Three Basic Epidemiological Models

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February 28, 2023

Introduction

- An epidemiological modeling is a simplified means of describing the transmission of communicable disease through individuals.
- These simplest models are formulated as initial value problems for system of ordinary differential equation are formulated mathematically.
- Parameter are estimated for various diseases and are used to compare the vaccination levels necessary for herd immunity for these disease.
- The study of disease occurrence is called epidemiology. An epidemic is an unusually large, short term outbreak of a disease. A disease is called endemic if it persists in a population.

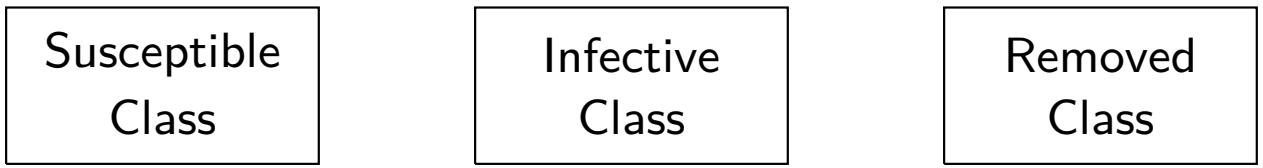
Why do Epidemiologic Modeling?

- The transmission interactions in a population are very complex so that it is difficult to comprehend the large scale dynamics of disease spread without the formal structure of mathematical model.
- An epidemiological model uses a microscopic description (The role of an infectious individual) to predict the macroscopic behavior of disease spread through a population.
- Experiments with infectious disease spread in human populations are often impossible, unethical or expensive that is why epidemiological modeling become a need.
- Modeling can often be used to compare different diseases in the same population, the same disease in different populations, or the same disease at different time.
- Epidemiological models are useful in comparing the effects of prevention or control procedures.

Assumption and Notation

Notation

- The population under consideration is divided into disjoint classes which change with time t.



- **The susceptible class** consists of those individuals who can incur the disease but are not yet infective, this fraction of population denoted as $S(t)$.
- **The infective class** consists of those who are transmitting the disease to others, this class denoted as $I(t)$.
- **The removed class** denoted by $R(t)$, consists of those who are removed from the susceptible infective interaction by recovery with immunity, isolation or death.

