ANALYSIS OF THE SPREAD OF MALARIA DISEASE

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Abstract. We construct a model that captures the spread of malaria disease, find the disease free and disease endemic equilibrium points, and find the conditions under which these points are stable. We define a number called the basic reproduction number and show that this number determines the stability of the system.

1. Introduction

Malaria is an infectious disease that is transmitted through human interactions with infected mosquitos and mosquito interactions with infected humans. We study an SIS (susceptible, infected, susceptible) model that captures these interactions. We assume that there is no death due to the infection, but that there are natural deaths. A susceptible human becomes infected by coming into contact with an infected mosquito at some constant rate. Similarly, a susceptible mosquito is infected when it comes into contact with an infected human at some different rate. We allow for a rate at which humans may recover from the disease, in which case they immediately become a member of the susceptible class again. In our model, we have chosen to make birth rates and death rates distinct, so we do not have a constant population.

In a system of differential equations, an equilibrium point is a point at which the equations all equal zero. Intuitively, this means that the state of the system is not changing. An equilibrium point where the infected populations are zero is referred to as a disease free equilibrium point. Otherwise, it is known as a disease endemic equilibrium point. If the solutions near the equilibrium points tend toward the points with time, then they are said to be locally stable. An equilibrium point is said to be globally asymptotically stable if the behavior of the system at any point tends toward the equilibrium point as time tends toward infinity.

We further analyze the model by examining the number of individuals that become infected from introducing one infected into a totally susceptible population. We find that if the number of new infections is greater than one, then the disease will persist. Alternatively, if the number of new infections is less than one, then the disease will die out. We refer to this number as the basic reproduction number and it determines the stability of the system.

2. The Model

Our populations are broken into total human population (N_h) and the total mosquito population (N_m). The total human population is further divided into susceptible individuals (S_h) and infected individuals (I_h). Similarly, the total mosquito population consists of

susceptible members (S_m) and infected members (I_m). Our model is displayed in Figure 1 with parameters given by Table 1.

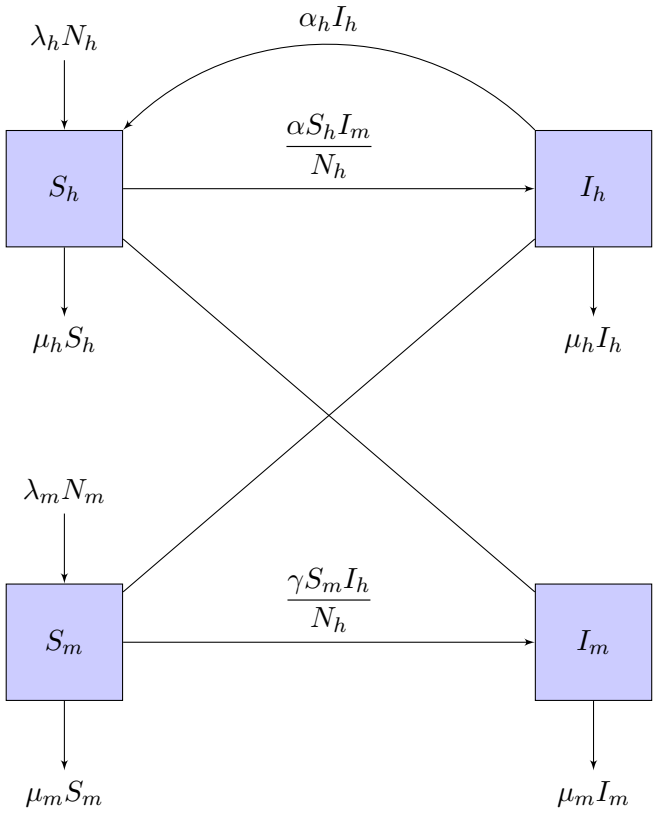


Figure 1. Susceptible humans are bitten by infected mosquitos and move to the infected class of humans at the rate $\frac{\alpha S_h I_m}{N_h}$. Also, susceptible mosquitos bite infected humans and move to the infected class of mosquitos at the rate $\frac{\gamma S_m I_h}{N_h}$. Infected humans recover from the disease and once again become susceptible at the rate $\alpha_h I_h$.

Table 1. Constant parameters for the malaria model.

