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Research Article

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Mathematical Modelling of Multi-Region Spread of Epidemic

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Abstract

SAIR model of growth of an epidemic is extended to a system of many interacting regions. Interactions are described by exchange of populations between various regions. Differences caused by the exchange of susceptible population, in addition to infected individuals are noted. It is shown that initial phase of the epidemic is governed by a linear system. Analysis of linear system shows that a fundamental mode gets established that governs the spatial profile of the spread of the disease.

1. Introduction

Covid-19 pandemic has given rise to renewed interest in the Mathematical Mod- elling of spread of a contagious disease, Yang and Wang [2020], Lobato et.al. [2021], Agrawal et.al. [2021], Peter et.al. [2021] [1-4]. This is an old topic, dating back to the work of Kermack and Meckendrick [1927] who proposed the SIR model [5]. In this model the population Π of a region under study is divided in three groups, namely Susceptible (S), Infected (I) and Removed (R). It is pos- tulated that the disease spreads through a contact between a susceptible person and an infected individual with the probability $\beta' dt/\Pi$ in an infinitesimal time in- terval dt. Thus the number of people getting infected in a time dt is given by $\beta' SIdt$, where S and I denote the number of susceptible and infected individuals at time t. The infected individuals are transferred to the Removed (R) group at the rate γIdt, either through recovery or death. One then sets up non-linear, first order, ordinary differential equations (ODE) describing how people go over from one group to another. These equations merely state the conservation of the total number of people in three groups. Their non-linearity makes it diffi- cult to analyse them theoretically and hence are generally studied numerically. In what follows we will set $\beta = \beta'/\Pi$ which is equivalent to the normalization $\Pi = 1$.

This basic model has been improved by various authors by including addi- tional groups to account for the specific characteristics of a particular disease. Thus for example in the SEIR model, Li and Muldowney [1995], one introduces another group of Exposed (E) people On contacting the disease a susceptible individual moves to Exposed (E) group for a certain incubation period before moving to the Infected (I) group [6]. The SAIR model was introduced by Robinson and Stilianakis [2013] to account for Asymptomatic (A) individuals [7]. Suscepti- ble individuals can contact disease by a contact with either the Asymptomatic person or an infected one and join the Asymptomatic group. Asymptomatic individuals either recover from the infection and directly move to Removed (R) group or move to Infected (I) group. The Infected persons move to the removed group either through recovery or death. Once again one can set up ODE describing conservation of people in these four groups.

Most of the studies consider only one region, which can be a town, city, state or a country. Few authors have considered the spatial and temporal de- velopment of the epidemic which is the subject of this paper. Thus e.g. Noble [1974], added diffusion terms to the balance equations for both Susceptible and Infected persons of basic SIR model [8]. This converts these two equations to time-dependent partial differential equations (PDE). Recently Besse and Faye [2021] used diffusion equation to account for migration of (only) infected indi- viduals on connected graphs, a system of cities connected by a transportation network [9]. This converts the infected (I) population equation for each node (city) to a non-linear PDE, coupling the neighbouring parts of the transportation net- work The equations for Susceptible (S) and Removed (R) groups remain the non-linear ODE. A much simpler approach was followed by Zakary, Richik and Elmouki [2017] who considered a discrete time evolution of Multi-region SIR model, allowing for the migration of only infected individuals [10-11]. We follow this approach but over continuous time, using classical mathematical physics meth- ods. Further we will examine the consequences of allowing movement of all, the Susceptible, Asymptomatic carriers and Infected people to different regions, i.e. with SAIR model.

In the next section we first briefly recall the basic SAIR model and then set out its generalization to multi-region case. All individuals are assigned a home region and the population of the regions is divided in S, A, I and R groups. Interactions between different regions is described in terms of a ”population exchange matrix”, that accounts for the people of one home region that are present in another region. We write down the equations of evolution of S, A, I and R groups in each region for model (a) that allows for migration of S, A and I persons. Thus a Susceptible individual can catch infection in his home region by a contact with an individual belonging to A and I groups of all regions that are present in his home region. In addition he can also be infected in some other region if he happens to be present in that region. We also consider a model (b) when only A and I groups migrate while Susceptible are confined to home region. They catch infection only in their home region by contact with A and I individuals belonging to any region. In either model we obtain a set of 2N coupled. non-linear equations for the S and A populations of N regions. Remaining 2N equations governing the populations of I and R groups of N regions are linear equations, each region is also decoupled from others. Then in section 3 we observe that in the initial stages of the epidemic the Infected and Asymptomatic (A) populations of all regions are much smaller than the Susceptible (S) populations. This allows us to obtain a linearized model involving "population exchange matrix". We note a central role played by the eigenvalue spectrum of this matrix on the future growth of the epidemic. We obtain the modes of this linearized model and show that a dominant fundamental mode exists with all non-negative elements. This fundamental mode grows much more rapidly than other modes. This concept of Fundamental Mode is borrowed from Reactor Physics describing the growth of neutron population in a nuclear reactor. We then set up the development of the solution of non-linear equations by a perturbation series expansion. In section 4, we illustrate our theoretical conclusions by numerical computations. We consider a system of just two regions when all migration from one region is to the only other region. This results in a particularly simple form of equations that can be easily solved. It is seen that model predicts all the features of the phenomenon, in quantitative terms, which one feels intuitively. Lastly in section 5 we state our conclusions.

2. Basic Equations

As mentioned in the Introduction, the SAIR model divides the population of a region i in four groups, namely, Susceptible (S), Asymptomatic (A), Infected
(I) and Removed (R). Let these symbols also denote the number of individuals in the region. One can easily write down the equations governing the time evolution of these four groups as

$$\frac{dS}{dt} = -[\beta_A A + \beta_I I]S \qquad \frac{dA}{dt} = [\beta_A A + \beta_I I]S - \gamma_A A - \alpha A$$

$$\frac{dI}{dt} = \alpha A - \gamma_I I; \qquad \frac{dR}{dt} = \gamma_A A + \gamma_I I \qquad \frac{dD}{dt} = \gamma_I (1-\mu) I \qquad (1)$$

Here β_A, β_I denote the rate at which an Asymptomatic or Infected individ- ual causes infection in a Susceptible person. γA denotes the rate at which an asymptomatic person recovers from the disease and moves directly to the re- moved group while α measures the rate at which asymptomatic persons move to infected group after showing symptoms of the disease. γ_I measure the rate of removal of infected persons by recovery (fraction μ) and death with frac- tion $(1-\mu)$. For simplicity we will consider the simplified SAIR model when $\beta_A = \beta_I = \beta$ and $\gamma_A = \gamma_I = \gamma$ though this assumption can be relaxed without any additional difficulties. Eq. (1) then reduce to

$$\frac{dS}{dt} = -\beta[A+I]S; \qquad \frac{dA}{dt} = \beta[A+I]S - \gamma A - \alpha A$$

$$\frac{dI}{dt} = \alpha A - \gamma I; \qquad \frac{dR}{dt} = \gamma[A+I] \qquad \frac{dD}{dt} = \gamma(1-\mu)I \qquad (2)$$

We observe that first two equations are non-linear and coupled while the re- maining three are linear and are essentially driven by a "source" αA. We now describe the extension of Eq. (2) to multi-region case.

2.1 Model (a) Movement of Susceptible, Asymptomatic and Infected Groups

Let us now consider a collection of N regions. Let us assume that a fraction $\xi_{i,j}$ of the population of the region j is visiting the region i at any given time. We will assume that this fraction is time-independent. For simplicity we will also assume that same fraction is applicable to susceptible, asymptomatic and infected groups, though this assumption can be easily relaxed. We also denote $\xi_i = \sum_{j=1,j\neq i}^{N} \xi_{j,i}$. Let S_i, A_i, I_i and R_i denote the susceptible, asymptomatic, infected and removed populations in the i-th region, $i = 1, 2,.........N$. Let us also for the moment assume that the people who show symptoms of the disease i.e. the infected individuals, isolate themselves and avoid further contacts. Then the time evolution of the S_i is governed by the equation

$$\frac{dS_i}{dt} = -(1-\xi_i)\Big[\beta_{i,i}(1-\xi_i)A_i + \sum_{j=1,j\neq i}^{N} \xi_{i,j}\beta_{i,j}A_j\Big]S_i$$

$$-\Big(\sum_{j=1,j\neq i}^{N} \xi_{j,i}[\beta_{i,j}(1-\xi_j)A_j + \sum_{k=1,k\neq j}^{N} \xi_{j,k}\beta_{i,k}A_k]\ S_i\Big) \qquad (3)$$

Eq. (3) states that the rate of change of susceptible population in the region i consists of two parts. A fraction $(1 - \xi_i)S_i$ catches infection locally from the asymptomatic people of the same region whose number is $(1 - \xi_i)A_i$ and rate βi,i. Thus this rate is $(1 - \xi_i)^2\beta_{i,i}A_iS_i$. Another set of susceptible is affected by the fraction $\xi_{i,j}$ of asymptomatic people of region j who were visiting the region i, and that totals to $\beta_{i,j}\xi_{i,j}A_j(1-\xi_i)S_i$. The second term accounts for the fraction $\xi_{j,i}$ of susceptible of region i contacting infection in some other region j, from the asymptomatic carriers of that region (rate $\beta_{i,j}\xi_{j,i}A_j(1-\xi_j)S_i$) as well as from the asymptomatic individuals visiting region j, including those from region i. We Separate the contribution from region i, set $\zeta^2_i = \Sigma^N_{j=1, j\neq i} \xi^2_{j,i}$ and define $\xi_{k,i}\eta_{i,k} = \Sigma^N_{j=1, j\neq i, j\neq k} \xi_{j,i}\xi_{j,k}$. With this notation we can write Eq. (3) as

$$\frac{dS_i}{dt} = -\Big[\beta_{i,i}[(1-\xi_i)^2 + \zeta_i^2]A_i$$

$$+ \sum_{j=1, j\neq i}^{N} \{(1-\xi_i)\xi_{i,j} + (1-\xi_j)\xi_{j,i} + \eta_{i,j}\xi_{j,i}\}\beta_{i,j}A_j\Big]S_i \tag{4}$$

This is an extension of a slightly modified form of SAIR model. A straight forward extension of SAIR model of Eq. (2) wherein asymptomatic carriers and infected individuals both come in contact of susceptible population can also be worked out and is given below. As we will see there is no material difference between these two versions of generalised SAIR models. The growth of Asymptomatic people A_i of region i is given by

$$\frac{dA_i}{dt} = \Big[\beta_{i,i}[(1-\xi_i)^2 + \zeta_i^2]A_i$$

$$+ \sum_{j=1, j\neq i}^{N} \{(1-\xi_i)\xi_{i,j} + (1-\xi_j)\xi_{j,i} + \eta_{i,j}\xi_{j,i}\}\beta_{i,j}A_j\Big]S_i - (\gamma_i + \alpha_i)A_i \tag{5}$$

