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Modeling infectious diseases in mixed household structures

Master Thesis
Mathematical Modeling Of Complex Systems

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Declaration of authorship

I herewith confirm that I alone have authored this thesis, that I did not use any resources other than those I have cited - in particular, no online sources not listed in the bibliography section - and that I have not previously submitted this thesis in association with any other examination procedure.

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Abstract

We studied SIS model of infectious disease in single household of size two. For this we introduced master equation and studied the transition of household state with focus on the influence of infection and recovery parameters. We performed a simulation using Runge-Kutta method to observe the influence of these parameters. The steady state observed in the simulation was further investigated by Linearization around equlibrium points which showed the existence of disease-free equilibrium and endemic equilibrium. Notably, our observations indicated that an increase in infection parameters lead to endemic equilibrium and an increase in recovery parameter leads disease-free equilibrium.

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1 Introduction

Throughout historical recorded event, the abrupt emergence of infectious diseases have been concerning for human population[13]. The regions where diseases occur might gradually decrease possibly due to immunity or development of vaccine but also might become endemic due to possible lack of health care facilities [12]. Epidemiological studies deals with the occurrence of epidemic diseases, its spread and control[13]. And, the goal of epidemiologists is to take the intial step by collecting the data of disease movement, observing the key events, analyzing the cause and predicting with realistic approach should become the ultimate goal in controlling it [12].

Brauer [12] credits public health physicians for using mathematical models such as compartmental models to understand the spread of infection. He also mention that the core idea of mathematical epidemiology of basic reproduction number was introduced by Dr.Ross for understanding dynamics of disease specially for malaria. Kermack and Mckendrick also formulated epidemic model where they established a threshold value for which an outbreak can be considered epidemic if it exceeded that value[16].

Mathematical modeling has become an integral part of understanding mechanisms and behaviour in epidemiology. In other words, mathematical models are valuable tools for estimating strategies to understand the transmission of infectious diseases. It is a comprehensive abstraction represented by the formulation of equations to estimate an event. The model's premise about variables and parameters may help in estimating the epidemic. Mathematical modeling is a useful tool to simulate and analyze events which help us reach conclusion. [16].

For applied mathematicians, the main question in disease models would be to solve solutions analytically and its qualitative behavior. And concerning question for mathematical epidemiologists would be about circumstances and persistence of a disease. Another concern for epidemic modelers would be investigation of models behavior at equilibrium on given initial conditions.[22]. The analytical approach to equilibrium begins with finding constant solutions [12]. Disease-free equilibrium and endemic equilibrium were studied in [15] using SIR Model by local stability of the equilibrium points and the basic reproduction number. Dadlani [13] also investigated disease-free equilibrium and endemic equilibrium with different models, including the SIS model with linear stability and re-

production number.

It is often observed and compared that the transmission rate of an infection is higher within a household which affects a small number of individuals to outside household which affects higher number of individuals. Wide-ranging studies of infectious disease model has been based on household-structured model. This study of discrepencies in household-structured of population has helped in understanding the pattern of diseases transmission to advise possible control policies and intervention strategies like household-based vaccination strategies for influenza and treatment of infected individual and their contacts for yaws[17].

A typical method for aligning a household model with data is to assume that the system is in a state of steady equilibrium. Followed by establishing a connection between the external force of infection and infections occurring in other households[17]. Limitations of household state in SIA model in finite number household size lead [17] to use SIS model in their studies with different numbers of household of same size using master equation. In thesis we also use master equation based on SIS model to analyze equilibria for household of size two.

The structure of this thesis unfolds in Chapter 2, where we present a section on the general derivation of master equation, its SIS dynamics within a single household approximation and analyzing solutions in terms of equilibrium. Chapter 3 delves into initial conditions through numerical simulations and analyze equilibria. In Chapter 4, we discuss the outcomes of Chapter 3 offering a comparative analysis of results and its limitations and suggestion for future research and Chapter 5 we concludes our thesis.

2 Model and Method

A model is a portray of events in simple structure to obtain the crucial fundamental characteristic factor of the system and to explain its noticeable phenomena. Based on biological nature of infection and demography in population there is transmission dynamic model and static model. Transmission dynamic model depends on prevalence of infection which changes with time as a function whereas static model is independent of time. In deterministic model, the average life of an infection whose course of infection is based on same predefined model of parameters and initial condtions while stochastic model is random processes. The state of disease with similar characteristic in an individual is considered in homogenous population and with different characteristic is consdidered in heterogenous popluation [20].

Kessler [18] compares two models susceptible-infected-susceptible (SIS) with susceptible-infected-recovered (SIR). In his comparision,reinfection to a recovered individual is allowed but in SIR model reinfection is not allowed. Similarity is shown in the case of SIS and SIR model when the infection level of diseases is below threshold value and infection dies out for both models. On the contrast outcome might be different for both model when infection level is above threshold value. While in the SIS model the number of susceptible individuals may increase, the number of susceptible individuals in the SIR model can only decrease.

In this chapter we derive general master equation for a single household (SHH) with view of SIS Model. The transmission of an infectious disease is viewed from its phenomenological derivation with concept of SHH approximation in equation (4) of [17].

2.1 Derivation of Master Equations for the Single Household Model(SHH)

In this section, we will apply idea of SIS model in single household structure with different sizes in population. An introduction to parameters influencing single household size SHH are given below with description.

Table 2.1: Defination of parameters

Parameter	Description
ϵ	External Infection Rate in which *individual* gets infected from an external source outside household and brings infection inside household
$\mathbf{T_p}$	Total individual in population
$\mathbf{N}$	Overall Number of Individuals in Household
β	The Internal Infection Rate in which an *individual* gets infected from an internal source inside household
γ	Recovery Rate in which a susceptible *individual* recovers

Dependence of External Infection Rate on the Probability Distribution

It is plausible that the external infection rate ϵ is not constant, but rather depends on the rate of infected people in the population. We may thus *assume* that epsilon is a linear function of the infection rate $\frac{I}{T_p}$, say $\epsilon = \tilde{\alpha}\frac{I}{T_p}$ with a suitable proportional factor $\tilde{\alpha}$.
However, in the SHH Model, in general we do not have the explicit number of infected people (I). Instead, we have expectation values for this number, so in what follows, we have to base the definition of external infection for our model on these expectation values.

Let P_k denote the probability that in a given household we have k infected individals. As the different households are indistinguishable, we can assume that the probability distribution $(P_0, P_1, ..., P_N)$ is the same in each household, and based on this assumption of homogeneous distributions we may approximate the number of infected people in each individual household (say $\mathbb{E}I_H$) by its expectation: $\mathbb{E}I_H = \sum_{k=0}^{N} k * P_k$.

The expectation value for the number of infected individuals in a given household by definition is $\mathbb{E}I_H = \sum_{k=0}^{N} k * P_k$.
Denoting ad-hoc the number of households in the model with M_H, the expectation for the overall number of infected people in the population becomes $M_H * \mathbb{E}I_H$, while the overall number of people in the population T_p can be written as $M_H * N$.
Thus, we get an approximation $\frac{I}{T_p} \approx \frac{M_H * \mathbb{E}I_H}{M_H * N} = \frac{\mathbb{E}I_H}{N} = \frac{1}{N}\sum_{k=0}^{N} kP_k$

Introducing the α Parameter

These considerations lead to assuming that there is a proportional factor α linking the external infection rate ϵ to the expectation value of infected individuals in a household:

For the external infection rate ϵ In the SHH-N Model we have

$$\epsilon = \frac{\alpha}{N}\mathbb{E}I_H = \frac{\alpha}{N}\sum_{k=0}^{N} kP_k$$

with a suitable parameter alpha.

Master Equations for the General SHH Case

We begin analyizing SIS dynamics in SHH with referring to set of master equations from equation (4) from [17]. For a system that can take on a finite number of states $S_0, .., S_N$, let P_k and P_l be the probabilities of the system in state k and state l. We then have the general form of the Master equations[4]:

$$\frac{dP_k}{dt} = \sum_{l \neq k}(T_{lk}P_l - T_{kl}P_k) \tag{2.1}$$

Where the T_{lk} is the transition probabilty for a state change from S_l to S_k and T_{kl} is the transition probabilty for a state change from S_k to S_l. In the case of a single household model where the state S_k means we have exactly k infected and $N - k$ susceptible individuals of the household, the master equations becomes more simple, as state transitions can appear from S_k to S_{k+1} or from S_{k+1} to S_k and also state transitions can appear from S_k to S_{k-1} or from S_{k-1} to S_k. The general form of the master equations can be written as:

$$\frac{dP_k}{dt} = T_{(k-1)k}P_{k-1} - T_{k(k-1)}P_k + T_{(k+1)k}P_{k+1} - T_{k(k+1)}P_k \tag{2.2}$$

Where the $T_{(k-1)k}$, $T_{k(k-1)}$, $T_{(k+1)k}$, $T_{k(k+1)}$ are the transition probabilties for a state change from S_{k-1} to S_k or S_k to S_{k-1} and S_{k+1} to S_k or from S_k to S_{k+1}. From here on, also the convention is taken that when dealing with households of size N, $P_k = 0$ if $k < 0$ and $N > k$ is adopted. For derivation of single household equation which we will use on indicator function[3]. Below shows the diagram of state transition in SHH

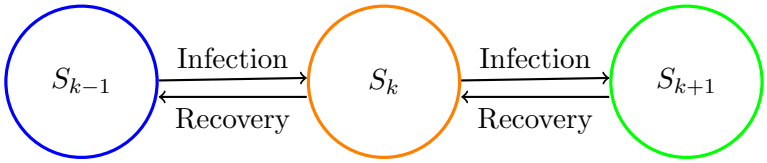


Figure 2.1: SHH diagram for state transition

The state transition of figure 2.1 is described in each positive and negative contribution. Postive contribution means number of individuals enter the state and negative contribution means exit the state. For our convenience we use term contribution. Contribution occurs when state transitions happens by external infection rate ϵ, internal infection rate β and recovery rate γ. Positive contribution means number of individuals enter the state and negative contribution means exit the state. A detailed explanation is given below:

Positive Contributions for $\frac{dP_k}{dt}$

We now investigate on the summands adding positively to $\frac{dP_k}{dt}$:

Positive Contribution from Infection, $T_{(k-1)k}P_{k-1}$

This case corresponds to the transition $S_{k-1} \to S_k$ between $k-1$ infected and $N-(k-1)$ susceptible individuals in the household, where one of them gets infected. There may be two different ways that this can happen:

Positive Contribution from External Infection : In positive contribution from external infection, one of the susceptible individuals in the household gets infected from outside. This can happen for state transition $S_{k-1} \to S_k$ for all $k \in \{1, 2, ..N\}$ at a rate of ϵ to any of the $N-(k-1)$ susceptible individuals in the household at the previous stage S_{k-1}. So the positive contribution of the external infection is:

$$\epsilon(N-(k-1))P_{k-1} \quad \text{for} \quad k \in \{1, 2, ..N\}$$

Positive Contribution from Internal Infection : Within household, one of the susceptible individual gets infected from inside. Obviously, this cannot happen at state transition $S_0 \to S_1$, as there is no one in the household to infect a susceptible at state S_0. For state transition $S_{k-1} \to S_k$ for all $k \in \{2, ..N\}$ at a rate of β to any of the N-(k-1) susceptible individuals in the household at the previous stage. So the positive contribution of the

external infection is:

$$\beta(N-(k-1))P_{k-1} \quad \text{for} \quad k \in \{2,..N\}$$

Positive Contribution from Recovery, $T_{(k+1)k}P_{k+1}$

In this case, one of the infected individuals in the household recovers. Obviously, this cannot happen at state transition $S_{k+1} \to S_k$, as there may not be more than N infected individuals in an Household. For state transition $S_{k+1} \to S_k$ for all $k \in \{0,..N-1\}$ to any of the $(k+1)$ infected individuals in the household at the previous stage at a rate of γ. So the positive contribution of recovery is:

$$\gamma(k+1)P_{k+1} \quad \text{for} \quad k \in \{0,..N-1\}$$

Negative Contributions

We now investigate the summands on adding negatively to $\frac{dP_k}{dt}$:

Negative Contribution from Infection, $T_{k(k+1)}P_k$

This corresponds to the transition $S_k \to S_{k+1}$, that is, while we have k infected and $N-k$ susceptible individuals in the household, one of them gets infected. There may be two different ways that this can happen:

Negative Contribution From External Infection One of the susceptible individuals in the household gets infected from outside. This can happen for state transition $S_k \to S_{k+1}$ for all $k \in \{0,..,N-1\}$ to any of the $N-k$ susceptible Individuals at a rate of ϵ So the negative contribution of the external infection is :

$$\epsilon(N-(k))P_k \quad \text{for} \quad k \in \{0,..,N-1\}$$

Negative Contribution From Internal Infection One of the susceptible individuals in the household gets infected from inside. Obviously, that cannot happen for $k \in \{0,N\}$ as for S_0 there is no one in the household to get infected from, and it also cannot happen for S_N, as there is nobody left to be infected. For state transition $S_k \to S_{k+1}$ for all $k \in \{1,..,,N-1\}$ to any of the $N-k$ susceptible individuals at a rate of β. So the

negative contribution of the external infection is:

$$\beta(N-k)P_k \text{ for } k \in \{1,..,,N-1\}$$

Negative Contribution from recovery, $T_{(k(k-1))}P_k$

One of the infected individuals in the household recovers. So this can happen for state transition $S_k \to S_{k+1}$ for all $k \in \{1,..N\}$
to any of the k infected individuals in the household at stage S_k with rate γ So the negative contribution of recovery is:

$$\gamma(k)P_k \text{ for } k \in \{1,..N\}$$

General Master Equation

To write down the Master Equation in a uniform way, we use "indicator functions":
For $j \in \mathbb{Z}$, we define the indicator functions :

$$X_{\{\leq i\}}(j) = \begin{cases} 1 \text{ for } j \leq i \\ 0 \text{ for } j > i \end{cases}$$

For $j \in \mathbb{Z}$, we define the indicator functions

$$X_{\{\geq i\}}(j) = \begin{cases} 0 \text{ for } j < i \\ 1 \text{ for } j \geq i \end{cases}$$

With this, the general Master Equation takes on the form:

$$\begin{aligned} \frac{dP_k}{dt} &= (X_{\{\geq 1\}}(k))\ \epsilon\ (N-(k-1))\ P_{k-1} \\ &+ (X_{\{\geq 2\}}(k))\ \beta\ (N-(k-1))\ P_{k-1} \\ &+ (X_{\{\leq N-1\}}(k))\ \gamma\ (k+1)\ P_{k+1} \\ &- (X_{\{\leq N-1\}}(k))\ \epsilon\ (N-k)P_k \\ &- (X_{\{\geq 1\}}(k))(X_{\{\leq N-1\}}(k))\ \beta\ (N-k))\ P_k \\ &- (X_{\{\geq 1\}}(k)\ \gamma\ (k)P_k \end{aligned} \tag{2.3}$$

General Master Equation for SHH

The general master equation 2.3 comprises ϵ, which is in general not known and must be assumed to depend on the number and distribution of the infected individuals in the population. However, for the special case of a single Household model (SHH) we have

found the identity $\epsilon = (\frac{\alpha}{\mathbf{N}} \sum_{k=1}^{\mathbf{N}} kP_k)$. Substituting ϵ in 2.3 with $(\frac{\alpha}{\mathbf{N}} \sum_{k=1}^{\mathbf{N}} kP_k)$ we get a version of the master equation for the SHH model, which gives us dependecy of the external infection in terms of the p_k:

$$\begin{aligned}
\frac{dP_k}{dt} &= (X_{\{\geq 1\}}(k))\ (\frac{\alpha}{\mathbf{N}} \sum_{k=1}^{\mathbf{N}} kP_k)\ (N-(k-1))\ P_{k-1} \\
&+ (X_{\{\geq 2\}}(k))\ \beta\ (N-(k-1))\ P_{k-1} \\
&+ (X_{\{\leq N-1\}}(k))\ \gamma\ (k+1)\ P_{k+1} \\
&- (X_{\{\leq N-1\}}(k))\ (\frac{\alpha}{\mathbf{N}} \sum_{k=1}^{\mathbf{N}} kP_k)\ (N-k)P_k \\
&- (X_{\{\geq 1\}}(k))(X_{\{\leq N-1\}}(k))\ \beta\ (N-k))\ P_k \\
&- (X_{\{\geq 1\}}(k)\ \gamma\ (k)P_k
\end{aligned} \tag{2.4}$$

Remark on Existence and Uniqueness of Solutions for the SHH Case

We note that with $P = (P_0, P_1, ...P_N)$ the general Master equations 2.4 are of the form $\frac{dP}{dt} = F(P)$, where $F : R^N \to R^N$ can be defined on the whole of R^N. Furthermore, the component functions f_k of F are polynominals (of at most second degree) of the P_k. Thus, the f_k are continiously differentiable, hence fulfill a local Lipshitz condition, and according to the Picard-Lindelöf therorem the system of ODEs 2.4 has a unique solution.

General Master Equation for SHH in case N=1

Setting N:=1 in equation (2.4) we get:

$\frac{dP_0}{dt}$ for SHH in case N=1

$$\frac{dP_0}{dt} = \gamma P_1 - \alpha P_1 P_0 \tag{2.5}$$

$\frac{dP_1}{dt}$ for SHH in case N=1

$$\frac{dP_1}{dt} = \alpha P_1 P_0 - \gamma P_1 \tag{2.6}$$

General Master Equation for SHH in case N=2

Setting N:=2 in equation (2.4) we get:

$$\begin{aligned}\frac{dP_k}{dt} &= (X_{\{\geq 1\}}(k))\ (\frac{\alpha}{\mathbf{2}}P_1 + \alpha P_2)\ (2-(k-1))\ P_{k-1} \\ &+ (X_{\{\geq 2\}}(k))\ \beta\ (2-(k-1))\ P_{k-1} \\ &+ (X_{\{\leq 1\}}(k))\ \gamma\ (k+1)\ P_{k+1} \\ &- (X_{\{\leq 1\}}(k))\ (\frac{\alpha}{\mathbf{2}}P_1 + \alpha P_2)\ (2-k)P_k \\ &- (X_{\{\geq 1\}}(k))(X_{\{\leq 1\}}(k))\ \beta\ (2-k))\ P_k \\ &- (X_{\{\geq 1\}}(k))\ \gamma\ (k)P_k\end{aligned} \tag{2.7}$$

$\frac{dP_0}{dt}$ for SHH in case N=2

$$\frac{dP_0}{dt} = \gamma P_1 - 2(\frac{\alpha}{\mathbf{2}}P_1 + \alpha P_2)P_0 \tag{2.8}$$

$\frac{dP_1}{dt}$ for SHH in case N=2

$$\frac{dP_1}{dt} = 2(\frac{\alpha}{\mathbf{2}}P_1 + \alpha P_2)P_0 + 2\gamma P_2 - (\frac{\alpha}{\mathbf{2}}P_1 + \alpha P_2)P_1 - \beta P_1 - \gamma P_1 \tag{2.9}$$

$\frac{dP_2}{dt}$ for SHH in case N=2

$$\frac{dP_2}{dt} = (\frac{\alpha}{\mathbf{2}}P_1 + \alpha P_2)P_1 + \beta P_1 - 2\gamma P_2 \tag{2.10}$$

2.2 Analytical Approach to Qualitative Analysis

The non-linear terms such as $P_0P_1, P_0P_2, P_1^2, P_1P_2$ in system of master equations 2.8, 2.9 and 2.10 of SHH of size two are indicators for non-linear differential equations. It is stated that equation (4) of [17] can be solved analytically to give steady states. Non-linear differential equation's explicit analytical solutions are hard to find for that we could also understand with stability analysis and by phase portraits [21]. An convenient approach used for the computation [2] of the master equations shows analytical solution at site [1] hard to interpret. System of differential equations can also be approximated by Euler method, Runge-Kutta method with computer simulation [20]. We will perform simulation in chapter 3 to understand behaviour of solution in long period of time. In chapter 3, we assume initial conditions for probability of household states P_0, P_1 and P_2 as well as three parameters between-household infection rate α, within-household infection rate β and recovery rate γ and show results for numerical approximation. We will plot flows(trajectories) by [9] and phase portraits. We will use [11] to plot normalized vectors fields and stream plot [10] with computation tool.

We also want to study infection presence and its recovery in the system in long term. For this we can also find their total infection rate and total recovered rate. With the each equilibrium solution of probability of household states reaching to steady values, we can analyze whether the state of system is disease-free or state becomes endemic.

For finding total infection rate represented as I_{Total} and total recovered rate as R_{Total}: Total infected rate in SHH size of two is understood from expectation $\mathbb{E}[I_H]$ with respect to time 't'.

$$\frac{d\mathbb{E}[I_H]}{dt} = \frac{dP_1}{dt} + 2\frac{dP_2}{dt}$$

with integration from intial time (0) to time (T) we get,

$$I_{Total} = \int_0^T \mathbb{E}[I_H(t)]\, dt \tag{2.11}$$

similarly for total recovered rate.

$$R_{Total} = \gamma I_{Total} \tag{2.12}$$

R_{Total} also represented that total number of people that got infected throughout the time got recovered.

Equilibrium

Brauer [12] describes an analytical approach to model for endemic diseases and epidemics starting with finding equilibria, which are constant solutions. With positive number of individuals being infected there can be one or more equilibria in endemic but there is a disease-free equilibrium. Further step is to linearize about each equilibrium and check its stability. We assume that the study of disease-free equilibrium and endemic equilibrium can be studied on system of equations 2.8, 2.9 and 2.10. We use abbreviated the form of disease-free equilibrium to DFE and endemic equilibrium to EE. The DFE and EE also can be describe as follows.

- DFE, $lim_{t\to\infty}(P_0(t), P_1(t), P_2(t)) = (1, 0, 0)$.
- In EE, $lim_{t\to\infty}(P_0(t), P_1(t), P_2(t)) \neq (1, 0, 0)$ (or (1,0,0) does not exist)

where t represents time. Finding equilibrium points in a system of SHH of size two and differentiating around those points gives us linearization at that point. The terms formed from linearization can be written as Jacobian Matrix which is 3 X 3 dimension in SHH of size two. Solving the characteristic equation, $|J - \lambda E| = 0$ and finding eigenvalues λ of the jacobian matrix (J) will determine stability and instability at that equilibirium point. By standard theory[23] eigenvalue λ's maximum real part of J indicates the stability, $\lambda(J) < 0$ represents stable and $\lambda(J) > 0$ represents unstable.

We follow morgan [21] and begin our notation dP_k/dt for introducing master equations, $dP_k/dt = f_k(P_k)$, where, $f_k(P_k) = (f_0(P_0), f_1(P_1), f_2(P_2))$ is function, and for all $k \in \{0, 1, 2\}$ in our SHH of size two is defined for $P_k = (P_0, P_1, P_2) \in \mathbb{R}^3$. Variables $P_0 = P_0(t), P_0 = P_1(t)$ and $P_2 = P_2(t)$ are dependent on time $t \in \mathbb{R}$. If function, f_k is differentiable and continuous defined in an interval, as stated in Theorem 1 in [21] there exists a unique solution of system of differential equations which satisfies initial condition.

In equilibrium :

$$dP_k/dt = f_k(P_k) = 0 \tag{2.13}$$

When dP_k/dt and $f_k(P_k)$ equal to zero defines the solution P_k as equilibrium solution also referred as critical point or equilibrium points. We take a critical point definition 1. from [21] of stable and unstable and restate below Let $P_k^* \in \mathbb{R}^3$ be a critical point of the form in 2.8, 2.9 and 2.10. We call P_k^* is stable if, for any $\epsilon > 0$, there is a $\delta > 0$ such that a solution $P_k = P_k(t)$ satisfies $\|P_k(0) - P_k^*\| < \delta$, then $\|P_k(t) - P_k^*\| < \epsilon$ for all $t > 0$.

Here $\|P_k\|$ denotes the Euclidean norm on $\mathbb{R}^3$, given by $\|P_k\| = \sqrt{P_0^2 + P_1^2 + P_2^2}$.

For unstable if P_k^* doesnot follow as defined above for stability.

Then we use linearization at critical points or equilibrium points to determine solution's stability.