λ_h	birthrate of humans
λ_m	birthrate of mosquitos
μ_h	natural death rate of humans
μ_m	natural death rate of mosquitos
α	human infection rate
γ	mosquito infection rate
α_h	human recovery rate

From Figure 1, we derive the following system of differential equations:

$$\begin{aligned}
\frac{dS_h}{dt} &= \lambda_h N_h - \frac{\alpha S_h I_m}{N_h} - \mu_h S_h + \alpha_h I_h \\
\frac{dI_h}{dt} &= \frac{\alpha S_h I_m}{N_h} - \alpha_h I_h - \mu_h I_h \\
\frac{dS_m}{dt} &= \lambda_m N_m - \frac{\gamma S_m I_h}{N_h} - \mu_m S_m \\
\frac{dI_m}{dt} &= \frac{\gamma S_m I_h}{N_h} - \mu_m I_m.
\end{aligned}$$

In order to ensure that our equilibrium points are not functions of time, we must eliminate the population variable from our equations. We let

$$s_h = \frac{S_h}{N_h},\ s_m = \frac{S_m}{N_m},\ i_h = \frac{I_h}{N_h},\ \text{and}\ \ i_m = \frac{I_m}{N_m}.$$

Then, since $S_h + I_h = N_h$ and $S_m + I_m = N_m$, we have $s_h + i_h = 1$ and $s_m + i_m = 1$, so that $s_h = 1 - i_h$ and $s_m = 1 - i_m$. With these new variables, the system becomes

$$\begin{aligned}
s_h' &= \lambda_h(1 - s_h) + \alpha_h i_h - \alpha_1 s_h i_m \\
i_h' &= \alpha_1 s_h i_m - \lambda_h i_h - \alpha_h i_h \\
s_m' &= \lambda_m(1 - s_m) - \gamma s_m i_h \\
i_m' &= \gamma s_m i_h - \lambda_m i_m,
\end{aligned}$$

where $\alpha_1 = \alpha\frac{N_m}{N_h}$. We use these identities to reduce our system to two equations by observing that $s_h' = -i_h'$ and that $s_m' = -i_m'$. After substituting $1 - i_h$ for s_h, and $1 - i_m$ for s_m, the system becomes

$$\begin{aligned}
i_h' &= \alpha_1(1 - i_h)i_m - \lambda_h i_h - \alpha_h i_h \\
i_m' &= \gamma(1 - i_m)i_h - \lambda_m i_m,
\end{aligned}$$

which is the system that we will analyze.

3. Equilibrium Points

To find our equilibrium points, we must set our system of equations, i_h' and i_m', equal to zero and solve for i_h and i_m. The simple case for which i_h' and i_m' are equal to zero is when $(i_h, i_m) = (0, 0)$, meaning that there are no infected humans or mosquitos. This is our disease free equilibrium point.

Now we consider the case in which $(i_h, i_m) \neq (0, 0)$ in order to obtain the disease endemic equilibrium point.

Solving $i_m' = 0$ for i_h, we obtain

$$i_h = \frac{\lambda_m i_m}{\gamma(1 - i_m)}.$$

Substituting this quantity into the equation $i_h' = 0$ gives the following expression for i_m^*:

$$i_m^* = \frac{\alpha_1\gamma - \alpha_h\lambda_m - \lambda_h\lambda_m}{\alpha_1\lambda_m + \alpha_1\gamma}.$$

The corresponding value of i_h^* is

$$i_h^* = \frac{\alpha_1\gamma - \lambda_m\alpha_h - \lambda_m\lambda_h}{\alpha_1\gamma + \alpha_h\gamma + \lambda_h\gamma}.$$

Thus, we obtain the endemic equilibrium point (i_h^*, i_m^*).

Let us examine the values of i_h^* and i_m^*. Because these values represent the infected human and mosquito populations, respectively, these numbers must be positive, which means their numerators must always be positive (note that i_h^* and i_m^* have the same numerator). For this to be true,

$$\alpha_1\gamma - \lambda_m\alpha_h - \lambda_m\lambda_h > 0.$$

From this inequality we see that

$$\frac{\alpha_1\gamma}{\lambda_m(\alpha_h + \lambda_h)} > 1.$$

We will label this quantity R_0. Analysis of the local asymptotic stability of the system will allow us to prove that R_0 is the basic reproduction number.