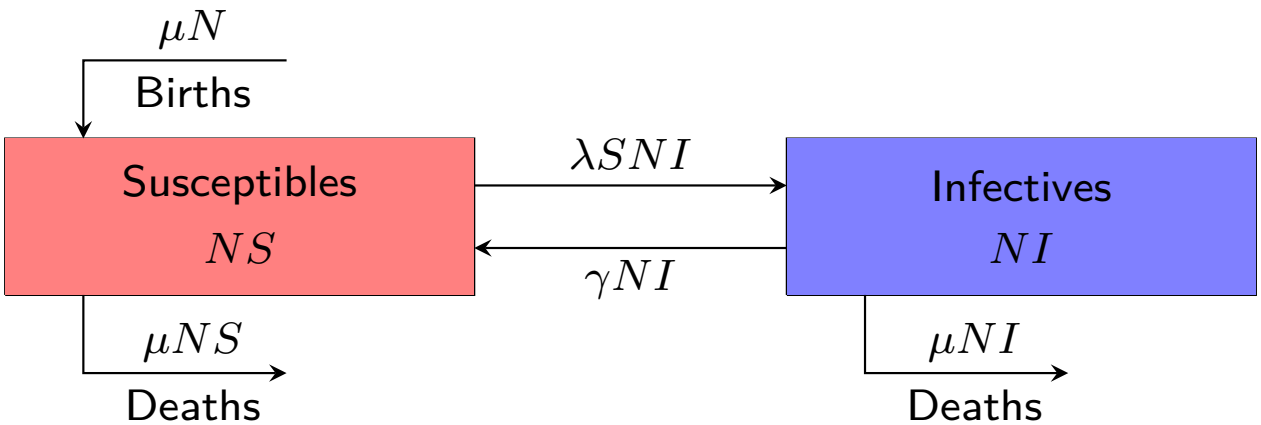
Assumption

- Let N be the population which is sufficiently large so that the sizes of each class can be considered as continuous variable.
- Let proportionality constant μ is the daily death removal rate.
- This corresponds to a negative exponential age structure with an average lifetime of $\frac{1}{\mu}$.
- Let λ is the average no. of adequate contacts per infective per day.
- The average no. of susceptible infected by an infective per day is λS.
- the average number of susceptible infected by the infective class with size NI per day in λSNI which is called the incidence.
- Let proportionality constant γ is the daily recovery removal rate.
- The average period of infectivity is $\frac{1}{\gamma}$.
- The removal rate from the infective class by both recovery and death is $\gamma + \mu$ so that the death-adjusted average period of infectivity is $\frac{1}{\gamma+\mu}$.
- The average number of adequate contacts of an infective during the infectious period is $\sigma = \frac{\lambda}{\gamma+\mu}$.
- Since the average number of susceptibles infected by an infective during the infectious period is σS which is called the replacement number.

The SIS Model

The first model is for diseases for which infection does not confer immunity. It is called an **SIS model** since individuals return to the susceptible class when they recover from the infection.

The compartmental diagram for the SIS model.



The initial value problem (IVP) for this SIS model formulated in terms of class size is

$$N\frac{dS}{dt} = -\lambda SNI + \gamma NI + \mu N - \mu NS$$
$$N\frac{dI}{dt} = \lambda SNI - \gamma NI - \mu NI$$
$$NS(0) = NS_0 > 0, \quad NI(0) = NI_0 > 0, \quad NS(t) + NI(t) = N$$

where λ is a positive constant and primes denote derivatives w.r.t time t. If each equations is divided by N then the IVP is

$$\frac{dS}{dt} = -\lambda SI + \gamma I + \mu - \mu S$$
$$\frac{dI}{dt} = \lambda SI - \gamma I - \mu I$$
$$S(0) = S_0 > 0, \quad I(0) = I_0 > 0, \quad S(t) + I(t) = 1.$$

Since $S(t) + I(t) = 1$ implies $S(t) = 1 - I(t)$
Then $\frac{dI}{dt} = [\lambda - (\gamma + \mu)]\, I - \lambda I^2, \quad I(0) = I_0 > 0.$

The given differential equation is a Bernoulli differential equation, which can be transformed into a linear differential equation by the substitution: Let $J(t) = \frac{1}{I(t)}$. Then, we have

$$\begin{aligned}\frac{dJ}{dt} &= -\frac{1}{I^2(t)} \times \frac{dI}{dt} \\ &= -\frac{1}{I^2(t)} \left[\lambda - (\gamma + \mu)\right] I(t) + \frac{1}{I^2(t)} \lambda I^2(t) \\ &= -\left[\lambda - (\gamma + \mu)\right] J(t) + \lambda.\end{aligned}$$

To solve this linear differential equation, we can use an integrating factor. Let $\mu(t) = e^{-[\lambda-(\gamma+\mu)]t}$. Then, multiplying both sides of the equation by $\mu(t)$, we get

$$\mu(t)\frac{dJ}{dt} + \left[\lambda - (\gamma + \mu)\right] \mu(t) J(t) = \lambda \mu(t).$$

Recognizing the left-hand side as the product rule of $(\mu(t)J(t))'$, we can integrate both sides to obtain

$$\mu(t)J(t) = \int \lambda \mu(t) dt + C,$$

where C is a constant of integration.