Linearization near equilibrium point A linearization is a technique to approximate nonlinear system as similar to approximate smooth function with tangent line [21].

At equilibrium point P_k^*,

1. $f_0(P_k) = f_0(P_0^*, P_1^*, P_2^*) = 0$
2. $f_1(P_k) = f_1(P_0^*, P_1^*, P_2^*) = 0$
3. $f_2(P_k) = f_2(P_0^*, P_1^*, P_2^*) = 0$

we use linearization techniques and linearize the system in the form

This form can be written in matrix form

$$\begin{bmatrix} \frac{dP_0}{dt} \\ \frac{dP_1}{dt} \\ \frac{dP_2}{dt} \end{bmatrix} = \begin{bmatrix} \frac{\partial f_0}{\partial P_0}(P_0^*, P_1^*, P_2^*) & \frac{\partial f_0}{\partial P_1}(P_0^*, P_1^*, P_2^*) & \frac{\partial f_0}{\partial P_2}(P_0^*, P_1^*, P_2^*) \\ \frac{\partial f_1}{\partial P_0}(P_0^*, P_1^*, P_2^*) & \frac{\partial f_1}{\partial P_1}(P_0^*, P_1^*, P_2^*) & \frac{\partial f_1}{\partial P_2}(P_0^*, P_1^*, P_2^*) \\ \frac{\partial f_2}{\partial P_0}(P_0^*, P_1^*, P_2^*) & \frac{\partial f_2}{\partial P_1}(P_0^*, P_1^*, P_2^*) & \frac{\partial f_2}{\partial P_2}(P_0^*, P_1^*, P_2^*) \end{bmatrix} \begin{bmatrix} (P_0 - P_0^*) \\ (P_1 - P_1^*) \\ (P_2 - P_2^*) \end{bmatrix}$$

The jacobian matrix(J) is ,

$$\begin{bmatrix} \frac{\partial f_0}{\partial P_0}(P_0^*, P_1^*, P_2^*) & \frac{\partial f_0}{\partial P_1}(P_0^*, P_1^*, P_2^*) & \frac{\partial f_0}{\partial P_2}(P_0^*, P_1^*, P_2^*) \\ \frac{\partial f_1}{\partial P_0}(P_0^*, P_1^*, P_2^*) & \frac{\partial f_1}{\partial P_1}(P_0^*, P_1^*, P_2^*) & \frac{\partial f_2}{\partial P_2}(P_0^*, P_1^*, P_2^*) \\ \frac{\partial f_2}{\partial P_0}(P_0^*, P_1^*, P_2^*) & \frac{\partial f_1}{\partial P_1}(P_0^*, P_1^*, P_2^*) & \frac{\partial f_2}{\partial P_2}(P_0^*, P_1^*, P_2^*) \end{bmatrix}$$

Disease-Free Equilibrium

In DFE, all individuals are susceptible. We find stability of system at equilibrium points (P_0^*, P_1^*, P_2^*) by Linearization. The valid equlibrium point is (1,0,0) where all the individuals are not infected. At equilibrium point $(P_0, P_1, P_2) = (P_0^*, P_1^*, P_2^*) = (1, 0, 0)$ using master equations 2.8, 2.9 and 2.10. Jacobian Matrix(J) at $(1, 0, 0)$ is shown below.

$$\begin{pmatrix} 0 & -\alpha+\gamma & -2\,\alpha \\ 0 & \alpha-\beta-\gamma & 2\,\alpha+2\,\gamma \\ 0 & \beta & -2\,\gamma \end{pmatrix} \tag{2.14}$$

The characteristic equation of the form is $|J-\lambda E|=0$, where J is 3 X 3 Jacobian matrix 2.14 and 'E' is 3 X 3 identity matrix and λ is 3 x 1 eigenvalues and in our thesis we deal with real eigenvalues. We find three eigenvalues, a zero eigenvalue does add information to our stability analysis therefore we looked at the other two eigenvalues to analyze stability. The submatrix which resulted into quadratic form with two eigenvalues is discussed as follows.

$$\begin{pmatrix} \alpha-\beta-\gamma & 2\,\alpha+2\,\gamma \\ \beta & -2\,\gamma \end{pmatrix} \tag{2.15}$$

We find the eigenvalues of the 2.15 as follows

$$\begin{aligned} \lambda_i &= \frac{Tr-\sqrt{Tr^2-4D}}{2} \\ \lambda_{ii} &= \frac{Tr+\sqrt{Tr^2-4D}}{2} \end{aligned} \tag{2.16}$$

Let A be 2 X 2 square matrix of form written in

$$\begin{pmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{pmatrix} \tag{2.17}$$

Where $Tr=a_{11}+a_{12}$ called as trace and $D=a_{11}a_{22}-a_{12}a_{21}$ called as determinant.

Trace(Tr) and Determinant(D) :
We compare 2.15 with 2.17 and write Tr as

$$Tr=\alpha-\beta-3\gamma \tag{2.18}$$

And also we compare 2.15 with 2.17 and write D as

$$D=2(\gamma^2-\alpha(\beta+\gamma)) \tag{2.19}$$

We find eigenvalues of 2.16 by replacing Tr in 2.18 and D in 2.19. Each output of elements in 2.15 is determined by parameter values between-household infection rate α, within-household infection rate β, and recovery rate γ. We can now evaluate variables/parameters analytically by infection rates and recovery rates. The calculation of two negative eigenvalues in 2.16, $\lambda_i<0$ and $\lambda_{ii}<0$ will show stability at equilibrium point. And any eigenvalue resulting positive will show instability at equilbrium point. We discuss further more about the parameters analytically and its interpretation.

Analysis of Eigenvalues For DFE In order to determine the stable and unstable regions in DFE, we use different cases in finding eigenvalues in equation 2.16. The stability and unstability regions can be determined from Tr , D and $\sqrt{Tr^2 - 4D}$ in . If eigenvalues calculated from 2.16 are negative would result into stability showing DFE and positve eigenvalues will result into instability. Based on Tr , D and $\sqrt{Tr^2 - 4D}$, in 2.16 we explain the following different cases.

case i : $Tr < 0$ **and** $Tr > \sqrt{Tr^2 - 4D}$: In this case both eigenvalues will show negative eigenvalues. Within this case , for $Tr > \sqrt{Tr^2 - 4D}$:

- if $D > 0$ and $Tr^2 > 4D$, then λ_i and λ_{ii} will have negative values which shows stability in DFE. For example, this would be applicable to $Tr < 0$, $\alpha < \beta + 3\gamma$ and $D > 0$, $\alpha < \frac{\gamma^2}{\beta+\gamma}$. In both Tr and D, α depends on β and γ where higher value in γ will decide the regions to be stable from the term $\alpha < \frac{\gamma^2}{\beta+\gamma}$ in D. This could mean that in high recovery rate , the system reaches to disease-free equilibrium.

- if $D < 0$, this will does not add information in our study. Here α will be higher is $D < 0$. At higher between-household infection rate system will not reach to disease-free equilibrium.

- if $-4D > Tr^2$, then it will lead to complex eigenvalues so we limit our studies to real number.

case ii : $Tr < 0$ **and** $Tr < \sqrt{Tr^2 - 4D}$:

- if $Tr < 0$ and $Tr < \sqrt{Tr^2 - 4D}$, $Tr^2 > 4D$ then an eigenvalue will be either both positive or another eigenvalue will be negative will lead to unstable in DFE.

- if $Tr^2 < 4D$, $D > 0$ then it will lead to complex pair of eigenvalue.

case iii : $Tr > 0$ **and** $Tr > \sqrt{Tr^2 - 4D}$: When $Tr > 0$ and $Tr > \sqrt{Tr^2 - 4D}$ will lead to unstable of which atleast one eigenvalue will be positive and lead to unstable in DFE. This will be because of higher α than β and γ.

case iv : $Tr > 0$ **and** $Tr < \sqrt{Tr^2 - 4D}$:

- if $Tr > 0$ and $Tr < \sqrt{Tr^2 - 4D}$, then negative output of $Tr^2 - 4D$ will create complex pair of eigenvalues.

- if output is positive $\sqrt{Tr^2 - 4D}$ and greater than Tr then it will lead to atleast one postive eigenvalue which shows instable in DFE.

Endemic equilibrium

For studying endemic equilibrium, we consider that probability of household states are in term $(P_0, P_1, P_2) \neq (1, 0, 0)$. For finding endemic equilibrium point, we set right hand side of master equations 2.8, 2.9 and 2.10 equal to zero.

Equilibrium point in endemic equilibrium The equilibria found at state P_k of $(P_0, P_1, P_2) = (P_0^*, P_1^*, P_2^*)$ are endemic which means the disease is always present in this system.
The rate of change of total probability of household states is equal to zero, in 2.13 integrating gives the form $P_0 + P_1 + P_2 = C$.
Since, the total probability of household states is always '1',
We write following approach in probability of household states P_2:

$$P_2 = 1 - P_1 - P_0 \tag{2.20}$$

At equilibirum condition, when k = 0 in equation 2.13 and 2.8,

$$\begin{aligned} \frac{dP_0}{dt} &= -\alpha(P_1 + 2P_2)P_0 + \gamma P_1 = f(P_0) = 0 \\ \text{or, } \alpha(P_1 + 2P_2)P_0 &= \gamma P_1 \end{aligned} \tag{2.21}$$

Similarly when k = 1 at equilibrium condition, in equation 2.13 and 2.9 we write

$$\begin{aligned} \frac{dP_1}{dt} &= f(P_1) = 0 \\ \text{or } \alpha(P_1 + 2P_2)P_0 - (\frac{\alpha}{2}(P_1 + 2P_2) + \beta + \gamma)P_1 + 2\gamma P_1 &= f(P_1) = 0 \end{aligned} \tag{2.22}$$

Then we solve 2.20 and 2.21, to get P_1 and P_0

$$P_1 = \frac{2\alpha P_0(1 - P_0)}{(\gamma + \alpha P_0)} \tag{2.23}$$

With equilibrium condition, when k = 2 at 2.13 and equation 2.10 we write,

$$\alpha(P_1 + 2P_2)P_0 + 2\gamma P_2 = (\frac{\alpha}{2}(P_1 + 2P_2) + \beta + \gamma)P_1 \tag{2.24}$$

Then solving equation 2.24 by substituting the equations of 2.20 and 2.23. We get quadratic equation.

$$\alpha^2\beta P_0^2 + \alpha\gamma(\alpha + \beta)P_0 - \gamma^3 = 0 \tag{2.25}$$

After solving 2.25, we only take the positive root or solution which is

$$P_0 = \frac{\gamma}{2\alpha\beta}(-(\alpha + \beta) + \sqrt{(\alpha + \beta)^2 + 4\beta\gamma}) \tag{2.26}$$

Analysis of endemic equilibrium solution The solution of P_0 in 2.26, P_1 in 2.23 and P_2 in 2.26 gives steady state solutions or equilibrium point or equilibrium solution of endemic equilibrium. We consider increasing one parameter and the other two parameter are kept fixed thus our calculation shows influence by one parameter and easier to analyze based on one parameter. The increase of recovery rate γ, in the term $\frac{\gamma}{2\alpha\beta}$ of the equation 2.26, will increase the value of P_0. However, while increase in infection rate α and β will obviously decrease the P_0 values. In the term $-(\alpha+\beta)+\sqrt{(\alpha+\beta)^2+4\beta\gamma}$ in P_0 , $+4\beta\gamma$ could influence the value of P_0 as $-(\alpha+\beta)$ and $\sqrt{(\alpha+\beta)^2}$ have similar terms. The value of P_0 will have direct affect on P_1 in equation 2.23 because of the term P_0 in P_1. In equation 2.23, increase in α might increase the value of P_1 due to decrease in P_0 value and increase in γ might decrease value of P_1. In equation 2.20,P_2 rely on value of P_1 and value of P_0. With this obviously, the low values of P_0 and P_1 will increase value of P_2.