4. Classification of Systems of Differential Equations

Before moving into asymptotic stability of our system, we will need to consider systems of first order linear differential equations of the form

$$x' = ax + by$$
$$y' = cx + dy.$$

Let

$$A = \begin{bmatrix} a & b \\ c & d \end{bmatrix}.$$

Then we can rewrite the system as

$$x' = Ax,$$

where

$$x = \begin{bmatrix} x \\ y \end{bmatrix}.$$

A nonzero vector $\vec{v}$ is called an **eigenvector** of A if $A\vec{v} = \lambda\vec{v}$. The constant λ is called an **eigenvalue** of A. Eigenvalues and eigenvectors may be used to give solutions to systems of differential equations of the form $x' = Ax$.

Theorem 4.1. *Suppose A has a pair of real eigenvalues $\lambda_1 \neq \lambda_2$ and associated eigenvectors $\vec{v_1}$ and $\vec{v_2}$. Then the general solution of the linear system $x' = Ax$ is given by*

$$x(t) = \alpha e^{\lambda_1 t}\vec{v_1} + \beta e^{\lambda_2 t}\vec{v_2}$$

where $\alpha, \beta \in \mathbb{R}$.

We can see that if λ_1 and λ_2 are both negative, then our solution will stabilize. The eigenvalues of A are given by the solutions λ to the equation

$$\det(\lambda I - A) = 0,$$

where **det** is the determinant and I is the 2×2 identity matrix. We call this equation the **characteristic equation** of A. Hence our characteristic equation is

$$(a - \lambda)(d - \lambda) - bc = 0,$$

which is equivalent to

$$\lambda^2 - (a + d)\lambda + (ad - bc) = 0.$$

From this, we observe that

$$\lambda^2 - \mathrm{tr}(A)\lambda + \det(A) = 0\,.$$

The roots of our characteristic equation are given by

$$\lambda_1 = \frac{\mathrm{tr}(A) + \sqrt{\mathrm{tr}(A)^2 - 4\det(A)}}{2}$$

and

$$\lambda_2 = \frac{\mathrm{tr}(A) - \sqrt{\mathrm{tr}(A)^2 - 4\det(A)}}{2}.$$

From this, we can see that

$$\lambda_1 + \lambda_2 = \mathrm{tr}(A)$$

and

$$\lambda_1\lambda_2 = \det(A).$$

Hence, for $\mathrm{tr}(A)^2 - 4\det(A) > 0$, if the trace is negative and the determinant is positive, then the eigenvalues will both be negative and by Theorem 4.1, the equilibrium point will be stable. However, in any other case the equilibrium point will be unstable.

Since we are working with a first order nonlinear system of differential equations, we can analyze the stability of our model at its equilibrium points by linearizing the system using the Jacobian matrix. We will then use this method of evaluating the trace and determinant to evaluate our system of equations without explicitly calculating eigenvalues.

5. Local Asymptotic Stability

In this section, we will study the local stability of both the disease free equilibrium point and the disease endemic equilibrium point.

Theorem 5.1. *i.) If $R_0 < 1$, then the disease free equilibrium point is locally asymptotically stable. ii.) If $R_0 > 1$, then the disease free equilibrium point is unstable and the disease endemic equilbrium point is locally asymptotically stable.*

Proof:

Taking partial derivatives of i_h' and i_m' with respect to i_h and i_m, we produce the following set of equations:

$$\begin{aligned}
\frac{\partial i_h'}{\partial i_h} &= -\lambda_h - \alpha_1 i_m - \alpha_h \\
\frac{\partial i_h'}{\partial i_m} &= \alpha_1(1 - i_h) \\
\frac{\partial i_m'}{\partial i_h} &= \gamma(1 - i_m) \\
\frac{\partial i_m'}{\partial i_m} &= -\lambda_m - \gamma i_h.
\end{aligned}$$

Using partial derivatives, we produce a Jacobian matrix of the form

$$J(i_h, i_m) = \begin{bmatrix} \dfrac{\partial i_h'}{\partial i_h} & \dfrac{\partial i_h'}{\partial i_m} \\ \dfrac{\partial i_m'}{\partial i_h} & \dfrac{\partial i_m'}{\partial i_m} \end{bmatrix}.$$