It is assumed that on contacting the infection a person moves initially to the asymptomatic group. A fraction recovers at the rate γ_iA_i while another fraction moves to the Infected category I_i at the rate α_iA_i. Hence other three equations of the set, Eq. (2), are generalised to

$$\frac{dI_i}{dt} = \alpha_iA_i - \gamma_iI_i; \qquad \frac{dR_i}{dt} = \gamma_i[A_i + I_i] \qquad \frac{dD_i}{dt} = \gamma_i(1-\mu_i)I_i \tag{6}$$

These are three linear equations for the region i, de-coupled from other regions and driven by a source term α_iA_i. It is seen that Eqs. (4) and (5) are a set of $2N$ coupled, non-linear equations and one cannot treat region i in isolation. It is not very hard to numerically solve Eqs. (4), (5) and (6) if the number of regions N is not too large. Fractions $\xi_{i,j}$ depend upon the geographical boundaries of the regions i,j and the number of people of region j that regularly visit region i for work, study and other purposes. This data can be inferred from normal monitoring of daily commute of people. A straight forward generalization of Eq.(2) is as follows. Define $M_i = A_i + I_i$, i = 1, 1, ...N. Using same arguments as before we arrive at the following equations in place of Eqs. (4), (5) and (6)

$$\frac{dS_i}{dt} = -\Big[\beta_{i,i}[(1-\xi_i)^2 + \zeta_i^2]M_i$$

$$+ \sum_{j=1, j\neq i}^{N} \{(1-\xi_i)\xi_{i,j} + (1-\xi_j)\xi_{j,i} + \eta_{i,j}\xi_{j,i}\}\beta_{i,j}M_j\Big]S_i \tag{7}$$

$$\frac{dM_i}{dt} = \Big[\beta_{i,i}[(1-\xi_i)^2 + \zeta_i^2]M_i$$

$$+ \sum_{j=1, j\neq i}^{N} \{(1-\xi_i)\xi_{i,j} + (1-\xi_j)\xi_{j,i} + \eta_{i,j}\xi_{j,i}\}\beta_{i,j}M_j\Big]S_i - \gamma_iM_i \tag{8}$$

and

$$\frac{dI_i}{dt} = \alpha_iM_i - (\gamma_i + \alpha_i)I_i; \qquad \frac{dR_i}{dt} = \gamma_iM_i \qquad \frac{dD_i}{dt} = \gamma_i(1-\mu_i)I_i \tag{9}$$

Remarks made for Eqs. (4), (5) and (6) are also applicable to Eqs. (7), (8) and (9). Eqs. (7) and (8) are a set of $2N$ coupled set of non-linear, first order equations while Eq. (9), a set of three linear first order ordinary differential equations determining I_i,R_i and D_i for the region i, isolated from other regions. Since the coupling of different regions is through Eqs. (7) and (8), we will concentrate only on these two equations. We also note that the treatment of Eqs. (4) and (5) is practically the same. It merely needs a redefinition of the parameters β_i, γ_i.

2.2 Model (b) Movements of only Asymptomatic and Infected Groups

Many authors study the effect of movement of infected groups (Asymptomatic and Symptomatic) only. The susceptible population remains confined to their home region. With the notation introduced earlier this model leads to the following differential equations in place of Eqs. (7) and (8).

$$\frac{dS_i}{dt} = -\Big[\beta_{i,i}(1-\xi_i)M_i + \sum_{j=1,j\neq i}^{N} \xi_{i,j}\beta_{i,j}M_j\Big]S_i \tag{10}$$

$$\frac{dM_i}{dt} = \Big[\beta_{i,i}(1-\xi_i)M_i + \sum_{j=1,j\neq i}^{N} \xi_{i,j}\beta_{i,j}M_j\Big]S_i - \gamma_i M_i \tag{11}$$

Eq. (9) remains unchanged and is written here for completeness

$$\frac{dI_i}{dt} = \alpha_i M_i - (\gamma_i + \alpha_i)I_i; \qquad \frac{dR_i}{dt} = \gamma_i M_i \qquad \frac{dD_i}{dt} = \gamma_i(1-\mu_i)I_i \tag{12}$$

For completeness let us also write down the solutions of Eq. (12). Thus we have

$$I_i(t) = \alpha_i \int_0^t M_i(t')e^{-(\alpha_i+\gamma_i)(t-t')}dt' \tag{13}$$

$$R_i(t) = \gamma_i \int_0^t M_i(t')dt' \tag{14}$$

and

$$D_i(t) = \alpha_i\gamma_i(1-\mu_i) \int_0^t M_i(t')e^{-(\alpha_i+\gamma_i)(t-t')}dt' \tag{15}$$

Eqs. (12), (13), (14) and (15) are applicable to both models (a) and (b). We thus have to study Eqs. (7) and (8) (or equivalently Eqs. (10) and (11)) and obtain $M_i(t)$, $i = 1, 2, ...N$ and we proceed to do that in the next section. We may add here that although we consider Eqs. (7) and (8), most of the analysis is also applicable to Eqs. (10) and (11). Any difference will be pointed out as we go along.

3. Linearization and Solution of Eqs. (7) and (8) by Perturbation Expansion

In the initial stages of the epidemic, the number of infected individuals $M_i(t)$ is small in all regions. The Susceptible populations S_i is close to their initial fixed values. We can therefore assume $S_i = S_{i,0} + \lambda_{si}(t)$ where the change $s_i(t)$ is small while $S_{i,0}$ are constants independent of time. We have introduced a perturbation parameter λ. We expand both M_i and s_i as power series in λ and write

$$M_i = \sum_{n=0}^{\infty} \lambda^n M_i^{(n)}(t); \qquad s_i = \sum_{n=0}^{\infty} \lambda^n s_i^{(n)}(t); \tag{16}$$

Eqs. (7) and (8) are modified to

$$\frac{ds_i}{dt} = -\Big[[(1-\xi_i)^2 + \zeta_i^2]\beta_{i,i}M_i + \sum_{j=1,j\neq i}^{N} \{(1-\xi_i)\xi_{i,j} + (1-\xi_j)\xi_{j,i} + \eta_{i,j}\xi_{j,i}\}\beta_{i,j}M_j\Big][S_{i,0} + \lambda s_i] \tag{17}$$

$$\frac{dM_i}{dt} = \Big[[(1-\xi_i)^2 + \zeta_i^2]\beta_{i,i}M_i + \sum_{j=1,j\neq i}^{N} \{(1-\xi_i)\xi_{i,j} + (1-\xi_j)\xi_{j,i} + \eta_{i,j}\xi_{j,i}\}\beta_{i,j}M_j\Big][S_{i,0} + \lambda s_i] - \gamma_i M_i \tag{18}$$

Substituting the expansions, Eq. (16), in Eqs. (17) and (18) and equating the coefficients of λ^n on both sides of equation we have

$$\frac{ds_i^{(n)}}{dt} = -\Big[[(1-\xi_i)^2+\zeta_i^2]\beta_{i,i}M_i^{(n)}$$

$$+\sum_{j=1,j\neq i}^{N}\{(1-\xi_i)\xi_{i,j}+(1-\xi_j)\xi_{j,i}+\eta_{i,j}\xi_{j,i}\}\beta_{i,j}M_j^{(n)}\Big]S_{i,0} \quad -\sum_{k=0}^{(n-1)}\Big[[(1-\xi_i)^2+\zeta_i^2]\beta_{i,}$$

$$+\sum_{j=1,j\neq i}^{N}\{(1-\xi_i)\xi_{i,j}+(1-\xi_j)\xi_{j,i}+\eta_{i,j}\xi_{j,i}\}\beta_{i,j}M_j^{(n-1-k)}\Big]s_i^{(k)} \qquad (19)$$

for $n = 0, 1, 2, ...$ and

$$\frac{dM_i^{(n)}}{dt} = \Big[[(1-\xi_i)^2+\zeta_i^2]\beta_{i,i}M_i^{(n)}$$

$$+\sum_{j=1,j\neq i}^{N}\{(1-\xi_i)\xi_{i,j}+(1-\xi_j)\xi_{j,i}+\eta_{i,j}\xi_{j,i}\}\beta_{i,j}M_j^{(n)}\Big]S_{i,0}-\gamma_i M_i^{(n)}$$

$$+\sum_{k=0}^{(n-1)}\Big[[(1-\xi_i)^2+\zeta_i^2]\beta_{i,i}M_i^{(n-1-k)}+\sum_{j=1,j\neq i}^{N}\{(1-\xi_i)\xi_{i,j}+(1-\xi_j)\xi_{j,i}+\eta_{i,j}\xi_{j,i}\}\beta_{i,j}M_j^{(n-1-k)}\Big]s_i^{(k)} \qquad (20)$$

In the zeroth order approximation

$$\frac{ds_i^{(0)}}{dt} = -\Big[[(1-\xi_i)^2+\zeta_i^2]\beta_{i,i}M_i^{(0)}+\sum_{j=1,j\neq i}^{N}\{(1-\xi_i)\xi_{i,j}+(1-\xi_j)\xi_{j,i}+\eta_{i,j}\xi_{j,i}\}\beta_{i,j}M_j^{(0)}\Big]S_{i,0} \qquad (21)$$

$$\frac{dM_i^{(0)}}{dt} = \Big[[(1-\xi_i)^2+\zeta_i^2]\beta_{i,i}M_i^{(0)}+\sum_{j=1,j\neq i}^{N}\{(1-\xi_i)\xi_{i,j}+(1-\xi_j)\xi_{j,i}+\eta_{i,j}\xi_{j,i}\}\beta_{i,j}M_j^{(0)}\Big]S_{i,0}-\gamma_i M_i^{(0)} \qquad (22)$$