Solving for $J(t)$, we get

$$J(t) = \frac{\int \lambda\mu(t)dt + C}{\mu(t)}.$$

Substituting back $I(t) = \frac{1}{J(t)}$ and using the initial condition $I(0) = I_0$, we have

$$I(t) = \frac{I_0 e^{[\lambda-(\gamma+\mu)]t}}{1 + \frac{I_0}{\lambda}(e^{[\lambda-(\gamma+\mu)]t} - 1)}.$$

Therefore, the solution to the given differential equation is

$$I(t) = \frac{I_0 e^{[\lambda-(\gamma+\mu)]t}}{1 + \frac{I_0}{\lambda}(e^{[\lambda-(\gamma+\mu)]t} - 1)}.$$

Since $\sigma = \frac{\lambda}{\gamma+\mu}$, substitute in $I(t)$
We get

$$I(t) = \begin{cases} \frac{e^{(\gamma+\mu)(\sigma-1)t}}{\frac{\sigma\left[e^{(\gamma+\mu)(\sigma-1)t}-1\right]}{\sigma-1} + \frac{1}{I_0}}, & \text{for} \quad \sigma \neq 1 \\ \frac{1}{\lambda t + \frac{1}{I_0}}, & \text{for} \quad \sigma = 1 \end{cases} \tag{1}$$

If taking $\lim_{t\to\infty} I(t)$, then we get

- $1 - \frac{1}{\sigma}$ if $\sigma > 1$
- 0 if $\sigma \leq 1$.

They means that for a disease without immunity with any positive initial infective fraction, the infective fraction approaches a constant endemic value if the contact number exceeds 1; otherwise, the disease dies out. Although the model (4.2) reduces to a one dimensional IVP (4.3), we show SI phase diagrams for this model in Fig. 2 so that they can be compared with the phase diagrams for the other models.

The SIR Model Without Vital Dynamics

If the individual recovers with permanent immunity, then the model is called **SIR** model. It is appropriate for viral agent such as measles, small pox, mumps. When such an SIR disease goes through a population in a relatively short time (less than one year), then this disease outbreak is called an **epidemic**.

The compartmental diagram for the SIR model without vital dynamics.

Since an epidemic occurs relatively quickly, the model does not include births and deaths (vital dynamics).
The initial value problem (VIP) for the SIR model without vital dynamics given is

$$N\frac{dS}{dt} = -\lambda SNI$$
$$N\frac{dI}{dt} = \lambda SNI - \gamma NI$$
$$N\frac{dR}{dt} = \gamma NI$$
$$N = NS(t) + NI(t) + NR(t)$$

$$NS(0) = NS_0 > 0, \quad NI(0) = NI_0, \quad NR(0) = NR_0 \geq 0$$

where λ and γ are positive constants. If each equation in (2) in divided by N, then the IVP is

$$\frac{dS}{dt} = -\lambda SI, \quad \frac{dI}{dt} = \lambda SI - \gamma I, \quad \frac{dR}{dt} = \gamma I \quad (1.1)$$

The epidemiological reasonable region in the SI plane is the triangle given by

$$T = \{(S, I) | S \geq 0,\ I \geq 0,\ S + I \leq 1\}.$$

Theorem

Let $(S(t), I(t))$ *be the solutions of* (1.1).

- *If* $\sigma S_0 \leq 1$, *then* $I(t)$ *decreases to* 0 *as* $t \to \infty$.
- *If* $\sigma S_0 > 1$, *then* $I(t)$ *first increases up to a maximum value*

$$I_{max} = 1 - R_0 - \frac{1}{\sigma} - \frac{\ln(\sigma S_0)}{\sigma}$$

and then decreases to 0 *as* $t \to \infty$.