Substituting with our partial derivatives, the resulting Jacobian matrix is

$$J(i_h, i_m) = \begin{bmatrix} -\lambda_h - \alpha_1 i_m - \alpha_h & \alpha_1(1 - i_h) \\ \gamma(1 - i_m) & -\lambda_m - \gamma i_h \end{bmatrix}.$$

Evaluating at our disease free equilibrium point $(0, 0)$, we obtain the Jacobian matrix

$$J(0,0) = \begin{bmatrix} -\lambda_h - \alpha_h & \alpha_1 \\ \gamma & -\lambda_m \end{bmatrix},$$

from which we obtain

$$\begin{aligned}
\det(J(0,0)) &= \lambda_m(\lambda_h + \alpha_h) - \alpha_1\gamma \\
\operatorname{tr}(J(0,0)) &= -(\lambda_m + \lambda_h + \alpha_h).
\end{aligned}$$

Our trace is always negative, so given the case that $R_0 < 1$, one sees that $\lambda_m(\lambda_h+\alpha_h) > \alpha_1\gamma$. If this is true, then our determinant is positive, making this equilibrium point locally asymptotically stable. Biologically, this means that the disease dies out.

Conversely, if $R_0 > 1$, then $\lambda_m(\lambda_h + \alpha_h) < \alpha_1\gamma$. This would cause our determinant to be negative, making the disease free equilibrium point unstable. Biologically, this means that the disease persists.

We now evaluate the Jacobian at the disease endemic equilibrium point (i_h^*, i_m^*):

$$J(i_h^*, i_m^*) = \begin{bmatrix} \dfrac{-\gamma(\alpha_1 + \lambda_h + \alpha_h)}{\lambda_m + \gamma} & \dfrac{\alpha_1(\alpha_h\gamma + \gamma\lambda_h + \alpha_h\lambda_m + \lambda_m\lambda_h)}{\gamma(\alpha_1 + \alpha_h + \lambda_h)} \\ \dfrac{\gamma\lambda_m(\alpha_1 + \alpha_h + \lambda_h)}{\alpha_1(\lambda_m + \gamma)} & \dfrac{-\alpha_1(\lambda_m + \gamma)}{\alpha_1 + \alpha_h + \lambda_h} \end{bmatrix},$$

from which we obtain

$$\det(J(i_h^*, i_m^*)) = \gamma\alpha_1 - \lambda_m(\alpha_h + \lambda_h)$$
$$\operatorname{tr}(J(i_h^*, i_m^*)) = -\left(\frac{\gamma(\alpha_1 + \lambda_h + \alpha_h)}{\lambda_m + \gamma} + \frac{\alpha_1(\lambda_m + \gamma)}{\alpha_1 + \alpha_h + \lambda_h}\right).$$

Again, our trace is always negative, so given the case that $R_0 > 1$, one sees that $\lambda_m(\lambda_h+\alpha_h) < \alpha_1\gamma$. If this is true, then our determinant is positive, making this equilibrium point locally asymptotically stable. Biologically, this means that the disease persists.

Conversely, if $R_0 < 1$, then $\lambda_m(\lambda_h + \alpha_h) > \alpha_1\gamma$. This would cause our determinant to be negative, making the disease free equilibrium point unstable. Biologically, this means that the disease dies out.

Given that R_0 satisfies the conditions set forth in Theorem 5.1, we can conclude that R_0 is the basic reproduction number.

□

6. Global Asymptotic Stability

If all solutions of a system that start out near an equilibrium point stay near the equilibrium point forever, then that point is considered globally asymptotically stable. In this section, we shall study the global stability properties of our disease free equilibrium point (0, 0) using Lyapunov's second method for stability.

Theorem 6.1. *Lyapunov Stability*

Let x^* be an equilibrium point for $x' = F(x)$, where $F(x)$ is a system of differential equations. Let $L : U \to \mathbb{R}$ be a continuous function defined on an open set U containing x^*. Suppose further that

(1) $L(x^*) = 0$ and $L(x) > 0$ if $x \neq x^*$

(2) $\dfrac{dL}{dt} < 0$ in $U \setminus x^*$

then x^* is globally asymptotically stable.

