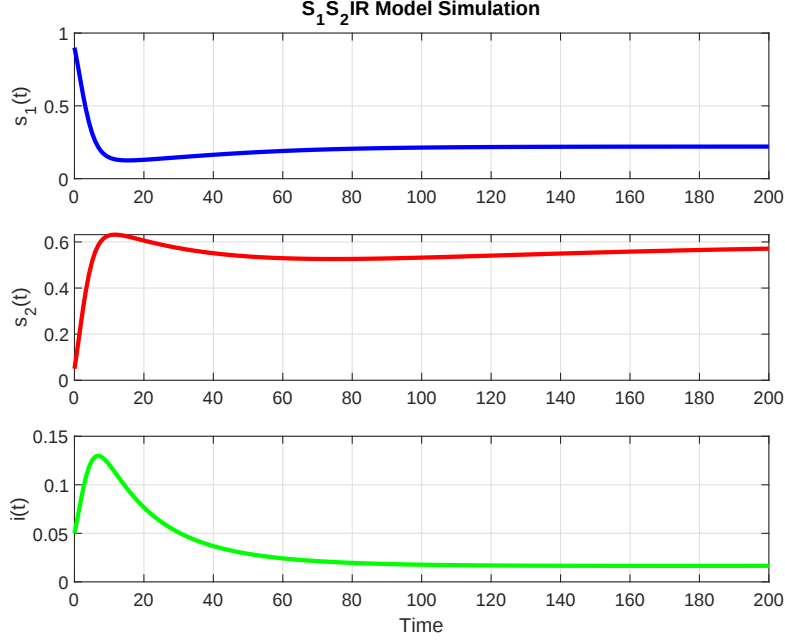


Figure 4: Time evolution of the normalized S_1S_2IR model variables over the interval $t \in [0, 200]$ showing the dynamics of the two susceptible classes $s_1(t)$, $s_2(t)$ and the infected population $i(t)$. The simulation illustrates convergence to a stable endemic equilibrium under the condition $R_{0_1} > 1$ and $R_{0_2} > 1$, with all compartments reaching steady-state values.

Simulation is for the DFE equilibrium case. The goal of this simulation is to demonstrate the long-term behavior of the S_1S_2IR model under conditions that lead to the eradication of the infection. This occurs when both basic reproduction numbers R_{0_1} and R_{0_2} are less than 1, resulting in the global stability of the disease-free equilibrium points. To assure the disease-free outcome we will decrease infection parameter values, compared to the endemic scenario. The chosen parameters are: Initial conditions are $s_1(0) = 0.9$, $s_2(0) = 0.05$ and $i(0) = 0.05$. These yield the following reproduction numbers $R_{0_1} \approx 0.33$ and $R_{0_2} \approx 0.45$. The smooth, monotonic evolutions of all three variables in figure5 imply that there is no oscillation or instability-from whence the global attractiveness of the disease-free steady state under the set of parameter conditions is consequently confirmed.

Table 2: Parameter values for simulation.

<i>Parameter</i>	<i>Value</i>	<i>Description</i>
μ	0.01	<i>Natural birth/death rate</i>
α_1	0.02	<i>Interaction rate between s_1 and s_2</i>
α_2	0.3	<i>Infection pressure due to behavior – modified transmission</i>
β	0.05	<i>Transmission rate</i>
γ	0.1	<i>Recovery rate</i>
d	0.05	<i>Transfer rate from s_1 to s_2</i>
k	0.1	<i>Saturation constant for incidence function</i>

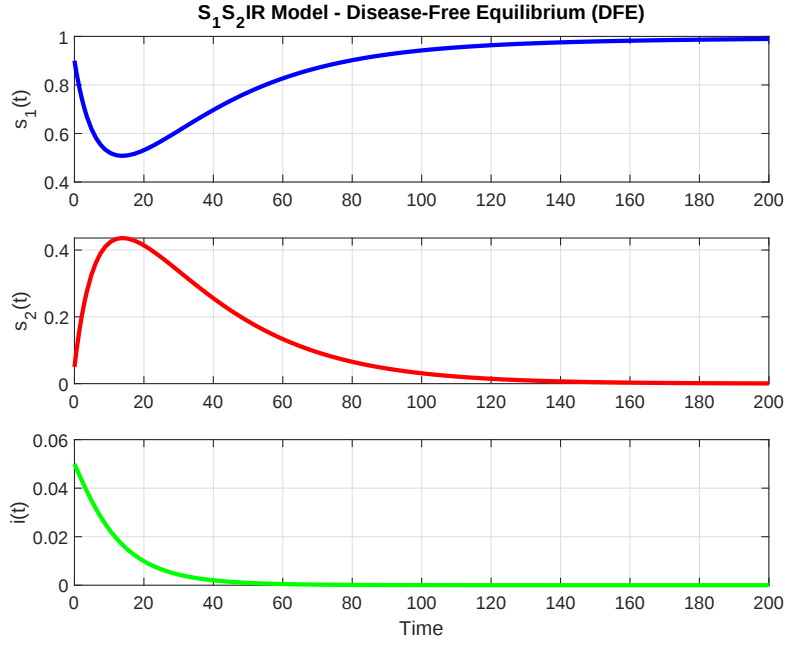


Figure 5: Simulation of the S_1S_2IR model under disease-free conditions where $R_{0_1} < 1$ and $R_{0_2} < 1$. The infected population $i(t)$ declines to zero over time, while the susceptible group $s_1(t)$ stabilizes near 1, and the behavior-modified class $s_2(t)$ gradually diminishes. This confirms the global asymptotic stability of the disease-free equilibrium points.

6 Conclusion

In this study, we derived and analyzed an extended SIR type epidemiological model, called the S_1S_2IR model, with two separated susceptible classes to

capture behavior adjusted transmission processes. Through mathematical analysis, we obtained conditions on local and global stability of the disease free equilibrium (DFE) and endemic equilibrium. Certain important thresholds, namely the basic reproduction numbers R_{0_1} and R_{0_2} . These were assumed to capture the long term dynamics of the system. The analysis showed that the DFE is globally asymptotically stable when $R_{0_1} < 1$ and $R_{0_2} < 1$, whereas the system possesses a locally stable and also unique endemic equilibrium whenever both reproduction numbers are larger than unity and certain inequality constraints exist.

Lyapunov functions were introduced to rigorously define global stability within proper parameter regimes. Numerical simulations supported theoretical results as well, confirming the model's predictions for the convergence dynamics of infected and susceptible individuals. This work demonstrates how heterogeneity in susceptibility due to behavior can qualitatively alter disease dynamics and presents a model for further study of even more complex epidemic scenarios with psychological or social behavioral effects.

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