Eq. (22) is a set of N coupled, first order, linear differential equations with constant coefficients. It can be solved easily by reducing it to a set of decoupled equations which we will outline below. Eq. (23) does not have the functions $s^{(0)}_i$ in its RHS. Thus its solution is straight forward when $M^{(0)}_i$ are known and we have (at time $t = 0$ we have $s^{(n)}_i(0) = 0$ for all n)

$$s_i^{(0)}(t) = -S_{i,0}\int_0^t \Big[[(1-\xi_i)^2+\zeta_i^2]\beta_{i,i}M_i^{(0)}(t')$$

$$+\sum_{j=1,j\neq i}^{N}\{(1-\xi_i)\xi_{i,j}+(1-\xi_j)\xi_{j,i}+\eta_{i,j}\xi_{j,i}\}\beta_{i,j}M_j^{(0)}(t')\Big]dt' \qquad (23)$$

let us now consider Eq. (22) and cast it in a matrix form. Let us define a Matrix H with matrix elements

$$H_{i,j} = \beta_{i,j}S_{i,0}\{(1-\xi_i)\xi_{i,j}+(1-\xi_j)\xi_{j,i}+\eta_{i,j}\xi_{j,i}\}, \quad i\neq j; \qquad H_{i,i} = S_{i,0}[(1-\xi_i)^2+\zeta_i^2]\beta_{i,i}-\gamma_i \qquad (24)$$

and a column vector $x^{(0)}(t)$ with components $M^{(0)}_i(t)$. Then Eq. (22) can be written in a compact for

$$\frac{d\mathbf{x}^{(0)}(t)}{dt} = \mathbf{H}\mathbf{x}^{(0)}(t) \qquad (25)$$

Time independent $N \times N$, real square matrix H has N eigenvalues v_1, v_2, ...v_N, real or complex, repeated or distinct. Complex eigenvalues occur in conjugate pairs and lead to oscillatory solutions. We will assume that it has N eigenvectors. Let P be an $N \times N$ matrix whose columns are the eigenvectors of H. The case of H having fewer eigenvectors can also be treated by including generalized eigenvectors. That will slightly modify the treatment given below. Pre-multiplying Eq. (25) by the time independent matrix P^{-1} we get

$$\frac{d\mathbf{y}^{(\mathbf{0})}}{dt} = \mathbf{\Lambda}\mathbf{y}^{(\mathbf{0})}; \qquad \mathbf{y}^{(\mathbf{0})} = \mathbf{P}^{-1}\mathbf{x}^{(\mathbf{0})}; \qquad \mathbf{HP} = \mathbf{P\Lambda} \tag{26}$$

where Λ is a diagonal matrix with entries v_1, v_2, ...v_N along the main diagonal. The differential equations in Eq. (26) are easily solved and we have

$$\mathbf{y}^{(\mathbf{0})}(t) = e^{\mathbf{\Lambda}t}\mathbf{y}^{(\mathbf{0})}(0); \tag{27}$$

where $e^{\Lambda t}$ is a diagonal matrix with entries $e^{v_1 t}$, $e^{v_2 t}$, ...$e^{v_N t}$ along the main diagonal. Thus we have

$$\mathbf{x}^{(\mathbf{0})}(t) = \mathbf{P}e^{\mathbf{\Lambda}t}\mathbf{P}^{-1}\mathbf{x}^{(\mathbf{0})}(0); \tag{28}$$

$x^{(0)}(0)$ is the column vector of known initial values of M_i, $i = 1, 2, ...N$ at $t = 0$. Eq. (28) describes the time evolution of infections as a superposition of eigenvectors of the matrix H. Each eigenvector evolves at the rate $e^{v_i t}$, with its eigenvalue v_i. If the real part $\Re(v_i)$ of the eigenvalue is negative the eigenvector decays with time or grows if $\Re(v_i) > 0$. Consequences of these are examined in next subsection. We observe from Eq. (23) that to compute $s^{(0)}_i$ we need to find expressions for integrals $\int_0^t M^{(0)}_i(t')dt$. These can be found easily when we notice

$$\int_0^t \mathbf{x}^{(\mathbf{0})}(t')dt' = \mathbf{P}\mathbf{\Lambda}^{-1}[e^{\mathbf{\Lambda}t} - \mathbf{I}]\mathbf{P}^{-1}\mathbf{x}^{(\mathbf{0})}(0); \tag{29}$$

where I is the identity matrix.

We now consider the evaluation of higher terms in the perturbation series, i.e evaluation of $n - th$ order terms $M^{(n)}_i$ and $s^{(n)}_i$ for $n = 1, 2, ...$We first observe that initial values at $t = 0$ of $M^{(n)}_i(0)$ and $s^{(n)}_i(0)$ vanish for all indices $i = 1, 2, ...N$ and $n = 1, 2, ...\infty$.. Defining the N dimensional vector $x^{(n)}(t)$ with components $M^{(n)}_i(t)$, $i = 1, 2, ...N$, we see that Eq. (20) can be written in matrix form as

$$\frac{d\mathbf{x}^{(\mathbf{n})}(t)}{dt} = \mathbf{H}\mathbf{x}^{(\mathbf{n})}(t) + \mathbf{b}^{(\mathbf{n})}(t) \tag{30}$$

where the source vector $b^{(n)}(t)$ involves functions $M^{(k)}_i(t)$ and $s^{(k)}_i(t)$ of previous orders $k = 0, 1, 2, ...n - 1$. An expression for $b^{(n)}(t)$ can be written down as follows. Let $S^{(k)}(t)$ be a sequence of $N \times N$ diagonal matrices with diagonal elements $(s^{(k)}_1(t)/S_{1,0}, s^{(k)}_2(t)/S_{2,0}, ...s^{(k)}_N(t)) / S_{N,0})$ for $k = 0, 1, 2, ...$ Then the vector $b(n)(t)$ is given by

$$\mathbf{b}^{(\mathbf{n})}(t) = \sum_{k=0}^{n-1} \mathbf{S}^{(\mathbf{k})}(t)\mathbf{H}\mathbf{x}^{(\mathbf{n-1-k})}(t) \tag{31}$$

Thus the vector $b^{(n)}(t)$ can be computed if the vectors $x^{(n-1-k)}(t)$ and matrices $S^{(k)}(t)$ of earlier terms in the series expansion are known. For the moment we will assume that these are known, though we have to devise methods for computing diagonal matrices $S^{(k)}(t)$, $k = 0, 1, 2, ..n - 1$ Pre-multiplying Eq. (30) by the matrix P^{-1} we get

$$\frac{d\mathbf{y}^{(\mathbf{n})}(t)}{dt} = \mathbf{\Lambda}\mathbf{y}^{(\mathbf{n})}(t) + \mathbf{P}^{-1}\mathbf{b}^{(\mathbf{n})}(t); \qquad \mathbf{y}^{(\mathbf{n})} = \mathbf{P}^{-1}\mathbf{x}^{(\mathbf{n})} \tag{32}$$

and the solution of Eq. (32) is given by

$$\mathbf{y}^{(\mathbf{n})}(t) = \int_0^t e^{\mathbf{\Lambda}(t-t')}\mathbf{P}^{-1}\mathbf{b}^{(\mathbf{n})}(t')dt'; \qquad \mathbf{x}^{(\mathbf{n})}(t) = \int_0^t \mathbf{P}e^{\mathbf{\Lambda}(t-t')}\mathbf{P}^{-1}\mathbf{b}^{(\mathbf{n})}(t')dt'; \tag{33}$$

We now turn our attention to the computation of the matrices $S^{(k)}(t)$, $k = 0, 1, 2, ..n-1$. Let $s^{(k)}(t)$, denote N dimensional vector with components $(s^{(n)}_1(t), s^{(n)}_2(t), ...s^n_N(t))$. It is clear that this vector immediately yields the diagonal matrix $S^{(k)}(t)$. We already have an expression for the vector $s^{(0)}$ from Eqs. (23) and (29). Thus we have

$$\mathbf{s}^{(\mathbf{0})}(t) = -[\mathbf{H} + \mathbf{\Gamma}]\mathbf{P}\mathbf{\Lambda}^{-1}[e^{\mathbf{\Lambda}t} - \mathbf{I}]\mathbf{P}^{-1}\mathbf{x}^{(\mathbf{0})}(0); \tag{34}$$

where Γ is a diagonal matrix with elements $\gamma_i\delta_{i,j}$, $i, j = 1, 2, ...N$. We see from Eq. (23) that

$$\frac{d\mathbf{s}^{(\mathbf{n})}(t)}{dt} = -[\mathbf{H} + \mathbf{\Gamma}]\mathbf{x}^{(\mathbf{n})}(t) + \mathbf{b}^{(\mathbf{n})}(t) \tag{35}$$

Hence we have

$$\mathbf{s^{(n)}}(t) = -[\mathbf{H}+\mathbf{\Gamma}]\int_0^t \mathbf{x^{(n)}}(t')dt' - \int_0^t \mathbf{b^{(n)}}(t')dt' \tag{36}$$

Substituting for $x^{(n)}$ from Eq. (33) we have

$$\mathbf{s^{(n)}}(t) = -[\mathbf{H}+\mathbf{\Gamma}]\int_0^t \mathbf{x^{(n)}}(t')dt' - \int_0^t \mathbf{b^{(n)}}(t')dt'$$

$$= -[\mathbf{H}+\mathbf{\Gamma}]\int_0^t \mathbf{P\Lambda^{-1}}[e^{\mathbf{\Lambda}(t-t")} - \mathbf{I}]\mathbf{P^{-1}b^{(n)}}(t")dt" - \int_0^t \mathbf{b^{(n)}}(t')dt' \tag{37}$$

We can now successively compute $M^{(n)}_i$ (t) (or the vectors $x^{(n)}$ (t)) i.e. all terms in perturbation expansion. We form the matrix H, given by Eq. (24), and find its eigenvalues (v_1, v_2, ..., v_N) and the corresponding eigenvectors and obtain the matrices $\mathbf{\Lambda}$,$\mathbf{P}$ and $\mathbf{P}^{-1}$. as defined in Eq. (26). We can then obtain the vector $x^{(0)}(t)$ from Eq. (28) and known initial values of M_i, i = 1, 2, ...N at t = 0. We also obtain the vector $s^{(0)}(t)$ from Eq. (34) and then compute the diagonal matrix $S^{(0)}$. We can then compute the vectors $b^{(1)}$, $x^{(1)}$ and $s^{(1)}$ from Eqs. (31), (33) and (37) for the case of n = 1.. Knowing these vectors for n = 1 we can compute the corresponding vectors for n = 2 and so on.