Theorem 6.2. *If $R_0 < 1$, then $(i_h, i_m) = (0, 0)$ is globally asymptotically stable.*

Proof:

First, let $\Omega = \{(i_h, i_m) \in \mathbb{R}^2_+ : 0 \leq i_h \leq 1, 0 \leq i_m \leq 1\}$ be all possible values of i_h and i_m. Define the *Lyapunov function* $L : \Omega \to \mathbb{R}$ by

$$L(i_h, i_m) = \gamma i_h + (\lambda_h + \alpha_h) i_m$$

We can see that $L(i_h, i_m) = 0$ at our disease free equilibrium point, $(0, 0)$, and for all $(i_h, i_m) \in \Omega \backslash (0, 0)$, we see that $L(i_h, i_m) > 0$. Therefore, condition (1) of Lyapunov stability is satisfied. Taking the total derivative of $L(i_h, i_m)$, we see

$$\frac{dL}{dt} = \frac{\partial L}{\partial i_h}\frac{di_h}{dt} + \frac{\partial L}{\partial i_m}\frac{di_m}{dt}.$$

Taking the partial derivatives of L and substituting in i_h' and i_m' gives

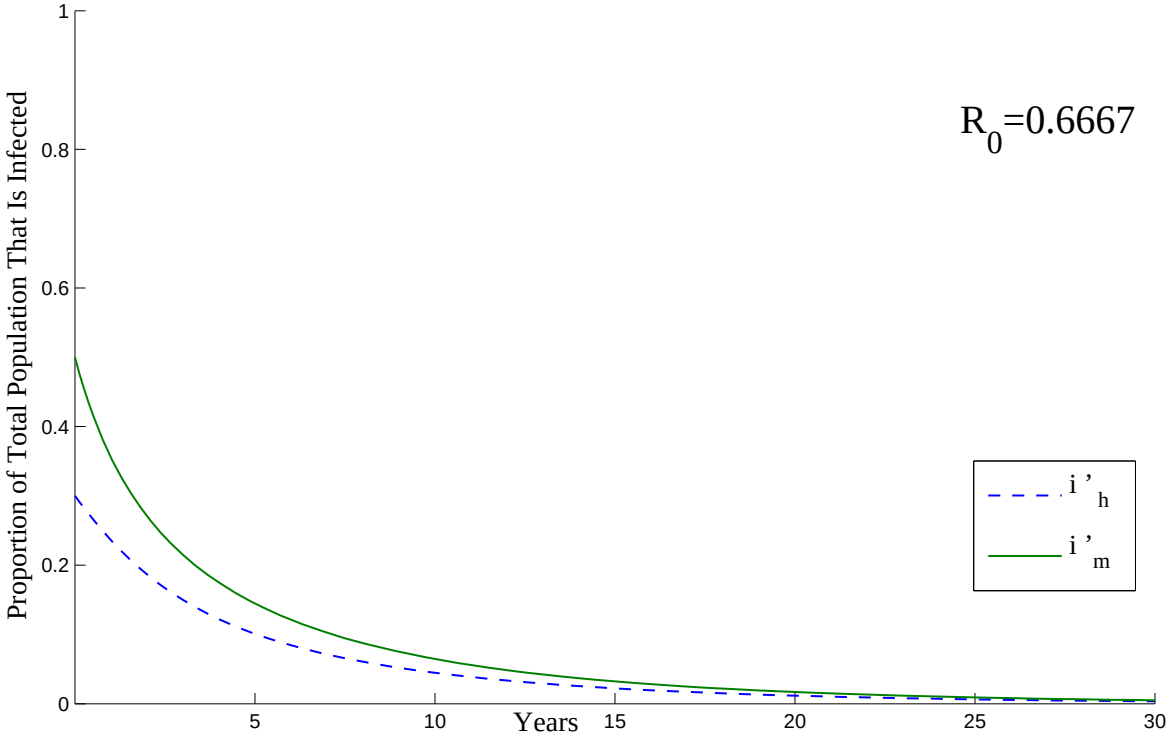
$$\begin{aligned} \frac{dL}{dt} &= \gamma\left[(\alpha_1 - i_h) - (\lambda_h + \alpha_h) i_h\right] - (\lambda_h + \alpha_h)(-\lambda_m i_m + \gamma i_h (1 - i_m)) \\ &= -[\lambda_m(\lambda_h + \alpha_h) - \alpha_1\gamma] i_m - \alpha_1 \gamma i_h i_m - \gamma(\lambda_h + \alpha_h) i_h i_m. \end{aligned}$$

Since $R_0 < 1$ implies that $\lambda_m(\alpha_h + \lambda_h) > \alpha_1\gamma$, it is evident that $\dfrac{dL}{dt} < 0$ in $\Omega \setminus (0, 0)$, so we may conclude that (0, 0) is globally asymptotically stable when $R_0 < 1$.