The linearization around endemic equilibirium points (P_0, P_1, P_2) from 2.26,2.23 and 2.20 will result in the form 2.27 and which helps in determine the stability. The condition for the system in endemic equilibrium to be stable is if all of its eigenvalues at equilibrium points are negative and resulting in any positive eigenvalue is consider unstable.
jacobian at endemic equilibrium point (P_0, P_1, P_2) or $(P_0, P_1, 1-P_0-P_1)$

$$\begin{pmatrix} -\alpha(2-2P_0-P_1) & -\alpha P_0+\gamma & -2\,\alpha P_0 \\ \alpha(2-2P_0-P_1) & P_0(1+\alpha)-1-\beta-\gamma & 2\,\alpha P_0-\alpha P_1+2\,\gamma \\ 0 & \alpha(1-P_0)+\beta & \alpha P_1-2\,\gamma \end{pmatrix} \tag{2.27}$$

3 Simulation and Results

3.1 Numerical Method with Example

We take a numerical approach in order to understand the behaviour of SIS dynamics in SHH of size two by setting up initial conditions as shown in table 3.1

Table 3.1: Initial conditions of SHH of size two

Name	Number	Fraction
Total population	1200	1
Total households	600	1
Probability of household state (P_0)	588	0.98
Probability of household state (P_1)	12	0.02
Probability of household state (P_2)	0	0

At timestep t,P_0 is $P_0(t)$,P_1 is $P_1(t)$ and P_2 is $P_2(t)$,
At intial timestep t = 0, P_0 is $P_0(0) = 0.98$, P_0 is $P_1(0) = 0.02$ and P_2 is $P_2(0) = 0$,
For understanding numerical approach, we perform simulation in python to plot trajectories of probabilities of household states with respect to time. We use scipy, numpy and matplotlib to solve the initial value problem of master equations 2.8,2.9 and 2.10. From scipy, *solve_ivp* is used to implement functional integration method which uses Runge-Kutta method. Generally RK45[9] is used as default method which also cites [14] and states that the error is controlled assuming accuracy of the fourth-order method, but steps are taken using the fifth-order. Another library 'numpy' is used for setting up items in array [6] and timestep [7] estimation. The other library matplotlib [5] is used for plotting figures.

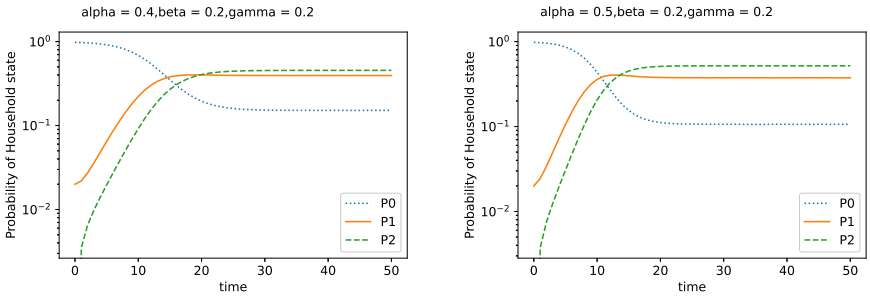
In following sections we will discuss three parameters which influence the probabilities of household states P_0, P_1 and P_2. Three parameters are between-household infection rate (α), within-household infection rate (β) and household recovery rate (γ). Initial conditions from table 3.1 and numerical values estimated parameters are substituted in the master equations 2.8, 2.9 and 2.10 and simulation is performed in long time till it reaches to equilibrium or steady values. The parameter's numerical values for SHH ap-

proximation is estimated from paper [17] as an initial and final range but with regular spaced(0.2,0.3,0.4,0.5,0.6,0.7,0.8).

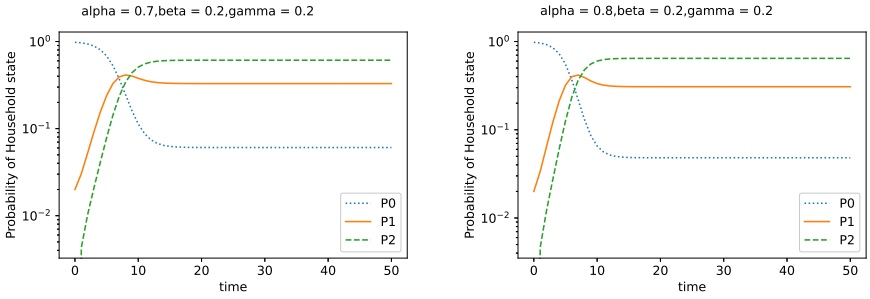
For our simulation, we assume that the disease is influenza where recovered individual becomes susceptible after infection. For example, we choose recovery rate as 0.2 which means the average time for an infected individual to recover is 5 days. Also, we assume between-household infection rate is 0.4 meaning it takes 3 days that an individual gets infected in household from outside. Similarly we assume within-household infection rate is 0.2 which means it takes 5 days for an infected individual to infect another susceptible individual inside an household. The other considered rates such as 0.3 is assumed to be 4 days and rates beyond 0.5 till 0.8 are considered to be less than 2 days.

Influence of between-household infection rate on Master Equation

In this section, we discuss about probability of household states P_0, P_1 and P_2 with varying α values while fixing γ and β at constant values. We observe the influence on the probablities in the figures below.



(a) $\alpha = 0.4, \beta = 0.2, \gamma = 0.2$ (b) $\alpha = 0.5, \beta = 0.2, \gamma = 0.2$



(c) $\alpha = 0.7, \beta = 0.2, \gamma = 0.2$ (d) $\alpha = 0.8, \beta = 0.2, \gamma = 0.2$

Figure 3.1: 'Probability of Household state' on $y-axis$ vs 'time' on $x-axis$ with varying α

At figure 3.1 y-axis is represented by probability of household state with logarithmic scaling values and x-axis by timestep (or days) is shown to observe movement of household states. We use notation 'P0' for P_0 by dotted (..) line, 'P1' for P_1 with connected line (-) and 'P2' by P_2 with dash line $(--)$ to represent them. In figure 3.1a P_0 decreases with change with time, whereas P_1 increases with change with time and state P_2 also shows increament with time. All four graphs at 3.1 shows similar trajectories that after relative period of time all three probability of household states become steady.

In figures: 3.1, parameters β and γ are kept fixed at 0.2 rate while α is varied at figure (a) with 0.4, figure (b) with 0.5, figure (c) with 0.7 and figure (d) with 0.8 rates to observe distinct influence of trajectories. We observed that the trajectory of P_0 decreases with time as rate α gradually increases before reaching to steady state. Similarly the trajectories of P_1 and P_2 gradually increases with time when α rate is increased gradually and forms crossover regions before reaching to steady state or equilbrium state. It is also observed that the time taken by the probability of household states to cross over each other happens in shorter duration time of gradual increase in α parameter.

Steady values The steady values is also studied by generating a text file from simulation. The values of each probability of household states and total infection rate 2.11 in each time step are recorded. We take output values of probability of household states aligned with total infection rate. This allignment will be considered as steady state value when approximated value defined as in 3.1. The total infection rate is calculated using 2.11. We use notation $P_{k_{t_i}}$ to represent the probability of household states $k \in \{0, 1, 2\}$ values in time step 't_i' where $i \in \{0, 1...\infty\}$. Equation shown below 3.1 defines the criteria to take the values.

$$|P_{k_{t_{i+1}}} - P_{k_{t_i}}| < 10^{-3} \tag{3.1}$$

where $P_{k_{t_{i+1}}}$ is probability of household state values at timestep t_{i+1} after one step further reaching the steady values and $P_{k_{t_i}}$ is the probability of household state values at time step t_i where we reach steady state values. For example in table 3.2 the values of all probabilities in household is approximately similar at $\alpha = 0.4$ to 35th timestep. And for total infection rate 3.2 we use criteria as follows

$$|I_{Total_{t_{i+1}}} - I_{Total_{t_i}}| < 10^{-3} \tag{3.2}$$

where $I_{Total_{t_{i+1}}}$ is total infection rate at time step t_{i+1} after one step further reaching the steady values and $I_{Total_{t_i}}$ is the total infection rate at time step t_i where we reach steady state values. Total infection rate 2.11 and total recovery rate 2.12 values with varying α are shown below in 3.2

Table 3.2: Total infection rate, Total recovered rate and time step taken by probabilities of household state to reach steady states with varying α

Name	$\alpha = 0.4$	$\alpha = 0.5$	$\alpha = 0.6$	$\alpha = 0.7$	$\alpha = 0.8$
Total infection rate (I_{Total})	(1.290)	(1.402)	(1.482)	(1.543)	(1.592)
Total recovered rate (R_{Total})	(0.258)	(0.280)	(0.296)	(0.308)	(0.318)
Total Timestep	(35)	(28)	(26)	(23)	(19)

We notice in table 3.2 that total infection rate and total recovered rate increases when α rate gradually increases while time taken to reach steady state decreases. After calculating total infection rate values we will show results of probability of household states distribution in table 3.3.

Table 3.3: Simulation : Probability of household state values with varying α

Probabilities of household states	$\alpha = 0.4$	$\alpha = 0.5$	$\alpha = 0.6$	$\alpha = 0.7$	$\alpha = 0.8$
P_0	0.151	0.106	0.078	0.060	0.048
P_1	0.394	0.375	0.351	0.328	0.307
P_2	0.453	0.518	0.569	0.610	0.644

We observed that the steady state values from 3.3 in P_0 decreases from 0.151 till 0.048 with increased α rates. Similarly the values of P_1 also decreases from 0.394 till 0.307 gradually in similar trend but P_2 values increases from 0.453 to 0.644 with gradual increase in α rate. We use graph 3.2 below to show probabilities of household states values with varying rates of α in table 3.3.

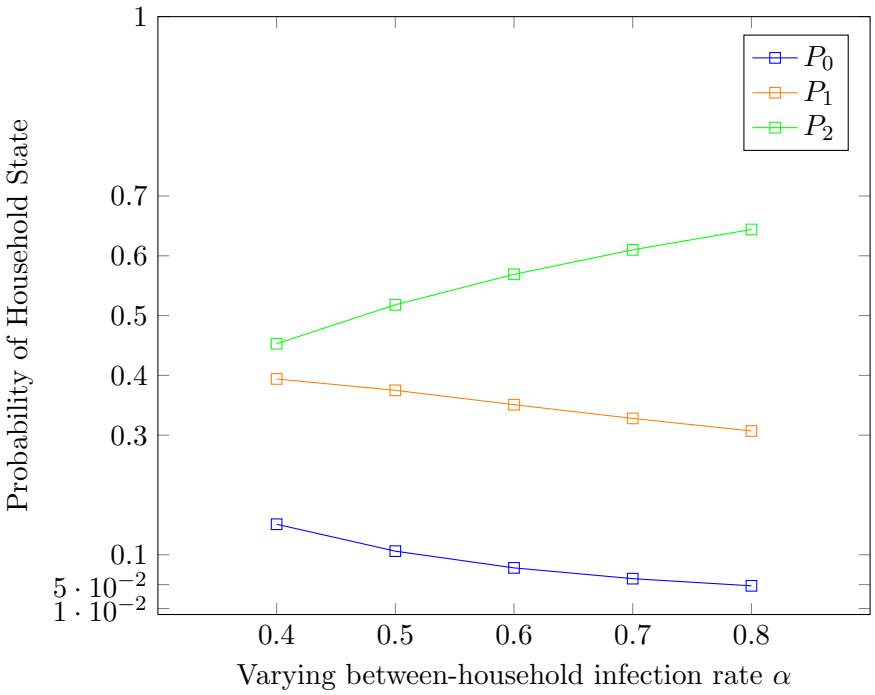
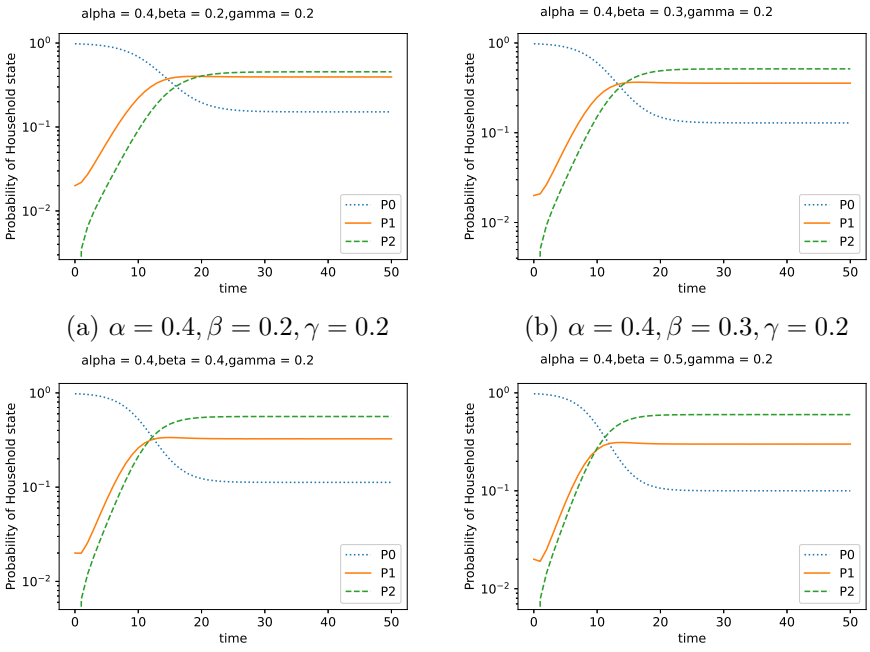


Figure 3.2: 'Probability of Household State' on $x - axis$ vs 'Varying between-household infection rate α' on $y - axis$

In figure 3.2 the values of P_0 and P_1 decreases with gradual increase in between-household infection rate α while value of 'P_2' decreases.