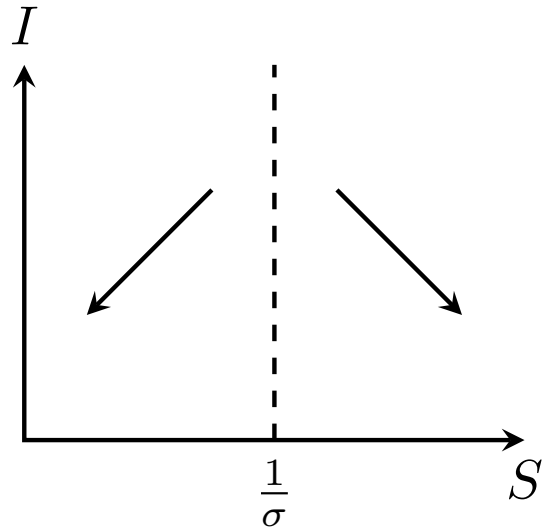
The susceptible fraction $S(t)$ *is a decreasing function and the limiting value* $S(\infty)$ *is the unique root in* $\left(0, \frac{1}{\sigma}\right)$ *of the equation*

$$1 - R_0 - S(\infty) + \frac{\ln\left(\frac{S(\infty)}{S_0}\right)}{\sigma} = 0.$$

Proof: Observe $\frac{dI}{dt} = I(\lambda S - \gamma)$

- If $\frac{dI}{dt} \leq 0$ then $I(\lambda S - \gamma) \leq 0$ or $S \leq \frac{\gamma}{\lambda} \leq \frac{1}{\sigma}$ or $\sigma S \leq 1$.
- If $\frac{dI}{dt} > 0$ then $I(\lambda S - \gamma) > 0$ or $S > \frac{\gamma}{\lambda} > \frac{1}{\sigma}$ or $\sigma S > 1$.

Diagram showing direction in the phase plane for the epidemic model.



From above diagram, we can conclude :

- If $\sigma S_0 \leq 1$, then $I(t)$ decreases to 0 as $t \to \infty$.
- If $\sigma S_0 > 1$, then $I(t)$ first increases and then decreases to 0 as $t \to \infty$.

We have $\frac{dS}{dt} = -\lambda SI$ and $\frac{dI}{dt} = \lambda SI - \gamma I$
Using chain rule,

$$\begin{aligned}\frac{dI}{dS} &= \frac{dI/dt}{dS/dt} \\ &= \frac{\lambda SI - \gamma I}{-\lambda SI} \\ &= -1 + \frac{\gamma}{\lambda S}\end{aligned}$$

Integrate both sides w.r.t S, then

$$\begin{aligned}I &= \frac{\gamma}{\lambda}\ln S - S + K \\ &= \frac{1}{\sigma}\ln S - S + K, \quad \left[\because\ \sigma = \frac{\lambda}{\gamma}\right]\end{aligned}$$

where K is an arbitrary constant.
By using initial value, we get

$$\begin{aligned}K &= I_0 + S_0 - \frac{1}{\sigma}\ln S_0 \\ &= 1 - R_0 - \frac{1}{\sigma}\ln S_0\end{aligned}$$