3.1 Model (b)

The analysis given above is also applicable to Model (b) wherein Susceptible population is confined to their home region i.e. the starting equations are Eqs. (10) and (11). For perturbation expansions, Eqs. (17) and (18) are replaced by

$$\frac{ds_i}{dt} = -\Big[(1-\xi_i)\beta_{i,i}M_i + \sum_{j=1,j\neq i}^{N}\xi_{i,j}\beta_{i,j}M_j\Big][S_{i,0}+\lambda s_i] \tag{38}$$

$$\frac{dM_i}{dt} = \Big[(1-\xi_i)\beta_{i,i}M_i + \sum_{j=1,j\neq i}^{N}\xi_{i,j}\beta_{i,j}M_j\Big][S_{i,0}+\lambda s_i] - \gamma_i M_i \tag{39}$$

Using the expansion, Eq. (16), in these equations we obtain the following equations for $s^{(n)}_i$ (t) and $M^{(n)}_i$ (t)

$$\frac{ds_i^{(n)}}{dt} = -\Big[(1-\xi_i)\beta_{i,i}M_i^{(n)} + \sum_{j=1,j\neq i}^{N}\xi_{i,j}\beta_{i,j}M_j^{(n)}\Big]S_{i,0}$$

$$-\sum_{k=0}^{(n-1)}\Big[(1-\xi_i)\beta_{i,i}M_i^{(n-1-k)} + \sum_{j=1,j\neq i}^{N}\xi_{i,j}\beta_{i,j}M_j^{(n-1-k)}\Big]s_i^{(k)} \tag{40}$$

for n = 0, 1, 2, ... and

$$\frac{dM_i^{(n)}}{dt} = \Big[(1-\xi_i)\beta_{i,i}M_i^{(n)} + \sum_{j=1,j\neq i}^{N}\xi_{i,j}\beta_{i,j}M_j^{(n)}\Big]S_{i,0} - \gamma_i M_i^{(n)}$$

$$+\sum_{k=0}^{(n-1)}\Big[(1-\xi_i)\beta_{i,i}M_i^{(n-1-k)} + \sum_{j=1,j\neq i}^{N}\xi_{i,j}\beta_{i,j}M_j^{(n-1-k)}\Big]s_i^{(k)} \tag{41}$$

Matrix formulation presented earlier (for zeroth and higher order approximations) is applicable to Eqs. (40) and (41) if we replace the matrix H with the matrix H_b whose matrix elements are given by

$$(\mathbf{H_b})_{i,j} = [\beta_{i,j}(1-\xi_i)S_{i,0} - \gamma_i]\delta_{i,j} + \beta_{i,j}\xi_{i,j}S_{i,0}[1-\delta_{i,j}] \tag{42}$$

Here $\delta_{i,j}$ is Kronecker's δ function, being unity when $i = j$ and zero otherwise. Thus for example Eqs. (25) and (26) are modified to

$$\frac{d\mathbf{x^{(0)}}(t)}{dt} = \mathbf{H_b x^{(0)}}(t) \tag{43}$$

$$\frac{d\mathbf{y^{(0)}}}{dt} = \mathbf{\Lambda_b y^{(0)}}; \qquad \mathbf{y^{(0)}} = \mathbf{P_b^{-1}x^{(0)}}; \qquad \mathbf{H_bP_b} = \mathbf{P_b\Lambda_b} \tag{44}$$

where $\mathbf{\Lambda_b}$ and $\mathbf{P_b}$ are the matrices of eigenvalues and eigenvectors of the matrix Hb respectively. Rest of the analysis, Eqs. (27) to (41) is same as before after replacing the matrices $\mathbf{H},\mathbf{\Lambda},\mathbf{P}$ and $\mathbf{P}^{-1}$ with $\mathbf{H_b},\mathbf{\Lambda_b},\mathbf{P_b}$ and $\mathbf{P}^{-1}_{b}$.

4. The Fundamental Mode

We now examine the eigenvalue problem of matrices $\mathbf{H}$ and $\mathbf{H_b}$ more closely as it is clear from above analysis that the eigenvalues of these matrices play a crucial role in the growth of the epidemic.

Our first observation is that if the fractions $\xi_{i,j}$ are symmetric i.e. $\xi_{i,j} = \xi_{j,i}$ then the matrices $\mathbf{H}$ and $\mathbf{H_b}$ are real symmetric matrices. All their eigenvalues are real and they have N distinct eigenvectors. Thus $\mathbf{P}$ and $\mathbf{P_b}$ exist and are orthogonal matrices and $\mathbf{P}^{-1} = \mathbf{P_T}$, the transpose of $\mathbf{P}$. Similarly $\mathbf{P}^{-1}_{b} = \mathbf{P}^{T}_{b}$. Since all the eigenvalues are real, one of them is the largest. Corresponding eigenvector constitutes the fundamental mode if all its elements are non-negative. This mode grows much faster than other eigenvectors and dominates after a few initial time steps. We will assume that the eigenvalues are ordered i.e. $\nu_1 > \nu_2 \geq \nu_3$, ...νN In case some of the eigenvalues are complex then their ordering is according to their real part. We also observe that all fractions ξi,j ≥ 0. Thus the off-diagonal elements of H and Hb are non-negative. If in addition the diagonal elements

$$\mathbf{H}_{i,i} = S_{i,0}[(1-\xi_i)^2+\zeta_i^2]\beta_{i,i}-\gamma_i \geq 0; \qquad (\mathbf{H_b})_{i,i} = [\beta_{i,i}(1-\xi_i)S_{i,0}-\gamma_i] \geq 0 \quad (45)$$

then $\mathbf{H} \geq 0, \mathbf{H_b} \geq 0$. Let us assume that $\mathbf{H}$ and $\mathbf{H_b}$ are Irreducible. Then we have from Perron-Frobenius theorem that these matrices have a largest positive eigenvalue, with one and only one corresponding eigenvector whose elements are non-negative. This eigenvector is the dominant fundamental mode which grows faster than all other modes. We note that Irreducible, non-negativity, Eq. (45), is a sufficient condition for the existence of fundamental mode. It is not necessary. Thus e.g. if all the parameters $\gamma_i = \gamma$, $i = 1, 2, ...N$ then also fundamental mode exists. This follows from the fact that in this situation

$$\mathbf{\Gamma} = \gamma\mathbf{I}; \qquad \mathbf{G} = \mathbf{H} + \gamma\mathbf{I} \geq 0; \qquad \mathbf{G_b} = \mathbf{H_b} + \gamma\mathbf{I} \geq 0 \qquad (46)$$

Thus the matrices $\mathbf{G}$ and $\mathbf{G_b}$ have a largest positive eigenvalue and a corresponding non-negative eigenvector. The eigenvectors of $\mathbf{G},\mathbf{G_b}$ are also the eigenvectors of $\mathbf{H},\mathbf{H_b}$. Thus $\mathbf{H},\mathbf{H_b}$ have the same eigenvector which is their fundamental mode.

It is easy to find this fundamental mode in some simple cases. Let us assume that all coefficients $\beta_{i,j} = \beta$ are equal, $\gamma_i = \gamma$ and all the initial Susceptible populations $S_{i,0} = S_0$ are also equal. Further we assume that the fractions $\xi_{i,j} = \xi_{j,i}$ are symmetric. Let $z = (z_1, z_2, ...z_N)$ denote an eigenvector of $\mathbf{H}$ corresponding to an eigenvalue ν

$$\mathbf{Hz} = \nu\mathbf{z} \qquad (47)$$

which is explicitly written

$$\beta S_0\Big[[(1-\xi_i)^2+\zeta_i^2]z_i + \sum_{j=1,j\neq i}^{N}\{(1-\xi_i)\xi_{i,j}+(1-\xi_j)\xi_{j,i}+\eta_{i,j}\xi_{j,i}\}z_j\Big] = (\nu+\gamma)z_i \qquad (48)$$

It is easily seen that the vector z = (1, 1, ...1), a positive vector, is a solution of Eq. (48). This follows from the definitions of ζ^2_i and $\eta_{i,j}$ given after Eq. (3) and symmetry of $\xi_{i,j}$. The corresponding eigenvalue is $\beta S_0 - \gamma$. We also note that under the conditions stated above, before Eq. (47), the matrix $\mathbf{H_b}$ also has same dominant eigenvector and same eigenvalue as $\mathbf{H}$. Remaining eigenvalues and eigenvectors, however, are different.

Other eigenvalues of $\mathbf{H}$ and $\mathbf{H_b}$ are also of interest. They determine the rate at which the fundamental mode gets established. As noted earlier, if $\Re(\nu_i) < 0$, $i = 1, 2, ..N$ then all these modes decay while if $\Re(\nu_i) > 0$ for some i, then that mode also grows. In that case the eigenvalue separation ν_1 (ν_i), between the fundamental eigenvalue and the particular eigenvalue is an important parameter. This parameter determines if the fundamental mode gets established before the non-linear effects become significant.

Before leaving this section we observe that main advantage of the above analysis is theoretical. By analysing initial phase of the epidemic we can iden- tify some characteristics of the solutions that can help us to decide which model fits the, observed data better. Thus e.g. we can find the influence of allowing movement of susceptible population in addition to that of infected people. We also expect that the relative proportion of infections in different regions will be similar to the fundamental mode, even when non-linear effects become im- portant, whatever be the initial distribution. In fact powerful computer codes are available that yield accurate numerical solutions of the coupled differential equations. The role of perturbation methods for obtaining numerical results is limited.

4.1 Two Region Problem

We now apply above considerations to a simple two region problem. Since there are only two regions, people going out of region 1 are only going to region 2. Thus $\xi_{2,1} = \xi_1$, $\xi_{1,2} = \xi_2$. It is seen that in this case $\eta_{1,2} = \eta_{2,1} = 0$ and $\zeta^2_1 = \xi^2_1$, $\zeta^2_2 = \xi^2_2$. To simplify the problem still further we will assume $\beta_{1,1} = \beta_{1,2} = \beta_{2,2} = \beta$ and $\gamma_1 = \gamma_2 = \gamma$. We will also assume that the initial susceptible populations in two regions are equal i.e. $S_{1,0} = S_{2,0} = S_0$. Eqs. (7) and (8) then take a simple form

$$
\begin{aligned}
\frac{dS_1}{dt} &= -\beta S_1(t)\Big[[(1-\xi_1)^2+\xi_1^2]M_1+\{\xi_1+\xi_2-2\xi_1\xi_2\}M_2\Big] \\
\frac{dS_2}{dt} &= -\beta S_2(t)\Big[\{\xi_1+\xi_2-2\xi_1\xi_2\}M_1+[(1-\xi_2)^2+\xi_2^2]M_2\Big] \qquad (49)\\
\frac{dM_1}{dt} &= \beta S_1(t)\Big[[(1-\xi_1)^2+\xi_1^2]M_1+\{\xi_1+\xi_2-2\xi_1\xi_2\}M_2\Big]-\gamma M_1 \\
\frac{dM_2}{dt} &= \beta S_2(t)\Big[\{\xi_1+\xi_2-2\xi_1\xi_2\}M_1+[(1-\xi_2)^2+\xi_2^2]M_2\Big]-\gamma M_2 \qquad (50)
\end{aligned}
$$

We solve non-linear equations, Eq. (49) and (50) for $S_1(0) = S_2(0) = S0$ and some initial values of $M_1(0)$, $M_2(0) << S0$. These numerical solutions provide us the reference solutions against which we check our theoretical conclusions based on the linearised model. It is seen that the Eqs. (49) and (50) are invariant with respect to the transformation $\xi_1 \to (1-\xi_1)$, $\xi_2 \to (1-\xi_2)$. Numerical results for any two cases corresponding to this transformation are identical.