Influence of within-household infection rate on Master Equation

In this section, we show figures of β's influence in Master Equations in figure :3.3 and figure 3.4. We will also show two tables of steady state values of total infection rate in table : 3.4 and probability of household states in table : 3.5 of β's influence in Master Equation.



(a) $\alpha = 0.4, \beta = 0.2, \gamma = 0.2$ (b) $\alpha = 0.4, \beta = 0.3, \gamma = 0.2$

(c) $\alpha = 0.4, \beta = 0.4, \gamma = 0.2$ (d) $\alpha = 0.4, \beta = 0.5, \gamma = 0.2$

Figure 3.3: "Probability of Household state' on $y-axis$ vs 'time' on $x-axis$ with varying β

We plot figures 3.3 to observe within-household infection rate β influence on Master equations and vary it at figure (a) with 0.2, figure (b) with 0.3, figure (c) with 0.4, figure (d) with 0.5 while fixing α constant at 0.4 and γ constant at 0.2. We observed that all probability of household states reaches to steady states. In addition, we observe that gradually increasing β in figures 3.3 shows the path of trajectories decreases in P_0 but increases in P_1 and P_2 before eventually reaching to steady paths.
The table shown below is steady values of the total infection rate and total recovery rate and their timestep to reach steady state are shown in 3.4.

Table 3.4: Total infection rate, Total recovered rate and time step taken by probabilities of household state to reach steady states varying β

Name	$\beta = 0.2$	$\beta = 0.3$	$\beta = 0.4$	$\beta = 0.5$
Total infection rate (I_{Total})	(1.290)	(1.375)	(1.441)	(1.493)
Total recovered rate (R_{Total})	(0.258)	(0.275)	(0.288)	(0.298)
Timestep	(35)	(31)	(30)	(27)

In table : 3.4 we observe that both total infection rate and total recoverd rate increases in values when the value of β is gradually increased and the time duration taken by household

states to reach steady state values gradually decreases. We show below probability of Household state values varying beta:

Table 3.5: Simulation : Probability of household state values with varying β

Probability of HouseHold state	$\beta = 0.2$	$\beta = 0.3$	$\beta = 0.4$	$\beta = 0.5$
P_0	0.151	0.128	0.112	0.100
P_1	0.394	0.356	0.325	0.299
P_2	0.453	0.514	0.561	0.599

We observe from the table 3.5 influence of gradual increase in β decreases the steady state values of P_0 and P_1 but P_2 values in steady states gets increased. We show the figure 3.4.

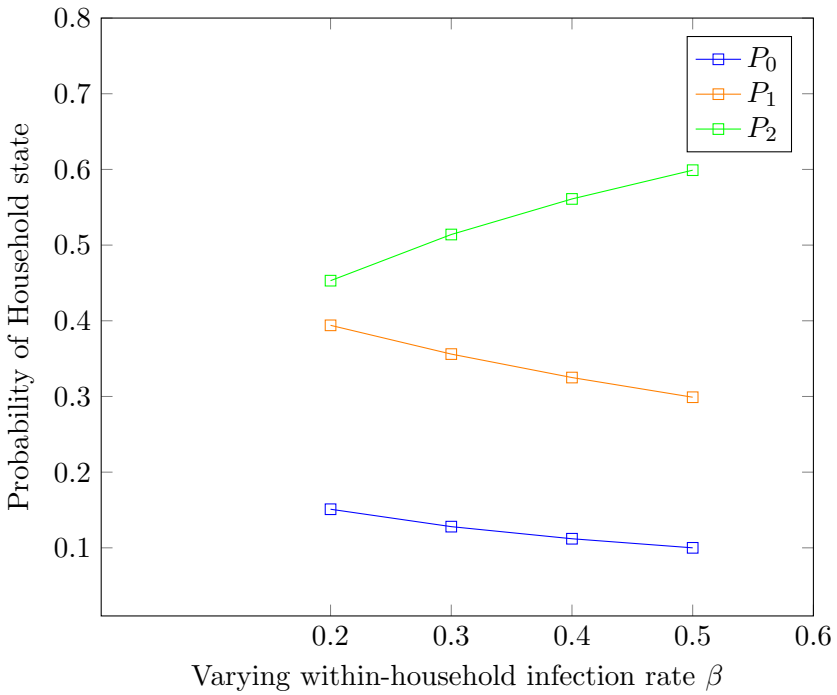
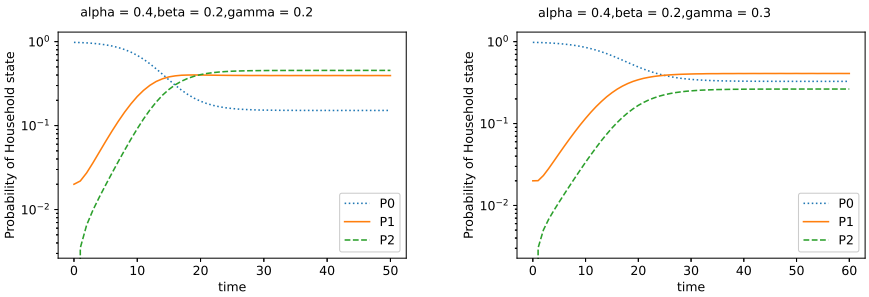


Figure 3.4: 'Probability of Household State' on $x - axis$ vs 'Varying within-household infection rate β' on $y - axis$

In figure 3.4 it is clearly seen that P_1 and P_0 decreases with gradual increase in β but P_2 increases.

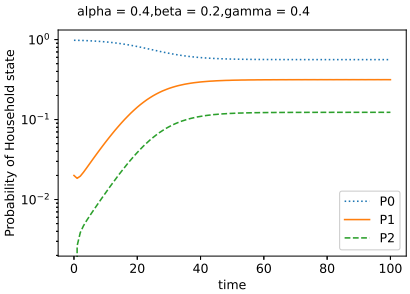
Influence of household recovery rate on Master Equation

In previous sections we discussed about gradual change in α and β on master equation now we will observe at the recovery parameter γ's influence on master equation in this section.

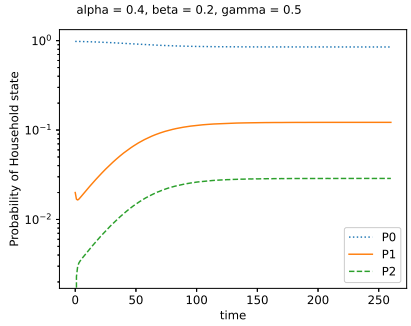


(a) $\alpha = 0.4, \beta = 0.2, \gamma = 0.2$

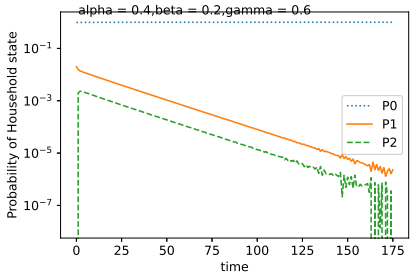
(b) $\alpha = 0.4, \beta = 0.2, \gamma = 0.3$



(c) $\alpha = 0.4, \beta = 0.2, \gamma = 0.4$



(d) $\alpha = 0.4, \beta = 0.2, \gamma = 0.5$



(e) $\alpha = 0.4, \beta = 0.2, \gamma = 0.6$

Figure 3.5: 'Probability of Household state' on $y-axis$ vs 'time' on $x-axis$ with varying γ

We observe an steady states in trajectories figure (a),(b), (c) and (d) in figure 3.5 but unstable trajectories in figure (e) when γ is gradually increased. In figure (a),(b) and (c) of figure 3.5, the timesteps taken by trajectories to reach steady states increases when γ increases. We can also observe values of total infected rate and total recovered rate

in table 3.6. Our observation of total infection rate and the criteria to take time steps referred from equation 3.2 to reach steady values or unsteady states are shown in table : 3.6

Table 3.6: Total infection rate, Total recovered rate and time step taken by probabilities of household state to reach steady states varying γ

Name	$\gamma = 0.3$	$\gamma = 0.4$	$\gamma = 0.5$	$\gamma = 0.6$
Total infection rate (I_{Total})	(0.922)	(0.545)	(0.161)	-
Total recovered rate (I_{Total})	(0.276)	(0.218)	(0.080)	-
Timestep	(54)	(74)	(185)	-

These steady state criteria values from table 3.6 are used to show the values of probability household states below table 3.7. In table 3.6 the steady state values in total infection rate sharply decreases as gradual increase in recovery rate while in total recovery rate slightly increases in $\gamma = 0.3$ but sharply decreases from $\gamma = 0.4$ onwards till approximately 0.5 and then it starts to show unsteady values or reach negligible to zero. The time step taken by total infection rate to reach steady state increases in gradual increase of recovery rate till $\gamma = 0.5$. At $\gamma = 0.6$, P_0 and P_1 reaches to negligible to zero. The household states values aligned with total infection rate is shown in table 3.7.

Table 3.7: Simulation : Probability of household state values varying γ

Probability of Household state	$\gamma = 0.3$	$\gamma = 0.4$	$\gamma = 0.5$	$\gamma = 0.6$
P_0	0.327	0.561	0.849	0.9999
P_1	0.408	0.315	0.121	-
P_2	0.264	0.123	0.028	-

We observe in 3.7 that in household state P_0 the equilibrium values increases sharply in gradual increase in recovery parameter. For P_1 there is slight increase in recovery rate from 0.2 to 0.3 but gets decreases significantly from 0.4 till 0.5 while for P_2 there is significant decrease till 0.5. At γ 0.6 the values of P_1 and P_2 is negligible to zero. The probability household states values gradual increase of recovery rate is shown in 3.6.

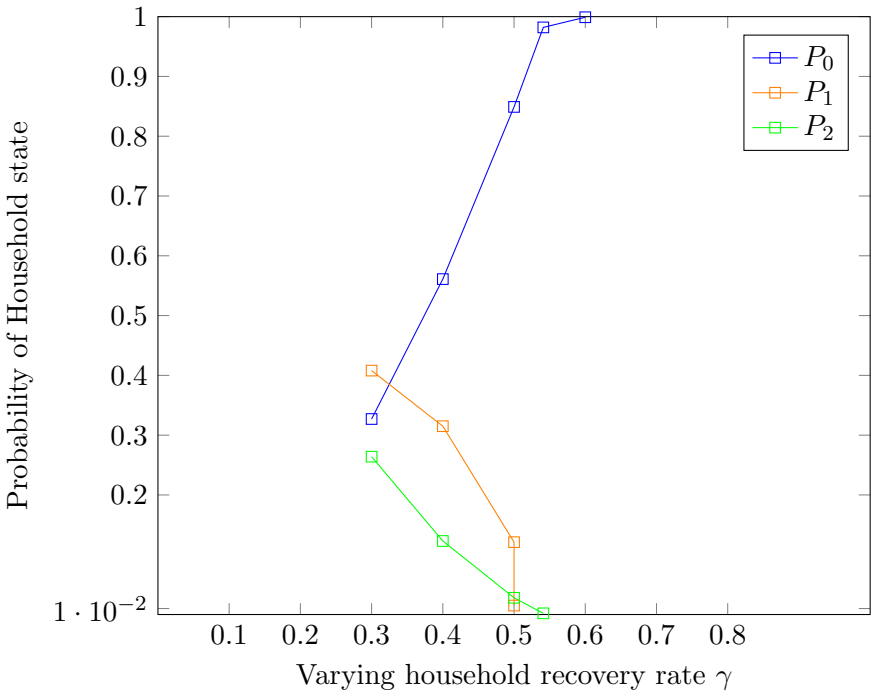


Figure 3.6: 'Probability of Household State' on $x - axis$ vs 'Varying household recovery rate γ' on $y - axis$

We can see in above 3.6 that P_0 state sharply rises but P_1 and P_2 falls down reaching stage reaching negligible to zero in timesteps towards infinity.