Finally, the solution is

$$I = \frac{1}{\sigma}\ln S - S + 1 - R_0 - \frac{1}{\sigma}\ln S_0$$

Now, we can determine the maximum point as follows

$$\frac{dI}{dS} = -1\frac{\gamma}{\lambda S} = 0$$

$$S = \frac{\gamma}{\lambda}$$

$$S = \frac{1}{\sigma}$$

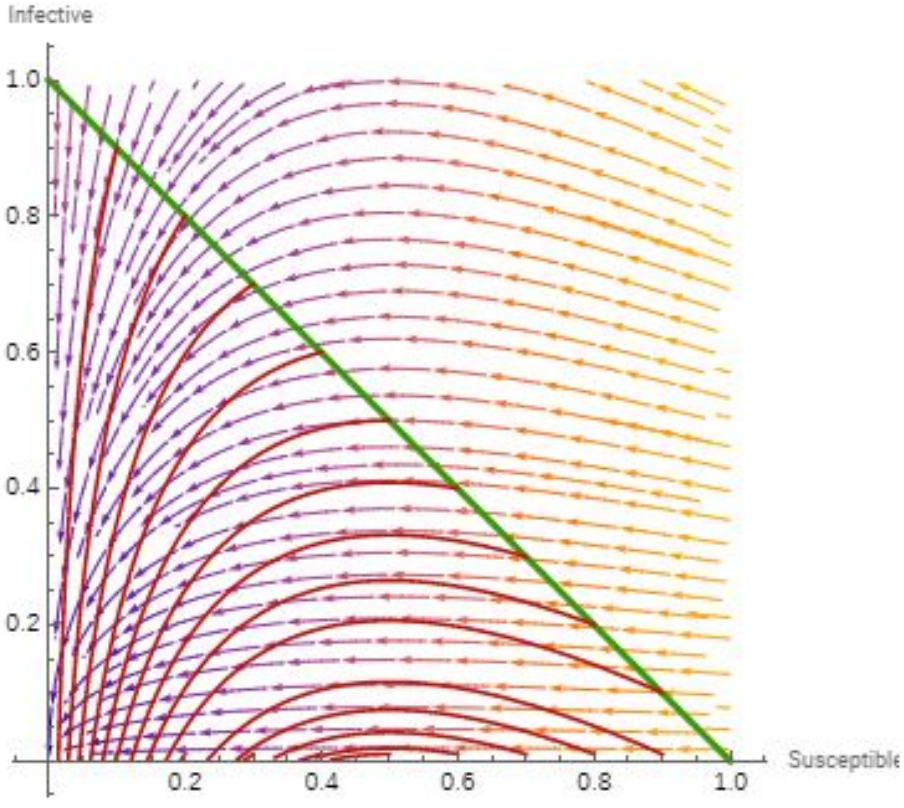
On the hand, the second derivative of I w.r.t S at $\frac{1}{\sigma}$ is

$$\frac{d^2I}{dS^2} = -\frac{1}{\sigma S^2} < 0$$

Hence, a maximum occurs at $S = \frac{1}{\sigma}$.
The maximum value is

$$I_{max} = \frac{1}{\sigma}\ln\left(\frac{1}{\sigma}\right) - \frac{1}{\sigma} + 1 - R_0 - \frac{1}{\sigma}\ln S_0$$