□

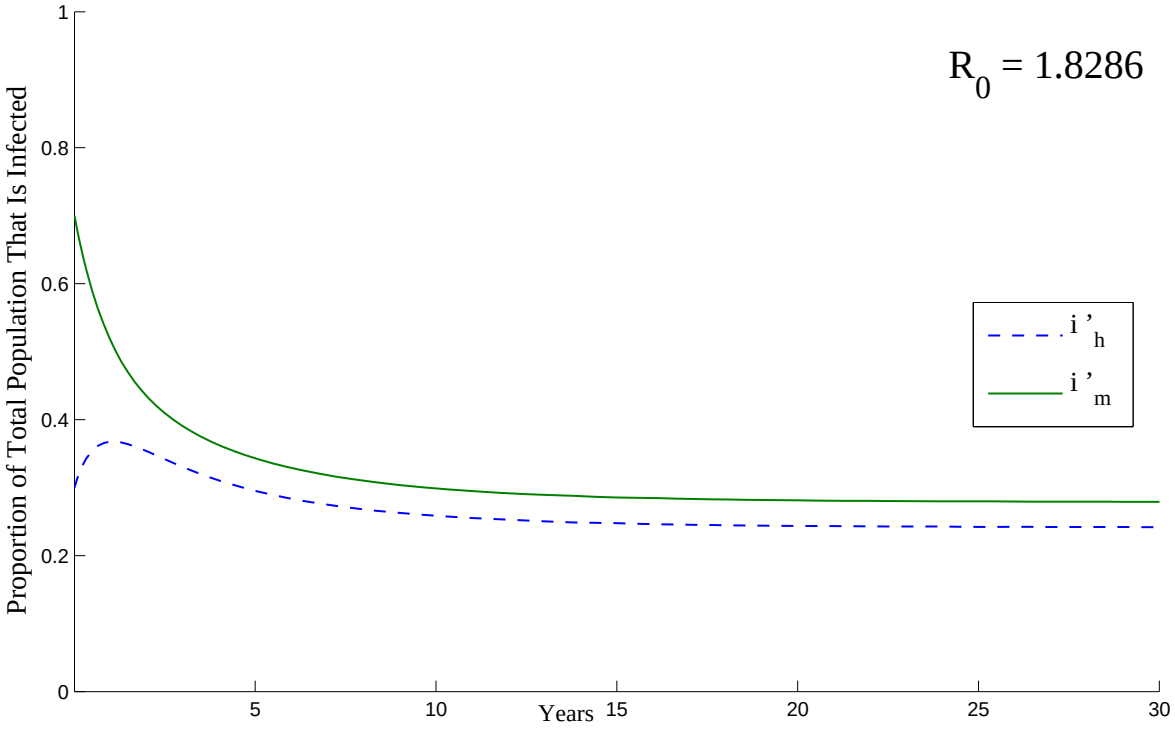
7. Application of Theoretical Findings

Based on our theoretical findings, we can predict realistic conditions under which the disease will either persist or go extinct. To illustrate this point, we will now provide graphical representations of our results for both the cases in which $R_0 < 1$ and $R_0 > 1$.



Parameter Values	
λ_h	0.4
λ_m	0.6
α_1	0.4
γ	0.7
α_h	0.3

This figure shows that over the time span of 30 years, when $R_0 < 1$ the solutions converge to the disease free equilibrium point, $(i_h, i_m) = (0, 0)$, and the disease goes extinct.



Parameter Values	
λ_h	0.4
λ_m	0.5
α_1	0.8
γ	0.9
α_h	0.3

Conversely, we note from this figure that over the same time span, when $R_0 > 1$ the solutions converge to the disease endemic equilibrium point, $(i_h, i_m) = (i_h^*, i_m^*)$, and the disease will persist.

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