Many details of the linearized model can be worked out analytically. The matrices $\mathbf{H}$ and $\mathbf{H} + \mathbf{\Gamma}$ can be written down explicitly

$$
\mathbf{H} = \begin{pmatrix} \beta S_0[(1-\xi_1)^2+\xi_1^2]-\gamma & \beta S_0(\xi_1+\xi_2-2\xi_1\xi_2) \\ \beta S_0(\xi_1+\xi_2-2\xi_1\xi_2) & \beta S_0[(1-\xi_2)^2+\xi_2^2]-\gamma \end{pmatrix}
$$

$$
\mathbf{H}+\mathbf{\Gamma} = \beta S_0 \begin{pmatrix} [(1-\xi_1)^2+\xi_1^2] & (\xi_1+\xi_2-2\xi_1\xi_2) \\ (\xi_1+\xi_2-2\xi_1\xi_2) & [(1-\xi_2)^2+\xi_2^2] \end{pmatrix}; \; = \beta S_0 \begin{pmatrix} a & b \\ b & c \end{pmatrix} \qquad (51)
$$

Matrix $\mathbf{H}$ is a real symmetric matrix. It has two real eigenvalues ν_1, ν_2 given by the equation

$$
\nu_1 = \beta S_0 \frac{a+c+r}{2} - \gamma; \qquad \nu_2 = \beta S_0 \frac{a+c-r}{2} - \gamma; \qquad r = \sqrt{(a-c)^2+4b^2} \quad (52)
$$

where the coefficients a, b, c are identified as the elements of the matrix $\mathbf{H} + \mathbf{\Gamma}$ in Eq. (51). $\mathbf{H}$ has two real eigenvectors and the orthogonal matrix $\mathbf{P}$ (of eigenvectors) and its inverse are given by

$$
\mathbf{P} = \sqrt{\frac{2}{r(r+c-a)}} \begin{pmatrix} b & -\frac{r+c-a}{2} \\ \frac{r+c-a}{2} & b \end{pmatrix} = \begin{pmatrix} p_0 & -p_1 \\ p_1 & p_0 \end{pmatrix}; \qquad \mathbf{P}^{-1} = \begin{pmatrix} p_0 & p_1 \\ -p_1 & p_0 \end{pmatrix} \quad (53)
$$

Here p_0, p_1 are the components of the normalised fundamental eigenvector. The eigenvalue $\nu_1 > \nu_2$ and the corresponding eigenvector is the fundamental mode. In general the eigenvalues ν_1, ν_2 and corresponding eigenvectors depend on the parameters ξ_1, ξ_2. These also conform to the transformation mentioned above. However in case $\xi_1 = \xi_2 = \xi$ we have $\nu_1 = \beta S_0 - \gamma$, independent of ξ_1, ξ_2 while $\nu_2 = \beta S_0(1-4\xi+4\xi^2)-\gamma$. In this case we have $c = a$ and $r = 2b$. The matrices $\mathbf{P}$ and $\mathbf{P}^{-1}$ then reduce to

$$
\mathbf{P} = \sqrt{\frac{1}{2}} \begin{pmatrix} 1 & -1 \\ 1 & 1 \end{pmatrix}; \qquad \mathbf{P}^{-1} = \sqrt{\frac{1}{2}} \begin{pmatrix} 1 & 1 \\ -1 & 1 \end{pmatrix} \qquad (54)
$$

Another interesting case is when $\xi_2 = (1-\xi_1)$. In this case the eigenvalue $\nu_1 = 2\beta S_0[\xi^2_1 + \xi^2_2] - \gamma > \beta S_0 - \gamma$ and $\nu_2 = -\gamma$. The matrix $\mathbf{P}$ of eigenvectors\ and its inverse $\mathbf{P}^{-1}$ are again given by Eq. (54). Thus the fundamental mode is same as that for the case $\xi_1 = \xi_2$ but is attained earlier in time as the separation of eigenvalues is larger.

If we consider the model (b) then we have the equations

$$
\begin{aligned}
\frac{dS_3}{dt} &= -\beta S_3(t)\Big[(1-\xi_1)M_3+\xi_2 M_4\Big] \\
\frac{dS_4}{dt} &= -\beta S_4(t)\Big[\xi_1 M_3+(1-\xi_2)M_4\Big] \qquad (55)\\
\frac{dM_3}{dt} &= \beta S_3(t)\Big[(1-\xi_1)M_3+\xi_2 M_4\Big]-\gamma M_3 \\
\frac{dM_4}{dt} &= \beta S_4(t)\Big[\xi_1 M_3+(1-\xi_2)M_4\Big]-\gamma M_4 \qquad (56)
\end{aligned}
$$

in place of Eqs. (49) and 50). Linearised treatment deals with the matrix $\mathbf{H_b}$ which in this case reduces to

$$\mathbf{H_b} = \begin{pmatrix} \beta S_0(1-\xi_1)-\gamma & \beta S_0\xi_2 \\ \beta S_0\xi_1 & \beta S_0(1-\xi_2)-\gamma \end{pmatrix} \tag{57}$$

The matrix $\mathbf{H_b}$ is not symmetric. It has two eigenvalues $v_3 = \beta S_0 - \gamma$ and $v_4 = \beta S_0[1-(\xi_1+\xi_2)] - \gamma$. Its matrix of eigenvectors $\mathbf{P_b}$ is not orthogonal. $\mathbf{P_b}$ and P_b^{-1} are given by

$$\mathbf{P_b} = \begin{pmatrix} \xi_2 & -1 \\ \xi_1 & 1 \end{pmatrix} \qquad \mathbf{P_b}^{-1} = \left(\frac{1}{\xi_1+\xi_2}\right)\begin{pmatrix} 1 & 1 \\ -\xi_1 & \xi_2 \end{pmatrix} \tag{58}$$

Clearly the first eigenvalue $v_3 > v_4$ and the vector $(\xi_2, \xi_1)^T$ is the fundamental mode. It is interesting to note that the eigenvalue v_3 is independent of ξ_1, ξ_2, but it is the second eigenvector that does not depend on these parameters.

4.2 Numerical Solutions

We solved non-linear equations, Eq. (49) and (50) on one hand and Eqs. (55) and (56) on other using Mathematica for the initial conditions $S_1(0) = S_2(0) = S_0 = 1.0$ and two different initial values of $M_1(0)$, $M_2(0) << S_0$, namely (i) $M_1(0) = M_2(0) = 0.001$ and (ii) M1(0) = 0.002, M2(0) = 0.0. We like to see if the dominant mode comes into play or the non-linear effects prevent it from getting established. We can resolve the initial distribution in two eigenvectors of the matrix **H**, given by the two columns of the matrix **P**, Eq. (53), and write down the zeroth order solution of the linearized model. Thus for the boundary condition $M_1(0) = 0.002$ (sometimes 0.0002), and $M_2(0) = 0.0$ we have

$$M_1(t) = M_1(0)\left[p_0^2 e^{\nu_1 t} + p_1^2 e^{\nu_2 t}\right]; \qquad M_2(t) = \{M_1(0)p_0p_1\}\left[e^{\nu_1 t} - e^{\nu_2 t}\right] \tag{59}$$

Likewise if we use the eigenvectors of $\mathbf{H_b}$ we have

$$M_3(t) = \frac{M_3(0)}{\xi_1+\xi_2}\left[\xi_2 e^{\nu_3 t} + \xi_1 e^{\nu_4 t}\right]; \qquad M_4(t) = \frac{M_3(0)\xi_1}{\xi_1+\xi_2}\left[e^{\nu_3 t} - e^{\nu_4 t}\right]; \tag{60}$$

We varied the parameters ξ_1, ξ_2 over a fairly wide range with values of 0.1, 0.3, 0.5, 0.7 and 0.9, considered three values of β = 0.15, 0.2, 0.25 but kept $\gamma = 0.1$. We observe that the roles of two regions 1 and 2 are interchangeable. We note that the solution of initial value problems governed by differential equations is quite sensitive to the number of digits retained in computations. We observed that retaining six digits in computations gives large errors in the number of infected persons. If eight digits are retained in all computations, the errors are still significant. Results reported in tables 4 - 8 were obtained with retaining 16 digits in all computations.

We now discuss our numerical results and our inferences from them. In Ta- bles 1, 2 and 3 we present the eigenvalues v_1, v_2 and the fundamental eigenvector of model (a) for various combinations of fractions ξ_1 and ξ_2. These tables corre- spond to three values of β (or βS_0 as $S_0 = 1$), namely 0.15, 0.2 and 0.25 respec- tively. For model (b) the eigenvalues are $v_3 = \beta S_0\ \gamma$, $v_4 = \beta S_0(1\ \xi_1\ \xi_2)\ \gamma$ and the fundamental eigenvector is $(\xi_2, \xi_1)^T$ and hence are not listed separately.

We see from these tables that the fundamental eigenvalue v_1 is positive while v_2 is always negative, except when ξ_1, ξ_2 both are small e.g. $\xi_1 = \xi_2 = 0.1$. Similarly $v_3 > 0$ and v_4 is generally negative. Hence only the fundamental mode grows with time while the second eigenvector decays. Further, $v_1 \geq v_3$ This implies that the movement of Susceptible population leads to a more rapid growth of disease, compared to the case of movement of infected people (asymptomatic or otherwise) only. We also note that even a slight increase in v_1 (v_3 does not vary with ξ_1, ξ_2) leads to a substantial increase in the number of infections because of the exponential behaviour.

Eigenvalue separation (v_1-v_2) or (v_3-v_4) increases with βS_0, being directly proportional to this parameter. This suggests that fundamental mode is estab- lished earlier for higher values of β. Variation of these two separations with ξ_1, ξ_2 is mixed. Sometimes we have $(v_1 - v_2) > (v_3 - v_4)$ while at other times reverse is true. Thus in some cases fundamental mode is attained earlier for model (a) while in other cases model (b) reaches this equilibrium first. Numerical com- putations confirm these trends though non-linear effects, due to reduction of $S_1(t)$, $S_2(t)$, $S_3(t)$ and $S_4(t)$ from their initial value S_0, also affect the results. Typically the linear model is a fair approximation when $S_1(t)$, $S_2(t)$, $S_3(t)$ and $S_4(t)$ decrease only by a few percentage points from their initial value S0.