3.2 Analysis of Numerical Results in Equilibrium

3.2.1 Analysis of Disease-Free Equilibrium(DFE)

With cases observed in 'Analysis of Eigenvalue for DFE' in analytical section of DFE, we show a figure to observe stable regions and instable regions for DFE in master equation SHH of size two. We take our intial parameter α being constant at 0.4 and set range of parameters β and γ from 0.1 to 1 dividing each by 1000. This is done in order to give smooth separation of regions to make a distinction of stable and unstable regions between gamma in y-axis and beta in x-axis. Each values given in α, β and γ represent trace values in 2.18 and determinant values in 2.19. The calculation of eigenvalue in both equation at 2.16 resulted in figure 3.7. According to the cases discussed in section 'Analysis of eigenvalues for DFE', we set up equation 2.16 such that if both eigenvalues are negative then we show stable region which is denoted by color blue and if anyone of the eigenvalues is positive then the regions are unstable which is denoted by color red.

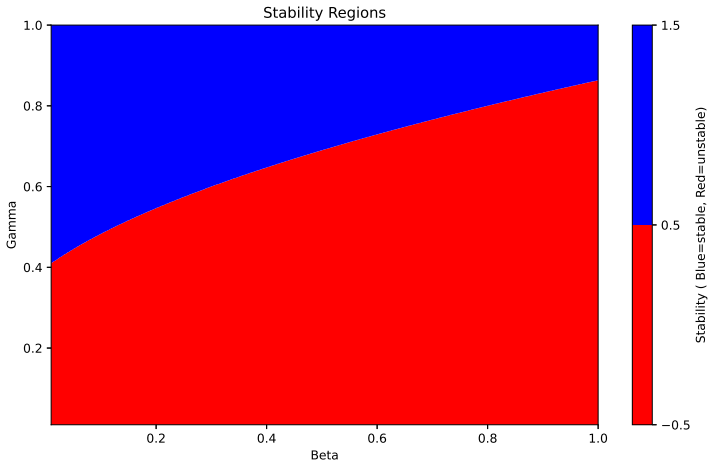


Figure 3.7: 'Gamma'(γ) as recovery rate on $y-axis$ and 'Beta'(β) as within-household infection rate on $x-axis$ with constant alpha(α) as between-household infection rate' at 0.4.

Figure 3.7 shows stable regions and unstable regions in disease-free equilibrium of SHH of size two.
The discussion of equilibrium case in disease-free equilibrium is as follows.

case : $Tr < 0$ **and** $Tr > \sqrt{Tr^2 - 4D}$ **, where** $D > 0$ **and** $Tr^2 > 4D$:

In this case we use term $Tr < 0$, which interchangeably means $\alpha < \beta + 3\gamma$ and $D > 0$ which means $\alpha < \frac{\gamma^2}{\beta+\gamma}$. In this case, when $Tr < 0$ and $Tr > \sqrt{Tr^2 - 4D} > 0$ with $D > 0$ and $Tr^2 - 4D > 0$, it shows the stable region because both eigenvalues are negative in 2.16 and for other cases, it shows unstable regions in 3.7. We limit our study to real eigenvalues and complex pair of eigenvalues are neglected. The α parameter has to be strictly less than $(\beta + 3\gamma)$ in $Tr < 0$ and for $D > 0$ in 2.19 to be positive. To fulfill the condition stated earlier, it is necessary for the value of β of $\alpha < \frac{\gamma^2}{\beta+\gamma}$ to be lower than γ. A higher rate of γ results in stable regions. This means higher recovery rate is needed for disease-free equilibrium. And the solution near the equilibrium point will result into stability. For example, if β is zero, γ is greater than 0.4 and α is 0.4 then the region is stable. Following up with previous example, to satisfy Tr condition the recovery rate has to be higher with (3γ). Also the difference of infection rates $(\alpha - \beta)$ has to lower greater than (3γ) . Only the higher recovery rates will make region stable. This case with $D > 0$ is significant criteria for γ to be high. This scenario is also seen in above figure. The other cases explored resulted in unstable region when $\alpha > \beta + 3\gamma$ and $\alpha > \frac{\gamma^2}{\beta+\gamma}$ i.e with betwee-household infection rates leading to unstable in DFE.

3.2.2 Analysis of Endemic Equilibrium(EE)

In section, we substitute the equations 2.26, 2.23 and 2.20 with parameters α, β and γ as shown in table 3.3, 3.5 and 3.7 which shows the following results.

Probability of household states values with varying α:
We take the rates of α, β and γ from table 3.3 and use them to find the solution of P_0 in equation 2.26, P_1 in equation 2.23 and P_2 in equation 2.20. We get the following results in table : 3.8

Table 3.8: Equilibrium : Probability of household states values with varying α

HouseHold states	$\alpha = 0.4$	$\alpha = 0.5$	$\alpha = 0.6$	$\alpha = 0.7$	$\alpha = 0.8$
P_0	0.151	0.106	0.078	0.060	0.048
P_1	0.394	0.375	0.351	0.328	0.307
P_2	0.454	0.518	0.569	0.610	0.644

We compared the values of simulation in Runge-Kutta method: 3.2 with endemic equilibrium values in table 3.8 and found them to be approximately similar.
Referencing equation 2.26, we gradually increase α but keep the other two parameters fixed. The increase in α rate of equation 2.26 decreases the value of P_0 while sum of between-household and within-household infection rate $(\alpha + \beta)$ in 2.26 should not make much difference. This decreases the value of P_0 by α in $\frac{\gamma}{2\alpha\beta}$ in equation 2.26 which have direct impact on P_0 and $(1 - P_0)$ in equation 2.23. The decrease in P_0 increases the value of P_1 at 2.23. The recovery rate remains constant in the $\gamma + \alpha P_0$ and the αP_0 term reduces the output in P_1. In equation 2.20, P_2 depends on the values of P_1 and P_0. The accumulation of low values of P_1 and P_0 leads to a high value of P_2. Therefore, it can be concluded that a gradual increase in the rate of α results in an increase in value of P_2 and in P_1.
For each rate, we computed the eigenvalues using the values at the endemic equilibrium point and also determined the Jacobian as per Equation 2.27. Our analysis revealed three eigenvalues, with one being zero and the other two being negative, indicating stable regions as possibility of endemic equilibrium. The gradual increase in the between-household infection rate resulted in a reduction of negative eigenvalues.

Probability of household states values with varying β:
We take the rates of α, β and γ from table 3.5 and use them to find the solution of P_0 in equation 2.26, P_1 in equation 2.23 and P_2 in equation 2.20. We get the following results in table : 3.9

Table 3.9: Equilibrium : Probability of household states values with varying β

HouseHold states	$\beta = 0.2$	$\beta = 0.3$	$\beta = 0.4$	$\beta = 0.5$
P_0	0.151	0.128	0.112	0.100
P_1	0.394	0.356	0.325	0.300
P_2	0.454	0.514	0.561	0.600

In this section we observe the effect of β on endemic equilibrium, we compared the values of table from simulation in Runge-Kutta method: 3.5 with endemic equilibrium values in table 3.9 and found them to be apporximately similar.
In table 3.9, the gradual increase in β rate equation 2.26 decreases the value of P_0. The decrease in value of P_0 increases P_1 in 2.23 but without direct influence of β in 2.23. In equation 2.20, P_2 depends on the values of P_1 and P_0. The sum of low values of P_1 and P_0 resulted in high values of P_2. We can see that the gradual increase in β rate increases value of P_2 in table 3.9.
We calculated the eigenvalues from β rates with endemic equlibrium solution or fixed point and from equation 2.27. We find three eigenvalues in which one eigenvalue is zero and the other two eigenvalues are negative which leads to stability which also shows possibility of endemic equilibrium. The gradual increase in the between-household infection rate decreases the negative eigenvalues.

Probability of household states values with varying γ:
We take the rates of α, β and γ from table 3.5 and use them to find the solution of P_0 in equation 2.26, P_1 in equation 2.23 and P_2 in equation 2.20. We get the following results in table : 3.10.

Table 3.10: Equilibrium : Probability of household states values with varying γ

HouseHold states	$\gamma = 0.3$	$\gamma = 0.4$	$\gamma = 0.5$	$\gamma = 0.5411$	$\gamma = 0.6$
P_0	0.327	0.561	0.849	0.982	-
P_1	0.408	0.315	0.121	0.014	-
P_2	0.263	0.123	0.028	0.002	-

In this section we observe the effect of γ on endemic equilibrium, we compared the values of table from simulation in Runge-Kutta method: 3.7 with endemic equilibrium values in table 3.10 and found them to be approximately similar.
In table 3.10, the gradual increase in recovery parameter γ is observed from equation 2.26. The increase of γ in equation 2.26 increases the value of P_0. The gradual increase in rate of γ will increase P_0 because of $+4\beta\gamma$ and $\frac{\gamma}{2\alpha\beta}$ in 2.26. The increase in recovery rate decreases the value of P_1 and in value of P_2. At $\gamma = 0.6$, P_1 and P_2 value are negligible to zero. We calculated eigenvalues of endemic equlibrium solution from equation 2.27 and

found three eigenvalues in which one eigenvalue is zero and the other two eigenvalues are negative until we increased γ to 0.5 which led to stable regions.This increase resulted in the gradual decrease in eigenvalues.

Phase portrait

Phase portraits in P_0 and P_1

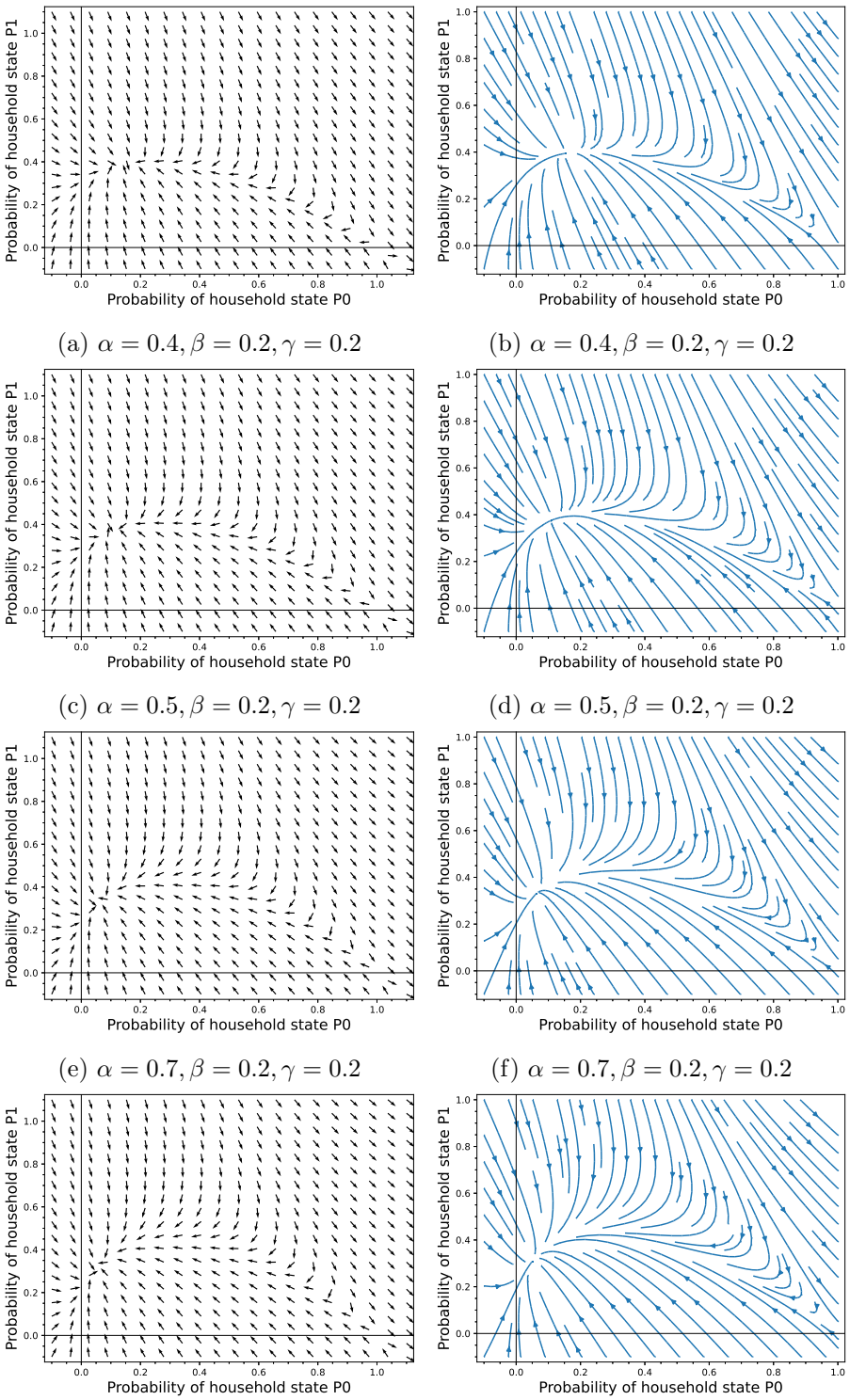
The dynamical system of differential equations of 2.8,2.9 and 2.10 could be geometrically represented in phase plane[8]. Phase portraits can be used for studying disease equilibrium to observe the stable and instable regions formed by linearization in DFE and in EE. The phase portrait formed from linearization is similar to the non-linear system [19]. We plot phase portraits in the plane of P_0 and P_1 to observe DFE and EE. By varying parameter values of α, β and γ in differential equations 2.8 as a function $f_0(P_0)$, 2.9 as a function $f_1(P_1)$. Their equation form is shown below