$$= 1 - R_0 - \frac{1}{\sigma} - \frac{1}{\sigma}\ln(\sigma S_0)$$

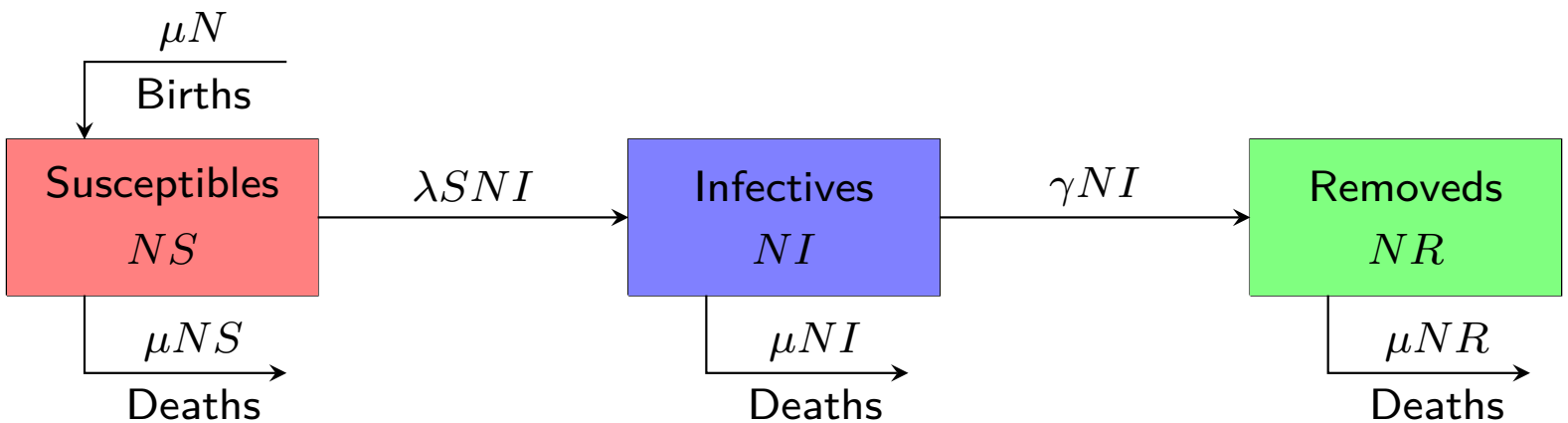


Phase diagram for the SIR model without vital dynamics.

The SIR Model with Vital Dynamics

If individuals recover with permanent immunity, then the model is an SIR model. But we model the disease behavior in the population over a long time period. A disease is called endemic if it is present in a population for more than 10 or 20 years. Because of the long time period involved, a model for an endemic disease must include births as a source of new susceptibles and natural deaths in each class.

The compartmental for the SIR model with vital dynamics.

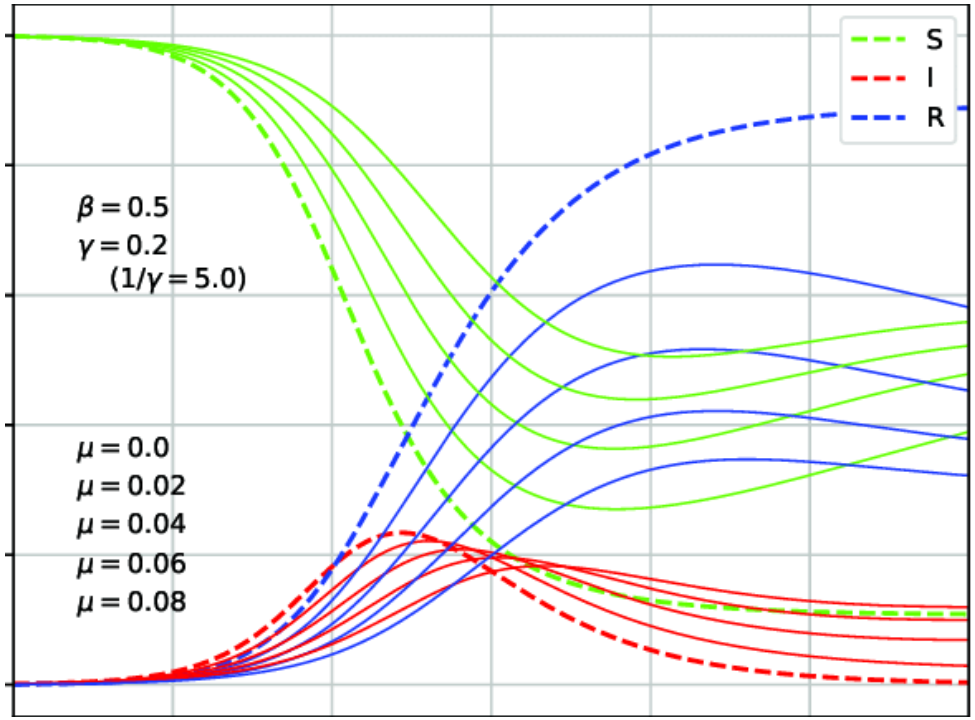


The initial value problem for SIR model with vital dynamics is :

$$\begin{aligned} N\frac{dS}{dt} &= -\lambda SNI + \mu N - \mu NS \\ N\frac{dI}{dt} &= \lambda SNI - \gamma NI - \mu NI \\ N\frac{dR}{dt} &= \gamma NI - \mu NR \\ N &= NS(t) + NI(t) + NR(t) \\ NS(0) = NS_0 > 0, &\quad NI(0) = NI_0 \geq 0, \quad NR(0) = NR_0 \geq 0. \end{aligned}$$

where the contact rate λ, the removal rate constant γ and the death rate constant μ are positive constants.
If each equation is divided by N, then the IVP is

$$\frac{dS}{dt} = -\lambda SI + \mu - \mu S, \quad \frac{dI}{dt} = \lambda SI - \gamma I - \mu I, \quad \frac{dR}{dt} = \gamma I - \mu R \qquad (1.1)$$



The solution of the SIR model with vital dynamics. The parameter μ is varied as $0.0, 0.02, 0.04, 0.06$, and 0.08, and the data of $\mu = 0.0$ are shown by thick dashed curves.