We present our results for some typical values of ξ_1, ξ_2 in tables 4, 5, 6 and 7 for the smallest value of $\beta = 0.15$ considered by us. It is in this case the fundamental mode is attained more slowly and is accompanied by a larger reduction of $S_i(t)$, $i = 1, 2, 3, 4$. Further we have chosen those cases when initial infections are all confined to region 1, while the fundamental mode predicts a much higher infections in region 2. Thus is a situation when non-linear effects are maximum during approach to equilibrium of linear models.

We begin by discussing table 4 where we tabulate $S_1(t)$, $S_2(t)$, $S_3(t)$ and $S_4(t)$ as well as $M_1(t)$, $M_2(t)$, $M_3(t)$ and $M_4(t)$ for $\xi_1 = 0.3$, $\xi_2 = 0.1$ and $t \in (0, 150)$ days for the initial conditions $M_1(0) = M_3(0) = 0.002$ and $M_2(0) = M_4(0) = 0.0$. In this case the fundamental eigenvalue $v_1 = 0.0590833$ of model (a) is somewhat larger than

v_3 = 0.05 but the second eigenvalue v_2 = −0.0490833 is much lower than the eigenvalue v_4 = 0.01. Thus it takes longer for model (b) to attain equillibrium than model (a). Numerical results show that it takes about 60 days for the fundamental mode to be established for model (a), i.e. infections are distributed in two regions in proportion to the fundamental eigenvector. In this time the susceptible population $S_1(t)$, $S_2(t)$, decreases by about 6%, 8% re- spectively. We see that at t = 60 the infected population $M_1(t)$ = 0.0197329 and $M_2(t)$ = 0.0272415. Their sum grows by a factor of 23.5 from its initial value of 0.002. However the zeroth order solution, Eq. (59), predicts $M_1(t)$ = 0.023181 and $M_2(t)$ = 0.032088. Clearly the zeroth order approximation is not a good measure of growth of the disease because of non-linear effects of reduction in $S_1(t)$, $S_2(t)$. In this interval about 4.2% of the population move to the "Re- moved" group by recovery or death. The ratio $M_1(t)/M_2(t)$ = 1.3805 at t = 60 though is closer to 1.413 predicted by fundamental eigenvector. For model (b) the infected population $M_3(t)$ = 0.00967471, $M_4(t)$ = 0.0247318 at t = 60 does not compare well with their Eq. (60) estimate of 0.010866, 0.029305 respec- tively while the growth factor is 17.2. The susceptible populations $S_3(t)$, $S_4(t)$ decrease by 3.24%, 7.1% respectively. This is in conformity with the eigenvalue v3 being somewhat less than v_1.The percentage of population that moves to Removed group in this time interval is 3.5%. The effect of larger second eigenvalue v_4 = −0.01 also shows up in the actual calculations. The ratio $M_4(t)/M_3(t)$ = 2.556 at t = 60 as against the value 3.0 predicted by the eigen-vector. This is partly due to slower decay of the second eigenvector and partly due to highly skewed fundamental eigenvector, three times in region 2 than in region 1. Reduction in $S_4(t)$ in this time interval also contributes. Overall we observe that the movements of susceptible increases the infections significantly, though not by an order of magnitude. It also leads to more even spatial dis- tribution of fundamental mode. Further this relative proportion of two regions is maintained much longer, beyond the applicability of linearized model. This suggests that one need not solve for different initial distributions of infected people. It is sufficient to consider initial distribution as given by fundamental mode.

Above conclusions are corroborated by comparing them with results for the initial conditions $M_1(0)$ = 0.0002, $M_2(0)$ = 0.0 in table 5. Since the initial infec- tions are an order of magnitude less, the non-linear effects are much less than in table 4. Thus at t = 60 the susceptible populations $S_1(t)$, $S_2(t)$, $S_3(t)$ and $S_4(t)$ all reduce by less than 1%. It is now seen that $M_1(t)$ = 0.00227942, $M_2(t)$ = 0.00320050 are much closer to their Eq. (59) estimates of 0.0023181, 0.0032088 and the ratio $M_2(t)/M_1(t)$ = 1.404 is much closer to theoretical value 1.413. However, more glaring difference is in the results of model (b). The ratio $M_4(t)/M_3(t)$ = 2.681 is higher than previos value of 2.556 at t = 60 and is still increasing with time. The value of this ratio 2.850 at t = 80, is still less than theoretical value 3.0. This is because of the slower decay of second eigenvector as v_4 = 0.01. At t = 60, the values $M_3(t)$ = 0.00107362 and $M_4(t)$ = 0.0028791 are close to their zeroth order estimates. Comparing the results of tables 4 and 5 we conclude that if the initial infections are high then non-linear effects come into play earlier and interfere with the settling of fundamental mode. In that case the solution will depend on the initial locations of infections. However if the epidemic starts from small initial infections, then its future growth is largely determined by the fundamental eigenvector and the initial location of outbreak has less significance.

We next discuss the case ξ_1 = ξ_2 = 0.3 in table 6. In this case the funda- mental eigenvalues v_1 = v_3 = 0.05 and hence the epidemic grows at the same rate for both models (a) and (b). Further the two eigenvectors are identical for both models, the fundamental mode is symmetric in regions 1 and (2) while the second eigenvector is antisymmetric. The eigenvalue v_2 = −0.076 is less than v_4 = 0.04 and hence the antisymmetric mode decays faster for model (a) than model (b). For both the models this second eigenmode decays faster than in previous tables 4 and 5 and the fundamental mode is nearly estab- lished by t = 50. The results show that indeed $M_1(t)$ = 0.0113069, $M_2(t)$ = 0.0112707 are nearly equal to one another at this time and are quite close to $M_3(t)$ = 0.0113959, $M_4(t)$ = 0.011176. Their zeroth order estimates, Eqs. (59) and (60), are $M_1(t)$ = 0.01220486, $M_2(t)$ = 0.01216012 and $M_3(t)$ = 0.0123178, $M_4(t)$ = 0.0120472 are much higher because of neglecting decrease in $S_1(t)$, $S_2(t)$, $S_3(t)$ and $S_4(t)$. If we reduce the initial infections to 0.0002, the reduction in $S_1(t)$, $S_2(t)$, $S_3(t)$ and $S_4(t)$ is less than 1% and the observed values of $M_1(t)$, $M_2(t)$, $M_3(t)$, $M_4(t)$ are much closer to their linearized estimates.

In previous cases the fundamental eigenvector for both models (a) and (b) are of similar nature. In table 4 it is greater in region 2 while in table 6 it is equal in both regions. Moreover the second eigenvector decayed faster in model (a) than in model (b). We now present a case where this eigenvector is higher in region 2 for model (a) while it is greater in region 1 for model (b). In table 7 we consider the case β = 0.15, ξ_1 = 0.5, ξ_2 = 0.7 and the eigenvalues v_1 = 0.0562396 > v_3 = 0.05 and v_2 = −0.09424 > v_4 = −0.13. Sharper decrease in v_4 implies that model (b) assumes equilibrium earlier than model (a). The fundamental eigenvector of model (a) assumes a value in region 2 which is 1.0832 times its value in region 1 while for model (b) its value in region 1 is 1.4 times that in region 2. Results of table 7 show that both models attain equilibrium by t = 40 the ratios $M_2(t)/M_1(t)$ = 1.0765, $M_3(t)/M_4(t)$ = 1.397 compare well those given by eigenvectors. The table shows that $M_1(t)$ = 0.0083692, $M_2(t)$ = 0.00900517 while $M_3(t)$ = 0.00827582, $M_4(t)$ = 0.00592471 at this time. The zeroth order linearized model, Eqs. (59) and (60) predict higher values $M_1(t)$ = 0.00875241, $M_2(t)$ = 0.0094306 and $M_3(t)$ = 0.009116, $M_4(t)$ = 0.0056621 because of slight reduction in susceptible populations during this interval. Fraction of people moving into Removed group is 0.0127318, 0.0137038 and 0.0132832, 0.0098403 respectively. There is an apparent mismatch between actual $M_4(t)$ value being higher than zeroth order estimate. This is observed for all t < 40 and disappears by t = 50 and is accompanied by significantly lower computed $M_3(t)$ compared to its zeroth estimate.

Lastly we observe that if the interaction between the regions is small, each region will evolve almost independently and thhe fundamental mode will hardly ever set in. In table 8 we present the results for the case β = 0.15, ξ_1 = ξ_2 = 0.1 with reduced initial conditions $M_1(0)$ = 0.0002, $M_2(0)$ = 0.0 so as to minimize the non-linear effects. Fundamental mode is symmetric in two regions for both the models (a) and (b) and so are the eigenvalues

$v_1 = v_3 = 0.05$. The second eigenvector is antisymmetric with $v_2 = -0.004$, small but negative, while $v_4 = 0.02$ is positive. Table 8 shows that $M_1(t) \approx M_2(t)$ only by $t = 100$ when they differ by less than 1%. By this time $S_1(t)$, $S_2(t)$ reduce by nearly 4%. Model (b) results show that there are more than 1% difference between $M_3(t)$ and $M_4(t)$ even for $t = 160$, suggesting that fundamental mode does not get established.