$$\begin{aligned} f_0(P_0) &= -\alpha(P_1 + 2(1 - P_0 - P_1))P_0 + \gamma P_1 \\ f_1(P_1) &= \alpha(P_1 + 2(1 - P_0 - P_1))P_0 \\ &\quad - ((\alpha/2)(P_1 + 2(1 - P_0 - P_1)) + \beta + \gamma)P_1 \\ &\quad + 2\gamma(1 - P_0 - P_1) \end{aligned} \tag{3.3}$$

We focus our analysis on the plane P_0 at the equilibrium point (1, 0, 0) to comprehend its behavior. At the endemic equilibrium point, both planes P_0 and P_1 play a significant role in influencing P_2. To illustrate this scenario, utilizing the equation in 2.20, we intend to create phase portraits in the phase plane of P_0 and P_1 within the domain [0,1] for both planes. In our investigation, P_0 is represented on the $x - axis$, and P_1 is on the $y - axis$. Our objective is to identify whether there are attractor regions or sink regions, repeller regions or source regions in this phase plane. We present two types of phase portraits. On the left side, a plot of normalized vector fields generated from [11] is displayed. This is complemented by a streamlined plot, again generated from [10].

Phase portraits of P_0 and P_1 with varying α

The phase portrait of P_0 is shown on the x-axis with a range of [-0.1, 1.1], and P_1 on the y-axis with a range of [-0.1, 1.1]. We vary α with rates $\alpha = 0.4, 0.5, 0.7$, and 0.8, while keeping $\beta = 0.2$ and $\gamma = 0.2$ fixed in Equation 3.3.



(a) $\alpha = 0.4, \beta = 0.2, \gamma = 0.2$ (b) $\alpha = 0.4, \beta = 0.2, \gamma = 0.2$

(c) $\alpha = 0.5, \beta = 0.2, \gamma = 0.2$ (d) $\alpha = 0.5, \beta = 0.2, \gamma = 0.2$

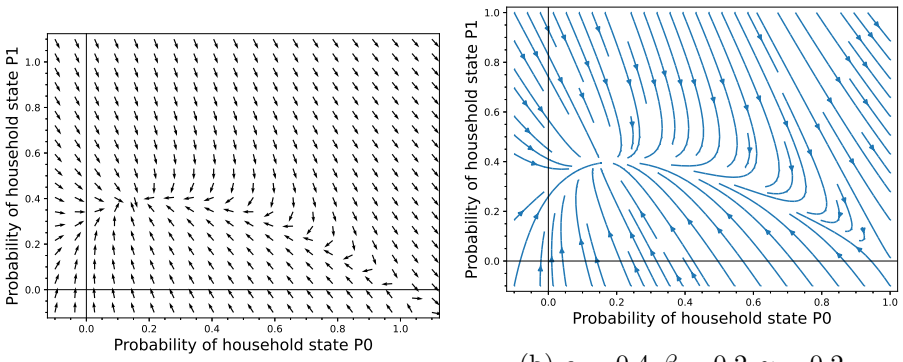
(e) $\alpha = 0.7, \beta = 0.2, \gamma = 0.2$ (f) $\alpha = 0.7, \beta = 0.2, \gamma = 0.2$

(g) $\alpha = 0.8, \beta = 0.2, \gamma = 0.2$ (h) $\alpha = 0.8, \beta = 0.2, \gamma = 0.2$

Figure 3.8: Probability of household state P0 $= P_0$ on $x - axis$ and Probability of household state P1 $= P_1$ on $y - axis$ varying α.

In the above Figure 3.8, within the P_0 and P_1 plane, we observe two distinct regions at equilibrium. At the equilibrium point (1,0), the disease-free equilibrium acts as a repellor region in the P_0 plane, commonly referred to as a saddle point. The attractor region in both P_0 and P_1 corresponds to the endemic equilibrium. In Figure 3.8, the gradual increase in α from 0.4 to 0.8 indicates a sink or attractor region at P_0 and P_1 plane, which is stable, signifying the existence of an endemic equilibrium.

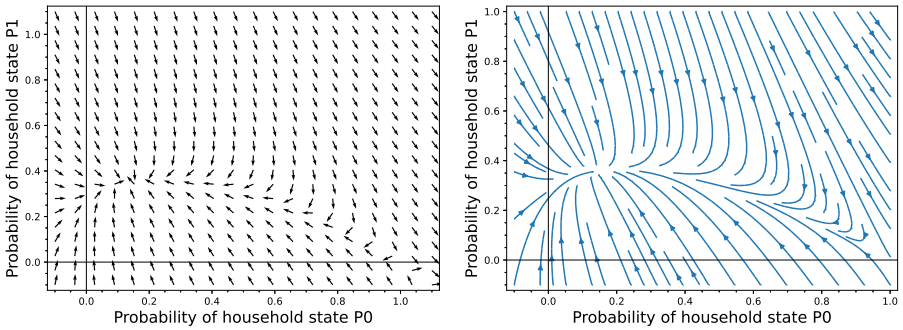
Phase portraits of P_0 and P_1 with varying β In this section, we present the phase portrait of P_0 and P_1, varying with β at 0.2, 0.3, 0.4, and 0.5, while keeping $\alpha = 0.4$ and $\gamma = 0.2$ fixed in Equation 3.3. The visualization includes vector fields and streamline plots.



(a) $\alpha = 0.4, \beta = 0.2, \gamma = 0.2$

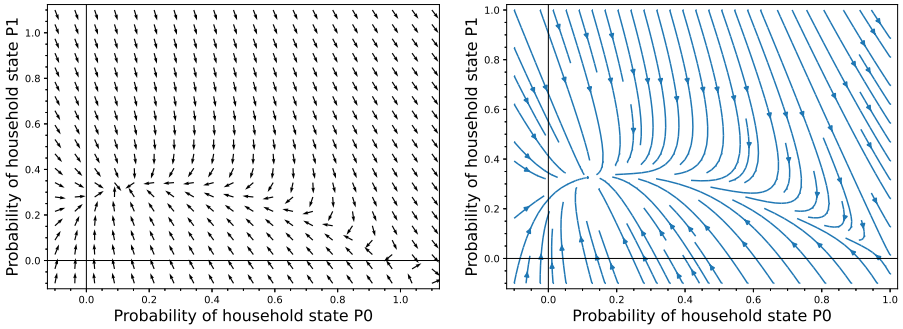
(b) $\alpha = 0.4, \beta = 0.2, \gamma = 0.2$

ex



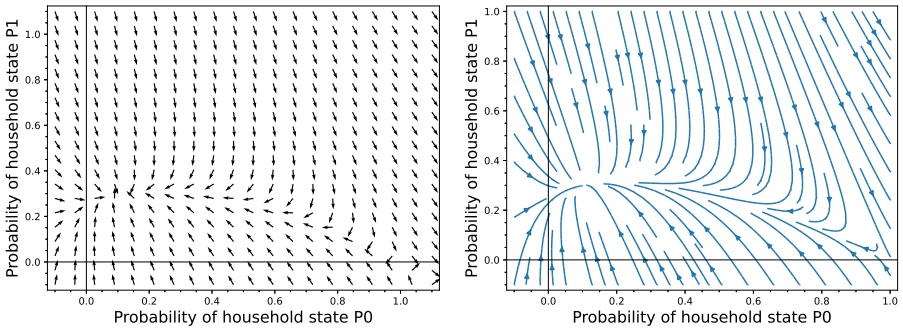
(c) $\alpha = 0.4, \beta = 0.3, \gamma = 0.2$

(d) $\alpha = 0.4, \beta = 0.3, \gamma = 0.2$



(e) $\alpha = 0.4, \beta = 0.4, \gamma = 0.2$

(f) $\alpha = 0.4, \beta = 0.4, \gamma = 0.2$



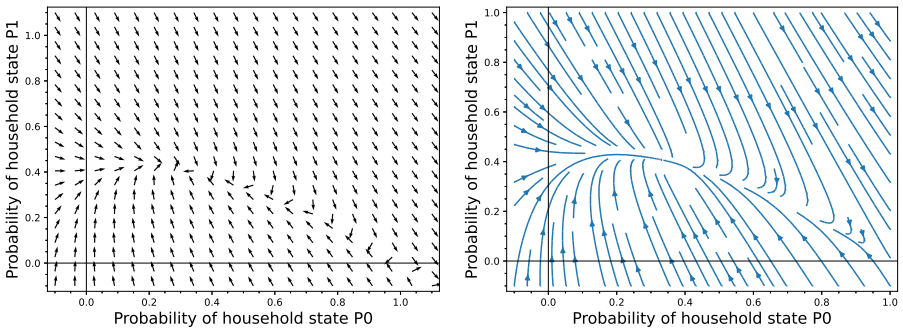
(g) $\alpha = 0.4, \beta = 0.5, \gamma = 0.2$

(h) $\alpha = 0.4, \beta = 0.5, \gamma = 0.2$

Figure 3.9: Probability of household state P0 $= P_0$ on $x - axis$ and Probability of household state P1 $= P_1$ on $y - axis$ varying β.

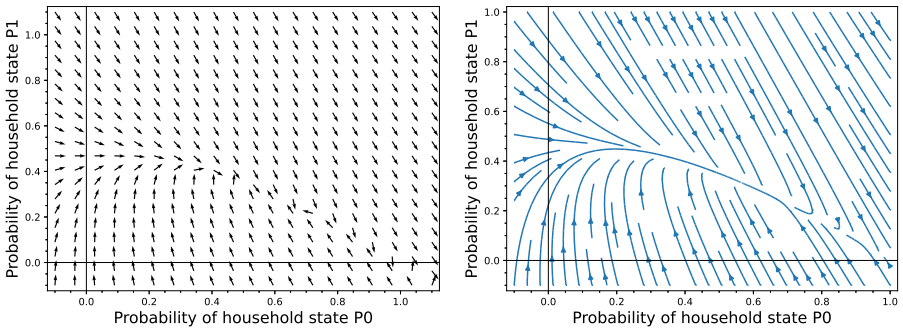
In the above Figure 3.9, similar regions are observed when compared to Figure 3.8. All figures demonstrate stable regions, attractor regions, or sink regions at 'P_0 and P_1' plane , where the disease becomes endemic with a gradual increase in β. The region at P_0 (1,0), representing the disease-free equilibrium, shows a repellor or saddle, implying that any introduction of the disease leads to an endemic state.