Equilibrium Points

Equilibrium points correspond to solutions of a coupled system of differential equations where the solutions are constant.

Theorem

- *If* $\sigma \leq 1$, *then the triangle* T *is an asymptotic stability region for the equilibrium point* $(1, 0)$.
- *If* $\sigma > 1$, *then* $T - \{(S, 0) | 0 \leq S \leq 1\}$ *is an asymptotic stability region for the equilibrium point*

$$\left(\frac{1}{\sigma}, \frac{\mu(\sigma - 1)}{\lambda} \right).$$

To prove this theorem, we first need to define some terms and concepts:

- An equilibrium point of a dynamical system is a state where the system remains constant over time.
- Asymptotic stability is a property of an equilibrium point in a dynamical system where any initial state that is sufficiently close to the equilibrium point will converge to the equilibrium point over time.
- The triangle T is defined as the set of all points (x, y) in the (x, y)-plane that satisfy $0 \leq x \leq 1$, $0 \leq y \leq \sigma(1 - x)$.

Now we can proceed to the proof of the theorem:
Case 1: $\sigma \leq 1$
In this case, the equilibrium point $(1, 0)$ lies within the triangle T.
To show that $(1, 0)$ is asymptotically stable, we need to show that any initial state (x_0, y_0) that is sufficiently close to $(1, 0)$ will converge to $(1, 0)$ over time.
Let $\epsilon > 0$ be given, and consider any initial state (x_0, y_0) that satisfies $\sqrt{(x_0 - 1)^2 + y_0^2} < \epsilon$. We need to show that the trajectory starting from (x_0, y_0) will converge to $(1, 0)$ over time.

The system of differential equations that describes the dynamics of this system is given by:

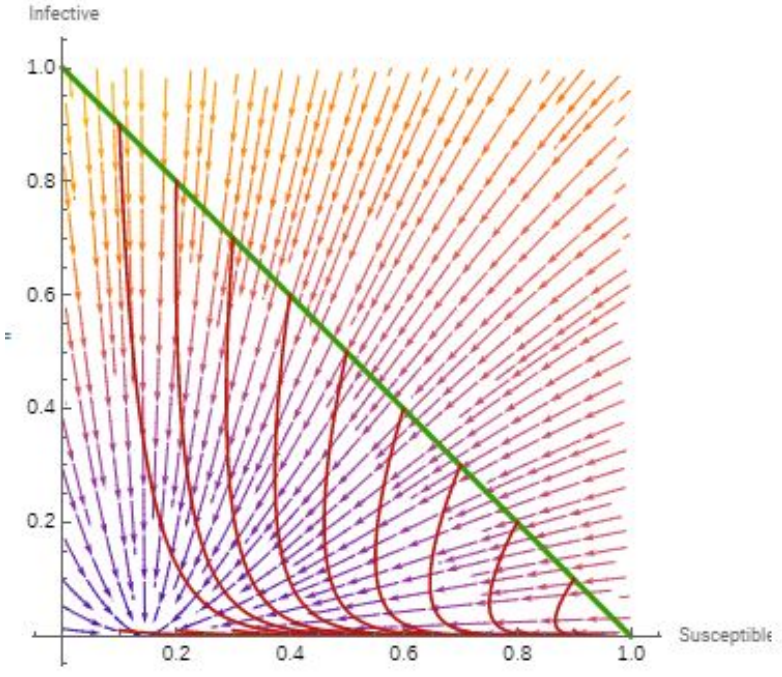
$$\dot{x} = \lambda x(1-x) - \mu xy$$
$$\dot{y} = \lambda y(\sigma - y/x).$$