β	ξ_1	ξ_2	ν_1	ν_2	p_0	p_1
0.15	0.1	0.1	0.05000000	-0.00400000	0.70710678	0.70710678
		0.3	0.05908327	-0.04908327	0.81633943	0.57757246
		0.5	0.07774643	-0.07974643	0.80770531	0.58958641
		0.7	0.10562306	-0.09562306	0.76775173	0.64074744
		0.9	0.14600000	-0.10000000	0.70710678	0.70710678
	0.3	0.1	0.05908327	-0.04908327	0.57757246	0.81633943
		0.3	0.05000000	-0.07600000	0.70710678	0.70710678
		0.5	0.05623962	-0.09423962	0.73476024	0.67832690
		0.7	0.07400000	-0.10000000	0.70710678	0.70710678
		0.9	0.10562306	-0.09562306	0.64074744	0.76775173
	0.5	0.1	0.07774643	-0.07974643	0.58958641	0.80770531
		0.3	0.05623962	-0.09423962	0.67832690	0.73476024
		0.5	0.05000000	-0.10000000	0.70710678	0.70710678
		0.7	0.05623962	-0.09423962	0.67832690	0.73476024
		0.9	0.07774643	-0.07974643	0.58958641	0.80770531
	0.7	0.1	0.10562306	-0.09562306	0.64074744	0.76775173
		0.3	0.07400000	-0.10000000	0.70710678	0.70710678
		0.5	0.05623962	-0.09423962	0.73476024	0.67832690
		0.7	0.05000000	-0.07600000	0.70710678	0.70710678
		0.9	0.05908327	-0.04908327	0.57757246	0.81633943
	0.9	0.1	0.14600000	-0.10000000	0.70710678	0.70710678
		0.3	0.10562306	-0.09562306	0.76775173	0.64074744
		0.5	0.07774643	-0.07974643	0.80770531	0.58958641
		0.7	0.05908327	-0.04908327	0.81633943	0.57757246
		0.9	0.05000000	-0.00400000	0.70710678	0.70710678

Table 1: Eigenvalues and Fundamental Eigenvector, Eqs. (52), (53) for $\beta = 0.15$

β	ξ_1	ξ_2	ν_1	ν_2	p_0	p_1
0.20	0.1	0.1	0.10000000	0.02800000	0.70710678	0.70710678
		0.3	0.11211103	-0.03211103	0.81633943	0.57757246
		0.5	0.13699524	-0.07299524	0.80770531	0.58958641
		0.7	0.17416408	-0.09416408	0.76775173	0.64074744
		0.9	0.22800000	-0.10000000	0.70710678	0.70710678
	0.3	0.1	0.11211103	-0.03211103	0.57757246	0.81633943
		0.3	0.10000000	-0.06800000	0.70710678	0.70710678
		0.5	0.10831949	-0.09231949	0.73476024	0.67832690
		0.7	0.13200000	-0.10000000	0.70710678	0.70710678
		0.9	0.17416408	-0.09416408	0.64074744	0.76775173
	0.5	0.1	0.13699524	-0.07299524	0.58958641	0.80770531
		0.3	0.10831949	-0.09231949	0.67832690	0.73476024
		0.5	0.10000000	-0.10000000	0.70710678	0.70710678
		0.7	0.10831949	-0.09231949	0.67832690	0.73476024
		0.9	0.13699524	-0.07299524	0.58958641	0.80770531
	0.7	0.1	0.17416408	-0.09416408	0.64074744	0.76775173
		0.3	0.13200000	-0.10000000	0.70710678	0.70710678
		0.5	0.10831949	-0.09231949	0.73476024	0.67832690
		0.7	0.10000000	-0.06800000	0.70710678	0.70710678
		0.9	0.11211103	-0.03211103	0.57757246	0.81633943
	0.9	0.1	0.22800000	-0.10000000	0.70710678	0.70710678
		0.3	0.17416408	-0.09416408	0.76775173	0.64074744
		0.5	0.13699524	-0.07299524	0.80770531	0.58958641
		0.7	0.11211103	-0.03211103	0.81633943	0.57757246
		0.9	0.10000000	0.02800000	0.70710678	0.70710678

Table 2: Eigenvalues and Fundamental Eigenvector, Eqs. (52), (53) for $\beta = 0.20$

β	ξ_1	ξ_2	ν_1	ν_2	p_0	p_1
0.25	0.1	0.1	0.15000000	0.06000000	0.70710678	0.70710678
		0.3	0.16513878	-0.01513878	0.81633943	0.57757246
		0.5	0.19624405	-0.06624405	0.80770531	0.58958641
		0.7	0.24270510	-0.09270510	0.76775173	0.64074744
		0.9	0.31000000	-0.10000000	0.70710678	0.70710678
	0.3	0.1	0.16513878	-0.01513878	0.57757246	0.81633943
		0.3	0.15000000	-0.06000000	0.70710678	0.70710678
		0.5	0.16039936	-0.09039936	0.73476024	0.6783269
		0.7	0.19000000	-0.10000000	0.70710678	0.70710678
		0.9	0.24270510	-0.09270510	0.64074744	0.76775173
	0.5	0.1	0.19624405	-0.06624405	0.58958641	0.80770531
		0.3	0.16039936	-0.09039936	0.67832690	0.73476024
		0.5	0.15000000	-0.10000000	0.70710678	0.70710678
		0.7	0.16039936	-0.09039936	0.67832690	0.73476024
		0.9	0.19624405	-0.06624405	0.58958641	0.80770531
	0.7	0.1	0.24270510	-0.09270510	0.64074744	0.76775173
		0.3	0.19000000	-0.10000000	0.70710678	0.70710678
		0.5	0.16039936	-0.09039936	0.73476024	0.6783269
		0.7	0.15000000	-0.06000000	0.70710678	0.70710678
		0.9	0.16513878	-0.01513878	0.57757246	0.81633943
	0.9	0.1	0.31000000	-0.10000000	0.70710678	0.70710678
		0.3	0.24270510	-0.09270510	0.76775173	0.64074744
		0.5	0.19624405	-0.06624405	0.80770531	0.58958641
		0.7	0.16513878	-0.01513878	0.81633943	0.57757246
		0.9	0.15000000	0.06000000	0.70710678	0.70710678

Table 3: Eigenvalues and Fundamental Eigenvector, Eqs. (52), (53) for $\beta = 0.25$

t	$S_1(t)$	$S_2(t)$	$S_3(t)$	$S_4(t)$	$M_1(t)$	$M_2(t)$	$M_3(t)$	$M_4(t)$
0	1.00000	1.00000	1.00000	1.00000	0.002000	0.*10∧-9	0.002000	0.*10∧-9
10	0.99777	0.99791	0.99762	0.99788	0.002156	0.001247	0.002232	0.001262
20	0.99439	0.99389	0.99468	0.99371	0.002926	0.003062	0.002685	0.003153
30	0.98891	0.98658	0.99078	0.98620	0.004661	0.005910	0.003499	0.006061
40	0.97946	0.97353	0.98519	0.97337	0.007907	0.010683	0.004886	0.010569
50	0.96317	0.95099	0.97689	0.95259	0.013450	0.018478	0.007120	0.017277
60	0.93712	0.91519	0.96479	0.92137	0.021996	0.030203	0.010456	0.026620
70	0.89715	0.86125	0.94725	0.87682	0.033961	0.046046	0.015150	0.038536
80	0.84195	0.78874	0.92305	0.81865	0.047972	0.063601	0.021078	0.051531
90	0.77468	0.70352	0.89205	0.75023	0.060626	0.077920	0.027559	0.062905
100	0.70283	0.61622	0.85521	0.67674	0.067981	0.084064	0.033632	0.069997
110	0.63520	0.53780	0.81504	0.60564	0.067659	0.080163	0.037973	0.070801
120	0.57810	0.47432	0.77458	0.54268	0.060985	0.069138	0.039670	0.065588
130	0.53319	0.42636	0.73682	0.49055	0.050441	0.054581	0.038681	0.056568
140	0.50012	0.39233	0.70344	0.44941	0.038823	0.040287	0.035455	0.045754
150	0.47723	0.36961	0.67525	0.41809	0.028200	0.028570	0.030857	0.035333

Table 4: Solution of Eqs. (49), (50) and (55), (56) WorkingPrecision 16 $\beta = 0.15$, $\xi_1 = 0.3$, $\xi_2 = 0.1$, $M_1(0) = M_3(0) = 0.002$, $M_2(0) = M_4(0) = 0$

t	$S_1(t)$	$S_2(t)$	$S_3(t)$	$S_4(t)$	$M_1(t)$	$M_2(t)$	$M_3(t)$	$M_4(t)$
0	1.00000000	1.00000000	1.00000000	1.00000000	0.00020000	0.*10∧-22	0.00020000	0.*10∧-22
10	0.99980167	0.99983341	0.99977424	0.99983653	0.00020203	0.00011253	0.00021814	0.00011158
20	0.99950776	0.99948758	0.99949774	0.99947169	0.00026723	0.00027191	0.00025859	0.00028476
30	0.99901686	0.99883639	0.99912866	0.99878474	0.00042256	0.00053240	0.00033473	0.00056006
40	0.99815667	0.99764712	0.99859928	0.99757749	0.00072480	0.00098442	0.00046851	0.00100328
50	0.99662560	0.99550123	0.99779982	0.99552731	0.00128060	0.00178407	0.00069566	0.00172033
60	0.99389463	0.99165929	0.99655295	0.99211504	0.00227942	0.00320050	0.00107362	0.00287891
70	0.98904889	0.98484493	0.99457511	0.98652054	0.00404505	0.00568595	0.00169314	0.00473734
80	0.98055576	0.97293781	0.99142104	0.97748614	0.00710092	0.00995806	0.00269312	0.00767491
90	0.96599794	0.95265248	0.98641304	0.96317675	0.01221130	0.01703052	0.00427556	0.01220230
100	0.94197188	0.91952689	0.97857176	0.94113302	0.02027469	0.02800171	0.00670828	0.01889891
110	0.90465623	0.86895825	0.96660053	0.90852859	0.03182571	0.04326612	0.01028826	0.02818329
120	0.85169824	0.79904349	0.94902513	0.86302108	0.04599567	0.06106886	0.01522333	0.03983967
130	0.78505184	0.71417803	0.92460784	0.80425743	0.05960611	0.07663777	0.02141055	0.05244321
140	0.71210806	0.62534263	0.89302185	0.73529740	0.06809916	0.08420260	0.02819839	0.06326605
150	0.64262529	0.54474330	0.85544970	0.66248052	0.06855830	0.08123850	0.03437389	0.06930110
160	0.58383435	0.47969771	0.81456679	0.59313751	0.06171852	0.07011592	0.03857092	0.06897278
170	0.53830121	0.43137480	0.77373870	0.53275108	0.05080277	0.05552027	0.03990701	0.06298839
180	0.50508325	0.39730004	0.73593719	0.48367491	0.03910810	0.04131850	0.03835699	0.05359563
190	0.48175403	0.37399212	0.70304751	0.44567718	0.02869274	0.02946602	0.03461726	0.04319717
200	0.46575091	0.35831738	0.67578403	0.41716732	0.02035415	0.02042420	0.02967509	0.03347375
210	0.45493150	0.34787365	0.65399124	0.39618166	0.01410647	0.01389592	0.02442325	0.02524126
220	0.44768270	0.34095062	0.63703030	0.38090347	0.00962123	0.00934148	0.01947711	0.01869083
230	0.44285406	0.33637438	0.62408313	0.36984631	0.00649050	0.00623184	0.01516379	0.01368038
240	0.43964946	0.33335409	0.61433719	0.36186703	0.00434572	0.00413724	0.01159351	0.00994232
250	0.43752792	0.33136252	0.60707476	0.35611539	0.00289477	0.00273834	0.00874416	0.00719639