Phase portrait of P_0 and P_1 with varying γ In this section, we present the phase plane plot with γ varying at rates γ with 0.3, 0.4, 0.6, and 0.8, while keeping $\alpha = 0.4$ and $\beta = 0.2$ fixed in Equation 3.3. The visualization includes vector fields and streamline plots.



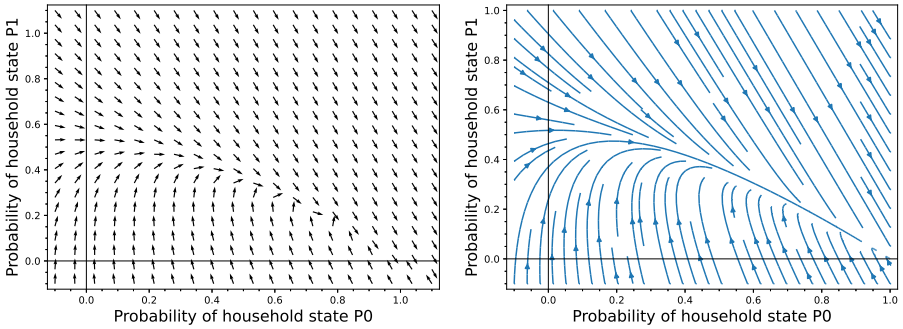
(a) $\alpha = 0.4, \beta = 0.2, \gamma = 0.3$

(b) $\alpha = 0.4, \beta = 0.2, \gamma = 0.3$



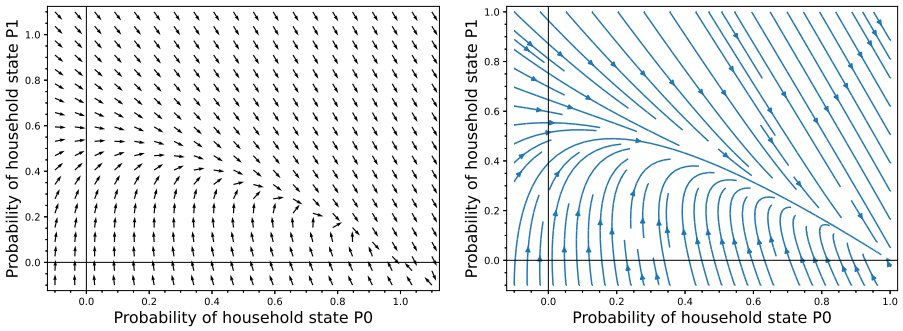
(c) $\alpha = 0.4, \beta = 0.2, \gamma = 0.4$

(d) $\alpha = 0.4, \beta = 0.2, \gamma = 0.4$



(e) $\alpha = 0.4, \beta = 0.2, \gamma = 0.6$

(f) $\alpha = 0.4, \beta = 0.2, \gamma = 0.6$



(g) $\alpha = 0.4, \beta = 0.2, \gamma = 0.8$

(h) $\alpha = 0.4, \beta = 0.2, \gamma = 0.8$

Figure 3.10: Probability of household state P0 $= P_0$ on $x-axis$ and Probability of household state P1 $= P_1$ on $y-axis$ of γ.

In Figures 3.10a and 3.10b, $\gamma = 0.3$, and in Figures 3.10c and 3.10d, $\gamma = 0.4$, stable regions are observed at plane 'P_0 and P_1' leading disease to endemic, which gradually degenerate at 3.10e and 3.10f. At $\gamma = 0.6$ it shows stability at P_0 (1,0) plane leading to disease-free equilibrium.

4 Discussion

We studied SIS dynamics in a single household of size two. We derived general master equations and applied them to a single household of size two to understand dynamical behaviour of the solutions. With numerical simulation performed on master equations, we analyzed parameter by varying between-household infection rate (α), within-household infection rate (β) and recovery rate(γ). We then took on the epidemiological perspective and assumed a situation where infectious disease enters by introducing 12 infected individuals to a small community of 600 households each of size two. Then we studied the disease prevalence with respect to long term and analyze equilibria in disease.

Numerical simulation results discussion We performed numerical simulation by using Runge-Kutta method to study master equations in long term behaviour. For simulation, we assumed initial parameters such as between-household infection at a rate of 0.4, within household infection at 0.2 and recovery rate at 0.2. This initial choice of parameters resulted in lower value in P_0 compared to P_1 and while comparing P_1 to P_2, P_1 has lower value than P_2.

Total Timestep :

We observed that the gradual increase in the between-household infection rate (α) leads to a decrease in the total timestep required for all the probability of household states to reach steady states. Similarly, the gradual increase in the between-household infection rate reduces the total timestep needed for the total infection rate and the total recovery rate to reach steady states. In comparison, the gradual increase in the within-household infection rate (β) results in a decrease in the total timestep for all household states to reach steady state. Likewise, the gradual increase in the within-household infection rate decreases the total timestep for the total infection rate and the total recovery rate to reach steady states.

When comparing the gradual increase in the within-household infection rate with the between-household infection rate, the total timestep taken by all the probability of household states is less in the between-household infection rate but more in the within-household infection rates. Similarly, when comparing the within-household infection rate

with the between-household infection rate, the total timestep taken by the total infection rate and the total recovery rate is more in the within-household infection rate but less in the between-household infection rate.
Meanwhile, the total timestep taken by all the probabilities of household states, considering both the total infection rate and the total recovery rate, increases gradually with the rise in the recovery rate until reaching steady states, up to a rate of 0.5.

Changes in the total values of a probability of household state, total infection rate and total recovered rate with parameters α, β and γ : The gradual increase in the between-household infection rate from 0.4 to 0.8 further decreases the values of P_0 and P_1 but increases the value of P_2, as illustrated in Figure 3.2.

Similarly, we observed that the gradual increase from 0.3 to 0.5 in the within-household infection rate decreases the values of P_0 and P_1 but increases the value of P_2, as shown in Figure 3.4.

Comparing the changes between the within-household and the between-household infection rates in all the probability of household states, P_0 decreases more with the gradual increase in the between-household infection rate but decreases less with the gradual increase in the within-household infection rate. Conversely, for P_1, it decreases less with the between-household infection rate but more with the within-household infection rate, as seen in Table 3.3 and 3.5. The value of P_2 remains similar with the gradual increase in both between-household and within-household infection rates. In the case of the total infection rate and the total recovery rate, both increase with the gradual increase in both between-household and within-household infection rates, but the gradual increase in the between-household infection is more than in the within-household infection rate.

Regarding the household recovery rate, a gradual increase from 0.3 to 0.6 resulted in a high increase in P_0 but a sharp decrease in both P_1 and P_2, as shown in Figure 3.6. The total infected rate and total recovery rate decrease with a gradual increase in the recovery rate. At the recovery rate $\gamma = 0.6$, P_1 and P_2 become negligible to zero.

Endemic Equilibrium(EE) : We interpreted the values for P_0, P_1 and P_2 in our results section with the equations at 2.26, 2.23 and 2.20. We used linearization near equilibrium points. And the Jacobian at equilibirum solutions to calculate eigenvalues. Among the three calculated eigenvalues, two negative eigenvalues confirm stability around the equilibrium solution. The other zero eigenvalue did not provide any qualitative analysis. We found that the calculated negative eigenvalues decrease with the gradual increase in the between-household infection rate. Similarly, we also found that the calculated negative eigenvalues decrease with the gradual increase in the within-household infection rate. Likewise, in the recovery rate, we also observed a decrease in the negative eigenvalues till recovery rate at 0.5.

Disease-Free Equilibrium(DFE) After the gradual increase in the recovery rate, P_1 and P_2 became negligible to zero, and at $\gamma = 0.6$, stable regions occured at P_0 (1,0,0). We computed the Jacobian at $(1, 0, 0)$ and found that eigenvalues depend on parameters α, β, and γ (see Figure 2.15). A case of $Tr < 0$ and $Tr > \sqrt{Tr^2 - 4D}$, where $D > 0$, $Tr^2 > 4D$, was crucial in finding negative eigenvalues as regions for stability. In this case, when $Tr < 0$, the α rate is strictly less than β and 3γ. This can be interpreted as the difference in the between-household infection rate and the within- household infection rate being smaller than compared to the recovery rate. Similarly, the lower rate of β and higher rate of γ in the of the expression $\alpha < \frac{\gamma^2}{\beta+\gamma}$ of $D > 0$ decides the stable region for the disease-free equilibrium. For a stable region to occur, the recovery rates should be high. Figure 3.7 shows that stable and unstable regions exist in γ vs β where α is fixed at 0.4. We interpret this scenario as when α is constant and β is lower compared to a higher recovery rate, the disease-free equilibrium occurs.

Phase portrait :

The influence of varying α, β, and γ in the 'P_0 and P_1' plane was also shown by the phase portrait. We observed the endemic equilibrium (EE) and disease-free equilibrium (DFE) at the domain of P_0 [0,1] and P_1 [0,1]. The gradual increase in α showed stable regions at endemic equilibrium solutions, forming attractor regions or sink regions. Similarly, the gradual increase in β showed stable regions at endemic equilibrium solutions but unstable regions at the fixed point (1,0) in the P_0 axis, which indicates a repellor or saddle. However, the gradual increase in the recovery rate shifted the stable regions from the P_0 and P_1 plane towards the fixed point (1,0). At the recovery rate $\gamma = 0.6$, the fixed point (1,0) showed stability regions, which have an attractor or sink region, referred to as disease-free equilibrium, as observed in the phase portrait section.

Limitations : At initial stage, we wanted to study about infectious disease in mixed household size rather than same household size but due to limited time, we analyzed equilibria in disease-free equilibrium and endemic equilibrium in a single household of size two. In a household, isolation policy is hard to implement, where everybody in a family interacts with one another. In SHH of size two it is obvious that inside household there is only one individual who is infective and transmit infection to the other susceptible but question arises what would happen with household of larger size where the chances are high that more individuals will be infected. Also the focus was not on crafting strategies or policies based on the results of simulation rather the focus was on analyzing equilbria. Lastly, we did not define the household structure and behavioural patterns of individuals.

Further research Further reseach on equilibrium can be done on higher dimensions having more than two individuals in a household, which leads to even more complexity in

the dynamics. A numerical approximation method like Runge-Kutta could be used to see overall scenario of disease in long term. It would be interesting to observe these scenario in large population and also in a small community.

Further research can be done on other epidemiological models of SIS varitaions SI, SIR, SEIR or other variation according to various form of diseases. Also finding modeling method for policies such vaccination, isolation, herd immunity etc would be beneficial in future for intervention strategies when disease outbreaks. We used linearization method for single household of size two in SIS, further research could be possible in calculating reproduction number and new generation matrix with spectral radius. Also, we studied with high rate of parameters but the study can also be done with low value of parameters to see significant changes in equilibrium.

5 Conclusion

In the thesis, we analyzed SIS dynamics in master equations for single household of size two to understand the dynamic behaviour of solutions at an equilibrium condition from the perspective of mathematical epidemiology. We considered the course of an infectious disease to be deterministic and homogenous. Then we derived general master equation to understand phenomenon for finite household size. Due to time limitation, we restricted our discussion to analyzing equilibria of disease in a single household of size two. In master equation, we graudally increased the rate between-household infection rate(α), within-household infection rate(β) and recovery rate(γ)'s and investigated the influence on a single household of size two. Our SHH approximation in SIS model showed both endemic equilibrium and disease-free equilibrium and confirmed it by analytical finding. We observed that P_0 and P_1 decreases with graudal increase in between-household infection rate and within-household infection rate. On the other hand P_2 and total infection rate increases with gradual increase in between-household infection rate and within-household infection rate. Moreover P_1, P_2 and total infection rate decreases with gradual increase in recovery rate. Conversely P_0 increases with gradual increase in recovery rate.
In summary, a transition from endemic equilibrium to a disease-free equilibrium is observed when the recovery rate is set at 0.6. This transition occurs within a specific range of household transmission rates, particularly when the between-household rate is set at 0.4 and the within-household rate is at 0.2.

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