To analyze the behavior of this system near $(1,0)$, we linearize the system by computing the Jacobian matrix evaluated at $(1,0)$:
The eigenvalues of $J(1,0)$ are λ and $\lambda\sigma$, which are both negative since $\lambda > 0$ and $\sigma \leq 1$. Therefore, the linearized system near $(1,0)$ is asymptotically stable, and by the Hartman-Grobman theorem, the nonlinear system near $(1,0)$ is also asymptotically stable.
Since any initial state (x_0, y_0) that is sufficiently close to $(1,0)$ will converge to $(1,0)$ over time, we have shown that $(1,0)$ is asymptotically stable within the triangle T when $\sigma \leq 1$.

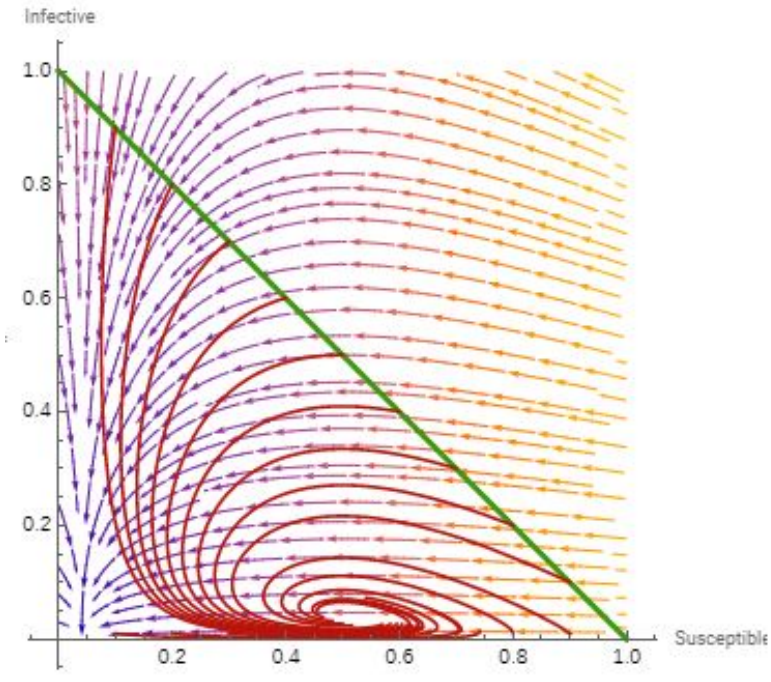
Case 2: $\sigma > 1$
In this case, the equilibrium point $(1, 0)$ lies outside the triangle T. To find the asymptotic stability region for the equilibrium point

$$P = \left(\frac{1}{\sigma}, \frac{\mu(\sigma - 1)}{\lambda} \right),$$

we need to identify the set of initial states that converge to P over time. Let $R = T - (S, 0) | 0 \leq S \leq 1$ be the region obtained by removing the x-axis from T. The boundary of R consists of three line segments: the segment from $(0, 0)$ to $(1, 0)$, the segment from $(1, 0)$ to $(1, \sigma - 1)$, and the segment from $(1, \sigma - 1)$ to $(0, \sigma)$.
To show that R is an asymptotic



Phase plane portrait for SIR model with vital dynamics when the contact number is $\sigma = 0.5 < 1$. From Hethcote (1976).



Phase plan portrait for SIR model with vital dynamics when the contact number is $\sigma = 2 > 1$. From Hethcore (1976).

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Moreover, I would like to thank my supervisor **Songheng ORN** for providing me guidance and feedback throughout this project work.

THANK YOU FOR YOUR PAYING ATTENTION !

Q & A !