Table 5: Solution of Eqs. (49), (50) and (55), (56) WorkingPrecision 16 $\beta = 0.15$, $\xi_1 = 0.3$, $\xi_2 = 0.1$, $M_1(0) = M_3(0) = 0.0002$, $M_2(0) = M_4(0) = 0$

t	$S_1(t)$	$S_2(t)$	$S_3(t)$	$S_4(t)$	$M_1(t)$	$M_2(t)$	$M_3(t)$	$M_4(t)$
0	1.00000	1.00000	1.00000	1.00000	0.002000	0.*10∧-9	0.002000	0.*10∧-9
10	0.99759	0.99791	0.99729	0.99822	0.002245	0.0012488	0.002436	0.001058
20	0.99395	0.99444	0.99339	0.99500	0.003132	0.0027082	0.003372	0.002467
30	0.98822	0.98875	0.98746	0.98951	0.004940	0.0046317	0.005082	0.004487
40	0.97898	0.97948	0.97809	0.98039	0.007945	0.007571	0.007948	0.007564
50	0.96427	0.96473	0.96330	0.96572	0.012558	0.0121169	0.012450	0.012219
60	0.94210	0.94256	0.94108	0.94354	0.019160	0.018778	0.019015	0.018905
70	0.90961	0.91011	0.90861	0.91101	0.028073	0.027891	0.027968	0.027965
80	0.86521	0.86572	0.86428	0.86654	0.038904	0.038877	0.038758	0.038849
90	0.80939	0.80988	0.80908	0.81113	0.050091	0.050115	0.049652	0.049820
100	0.74572	0.74616	0.74593	0.74773	0.059046	0.059079	0.058509	0.058728
110	0.68022	0.68061	0.68097	0.68252	0.063233	0.063272	0.062732	0.062973
120	0.61940	0.61976	0.62033	0.62165	0.061695	0.061736	0.061328	0.061559
130	0.56720	0.56752	0.56831	0.56945	0.055416	0.055453	0.055420	0.055621
140	0.52527	0.52556	0.52623	0.52722	0.046401	0.046432	0.046518	0.046679
150	0.49348	0.49375	0.49408	0.49498	0.036652	0.036676	0.036865	0.036987

Table 6: Solution of Eqs. (49), (50) and (55), (56) WorkingPrecision 16 $\beta = 0.15$, $\xi_1 = 0.3$, $\xi_2 = 0.3$, $M_1(0) = M_3(0) = 0.002$, $M_2(0) = M_4(0) = 0$

t	$S_1(t)$	$S_2(t)$	$S_3(t)$	$S_4(t)$	$M_1(t)$	$M_2(t)$	$M_3(t)$	$M_4(t)$
0	1.00000	1.00000	1.00000	1.00000	0.002000	0.*10∧-9	0.002000	0.*10∧-9
10	0.99768	0.99757	0.99753	0.99797	0.002179	0.001476	0.002203	0.001295
20	0.99380	0.99340	0.99299	0.99465	0.003256	0.003240	0.003522	0.002566
30	0.98725	0.98630	0.98577	0.98947	0.005642	0.005672	0.005874	0.004264
40	0.97602	0.97413	0.97456	0.98144	0.009773	0.009660	0.009495	0.006818
50	0.95718	0.95376	0.95699	0.96878	0.016256	0.016224	0.014971	0.010780
60	0.92782	0.92213	0.93030	0.94944	0.025570	0.026264	0.022888	0.016565
70	0.88399	0.87510	0.89172	0.92124	0.037825	0.040140	0.033446	0.024400
80	0.82464	0.81170	0.83966	0.88268	0.052079	0.055663	0.045902	0.033877
90	0.75320	0.73587	0.77532	0.83420	0.064875	0.068984	0.058118	0.043572
100	0.67753	0.65620	0.70365	0.77898	0.071918	0.075925	0.066962	0.051207
110	0.60693	0.58252	0.63197	0.72232	0.071133	0.074511	0.069852	0.054660
120	0.54724	0.52078	0.56802	0.67045	0.063610	0.066062	0.066617	0.053353
130	0.50058	0.47290	0.51423	0.62573	0.052293	0.053843	0.058912	0.048294
140	0.46628	0.43795	0.47097	0.58894	0.040193	0.041087	0.048815	0.040945
150	0.44213	0.41349	0.43776	0.56016	0.029401	0.029912	0.038426	0.032908

Table 7: Solution of Eqs. (49), (50) and (55), (56) WorkingPrecision 16 $\beta = 0.15$, $\xi_1 = 0.5$, $\xi_2 = 0.7$, $M_1(0) = M_3(0) = 0.002$, $M_2(0) = M_4(0) = 0$

t	$S_1(t)$	$S_2(t)$	$S_3(t)$	$S_4(t)$	$M_1(t)$	$M_2(t)$	$M_3(t)$	$M_4(t)$
0	1.00000000	1.00000000	1.00000000	1.00000000	0.00020000	0.*10∧-23	0.00020000	0.*10∧-23
10	0.99971131	0.99989947	0.99967259	0.99993820	0.00026092	0.00006879	0.00028696	0.00004274
20	0.99930037	0.99966911	0.99918996	0.99977963	0.00036387	0.00017943	0.00042063	0.00012261
30	0.99868590	0.99922768	0.99846479	0.99944924	0.00053577	0.00035893	0.00062883	0.00026561
40	0.99773487	0.99844194	0.99735700	0.99882121	0.00082050	0.00065137	0.00095642	0.00051472
50	0.99623068	0.99709472	0.99564217	0.99768686	0.00128914	0.00112816	0.00147530	0.00094022
60	0.99382309	0.99483453	0.99296213	0.99570393	0.00205547	0.00190362	0.00229958	0.00165564
70	0.98995322	0.99110013	0.98875153	0.99231989	0.00329794	0.00315716	0.00360678	0.00284047
80	0.98374795	0.98501429	0.98213556	0.98666293	0.00528712	0.00516081	0.00566387	0.00476911
90	0.97389105	0.97525406	0.97180704	0.97740662	0.00840947	0.00830330	0.00884880	0.00783713
100	0.95851434	0.95994118	0.95592699	0.96265074	0.01315956	0.01308218	0.01363973	0.01255692
110	0.93523040	0.93667491	0.93216807	0.93994108	0.02003861	0.02000177	0.02051179	0.01945884
120	0.90153496	0.90293706	0.89812096	0.90666499	0.02926932	0.02928600	0.02965630	0.02880249
130	0.85581361	0.85710542	0.85228155	0.86107617	0.04030179	0.04038114	0.04050404	0.04006445
140	0.79880139	0.79992236	0.79545717	0.80381370	0.05137371	0.05151350	0.05131310	0.05146534
150	0.73451274	0.73542835	0.73163657	0.73890806	0.05975504	0.05993711	0.05942503	0.06019487
160	0.66937363	0.67008506	0.66711944	0.67293028	0.06301857	0.06321366	0.06250035	0.06371670
170	0.60971241	0.61024939	0.60808009	0.61240385	0.06047722	0.06065724	0.05989696	0.06127766
180	0.55952332	0.55992748	0.55840938	0.56146714	0.05342786	0.05357585	0.05289354	0.05418653
190	0.51995687	0.52026764	0.51922557	0.52132667	0.04412479	0.04423642	0.04369328	0.04475754
200	0.49016766	0.49041595	0.48969720	0.49112907	0.03459883	0.03467805	0.03428076	0.03508199
210	0.46842533	0.46863293	0.46812387	0.46910954	0.02610582	0.02615977	0.02588591	0.02645303
220	0.45287664	0.45305807	0.45268124	0.45337784	0.01915787	0.01919366	0.01901253	0.01939729
230	0.44190388	0.44206853	0.44177366	0.44228611	0.01378429	0.01380768	0.01369127	0.01394491
240	0.43422707	0.43438094	0.43413636	0.43453260	0.00978132	0.00979650	0.00972315	0.00988716
250	0.42888657	0.42903348	0.42881955	0.42914283	0.00687396	0.00688379	0.00683821	0.00694292

Table 8 Solution of Eqs. (49), (50) and (55), (56) WorkingPrecision 16 $\beta = 0.15$, $\xi_1 = 0.1$, $\xi_2 = 0.1$, $M_1(0) = M_3(0) = 0.0002$, $M_2(0) = M_4(0) = 0$

5. Conclusions

In this paper we have extended the SAIR model of spread of an epidemic to a system comprising of many regions. Interaction between various regions is described by the fraction of population of any region that is present in other re- gions. We considered two models, one which allows for migration of Susceptible and Aymptomatic groups and the other which confines Susceptible population to their home region. We then developed ordinary differential equations that describe the time evolution of Susceptible, Asymptomatic carriers, Infected and Removed groups of people of all the regions. It is noted that only half the equations are non-linear that are also coupled for different regions. Further in the initial stages of the evolution of disease, the number of infected and asymp- tomatic carriers is much smaller than the susceptible population. This allows us to treat these equations by expanding in a perturbation series involving only linear equations in all orders of approximation. The zeroth order approximation yields a simple set of coupled, linear, first order ordinary differential equations involving a constant matrix of the interactions between various regions. We cast these equations in matrix form and note that same interaction matrix governs the evolution of all higher order terms, only the source terms are different. We then observed the crucial role played by the spectrum of this matrix and noted that a fundamental mode exists which grows much faster than other eigenvec- tors. This fundamental mode gets established if real part of other eigenvalues is sufficiently negative. Future spatial and temporal evolution of the disease then is governed by the shape of this mode only and the location of initial outbreak does not have much significance. If some other modes also grow, though slower than the fundamental one, then non-linear effects interfere with setting in of the dominant mode. It is noted that this is the case when the regions interact weakly with each other.

We then applied above analysis to a simple two region problem for which lot of work can be carried out analytically. We verified our theoretical conclusions and confirmed that restricting the movement even of susceptible population only does lead to a slower growth of the epidemic. It was also found that once the fundamental mode sets in, subsequent time evolution roughly maintains the spatial shape much longer, well beyond the applicability of linearized model.

An apparent limitation of this analysis is that the spread of disease during commute from one region to another is neglected. It is well known that every major city has a well-developed public transportation system where people come in close contact with each other. Likewise different cities and countries are linked through a travel network. This network makes a major contribution to spread of disease. It should be noted that this transport network can be regarded as another region with a population that equals the number of people normally using the network. The exchange of population from transport region to other regions and vice versa is high so that sum of people that go to (and from) other regions almost equals its entire population.

Declarations

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Availability of Data No Data.

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Authors' Contribution DCS formulated the problem and provided theoret- ical Analysis. RGT wrote the programs and performed calculations. Both contributed to theoretical and computational parts as well as in writing the paper..

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