UNIVERSITY OF AGDER

Impact of travel restrictions on the spread of infection

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University of Agder, 2022

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Acknowledgements

I would like to thank my supervisors, Yuriy and Josef, for their invaluable help throughout the process of writing this thesis. I would also like to thank you to my family, friends and colleagues, Hege and Swar, for the support throughout the process.

Abstract

With the outbreak of Covid-19 it has become more important to know how to deal with a large scale epidemic effectively. Governments utilize different methods to try and contain the spread of viruses, to different results. But what does modeling say about the way to approach the problem? The purpose of the thesis is to introduce a modification of a popular SIR model for the spread of infectious diseases which allows to explore the impact of travel. The group of susceptible individuals S is split into two subgroups in accordance with the travel patterns: S_1 (traveling individuals) and S_2 (not traveling individuals). Stability properties of infection-free and endemic equilibria are studied with respect to the basic reproduction number. Numerous numerical simulations illustrate the dynamics of the system, including its modifications based on the introduction of the delayed argument. The results of the theoretical analysis and numerical simulations are compared to the recent empirical data to provide practical advice to local and governmental policy makers.

Contents

Chapter 1

Introduction

1.1 Motivation

Since the Covid-19 epedemic started in 2019, governments in different countries, have imposed strict policies including locking down the entire country to prevent the spread of disease. For instance in Norway the country went into lockdown the 12.03.22, and the Prime Minister of Norway is quoted to have said these are the strictest measures in peacetime [13]. But how efficient have these measures been? How much do travel restrictions impact the spread of infections? The central and local governments implemented a number of measures to restrict travel, and required quarantine depending on the spread of the infection. These issues are important to address, and mathematical modeling helps us better prepare for similar situation in the future.

In the beginning when we were exploring the theory I became very interested in modeling infectious diseases. We explored different infectious diseases including those caused by viruses (Corona-19, Rhinovirus, etc.) but also computer viruses. Since the data about Corona-19 were in abundance whereas for computer viruses we would have used simulated data rather than real values we focused on the spread of infection. We also considered possibilities for having more compartments including quarantined and hospitalized in which case the number of equations and parameters would have increased making the anal-

ysis more demanding. Further research possibilities are discussed in the final part of the thesis.

1.2 Aims and objectives

Travel facilitates the transmission of disease from areas affected by the virus, to areas less affected, since the amount of contacts rises substantially. To take this into account, we create a model which splits susceptible into two groups, those who currently travel and those who do not. For simplicity we call them mobile and non-mobile subgroups. We assume that there is a higher infection rate in the mobile subgroup. We also analyse the data from different sources to more accurately find the parameters we should use in our model. To analyse travel patterns we used statistical data from the Statistisk Sentralbyrå (SSB), Transportation Security Administration (TSA) and Travel Leaders Corporate. Since there is a lot of data related to Covid-19 published in the last few years we model parameter values for Covid-19. The important parameters in the model were introduced on the basis of the data available, for example, for the incubation and infection periods in medical and other modeling papers. Furthermore, Covid-19 was the reason for introducing travel restrictions and this is why we were in particularly interested in the model describing Covid-19 were the different travel patterns for different groups affect the dynamics the most. The research question we address is how a reduction of mobility impacts the spread of infectious disease. We consider both ordinary and delay differential equations in our models.

1.3 Structure of the thesis

This thesis is organised as follows. In Chapter 1 we provide our motivation for the work, describe the aims and objectives, and describe the organisation of the thesis. Chapter 2 introduces basic mathematical models used in epidemiology. Chapter 3 deals with delay differential equations (DDEs). We introduce

several classes of DDEs along with the method of steps for solution of DDEs and conclude the chapter with an overview of methods used for their solution in Matlab.

Our main contributions are reported in Chapters 4 and 5. The design of the models with and without delay is described in Chapter 4. First, for the model without delay we prove positivity of all solutions with positive initial data. Then we find disease-free and endemic equilibria and study their stability properties. We also compute the basic reproduction number. In the final part of Chapter 4 we introduce the delay into our model. Since the analysis of the model with delay becomes very complicated we limit ourselves only to numerical simulations for this case. Numerical simulations for models without and with delay are presented in Chapter 5, where we analyse the impact of the variation of parameters on the behavior of solutions. We conclude the thesis with the discussion of the limitations of our models and suggestions for further work.

Chapter 2

Mathematical models in epidemiology

2.1 Compartmental models

Compartmental models are often used for modeling the spread of infectious diseases. The first models where introduced in the early twentieth century by Ross in 1916, Ross and Hudson in 1917, Kermack and McKendrick in 1927. The deterministic models are usually described by ordinary differential equations but if spacial distribution is important partial differential equations are used. Further extensions may include stochastic (random) perturbations. Compartmental models are used for example to predict the spread of the disease, the total number of infected, the duration of the epidemics etc. This information is useful for governmental and medical authorities and policy makers.

When modeling diseases we assign the population into compartments. Then there are equations to describe the flow between the different compartments. Denote the sum of all the compartments as N. We can either keep the total population (N) constant over time, or account for changes in the population. This can be due to natural death and birth or death linked to the disease. The most common type of model is the SIR Model, with a constant popula-

tion. The compartments in this model are given by $S(t)$, which is the number of susceptible at time t, $I(t)$ the number of infected at time t and $R(t)$ the number of infected at time t where t is described in days. There are always possibilities to expand this model making it more realistic, but also more difficult to study. Adding states, for instance a quarantine state, exposed state [6], and hospitalization state are some of the ideas that have been explored. Furthermore, one can also change the functions describing the flow between the states.

2.2 SIR-model

In the SIR model we assume that the population is split in three groups S, I and R, as defined above where the total population $N(t) = S(t) + I(t) + R(t)$. It is common for equations describing the transfer between the states that the transfer between the compartments of susceptible and infected is dependent on both states. This is to simulate that if there are no, or a low amount of either susceptible or infected then there are fewer getting infected. In this model we assume a constant (no deaths and births) population, the advantage of this is that $N(t)$ adds up to the same value for all times, making the system simpler to analyse and to simulate. For models describing the spread of infection over a short period of time, the births and deaths are less important to take into account, and these will not change dramatically over the period we try to model. We also normalise the four variables in our equations making assuming that $N(0) = 1$ by finding the proportions of people in different categories. Our initial conditions are given by:

$$\begin{bmatrix} S(0) \\ I(0) \\ R(0) \end{bmatrix} = \begin{bmatrix} 1-q \\ q \\ 0 \end{bmatrix}$$

where q is the proportion of infected at $t = 0$. Our presentation of an SIR model follows [3], see also [2]. Consider the system of differential equations:

$$\dot{S} = -\alpha I(t)S(t), \tag{2.1}$$

$$\dot{I} = \alpha I(t)S(t) - \delta I(t), \tag{2.2}$$

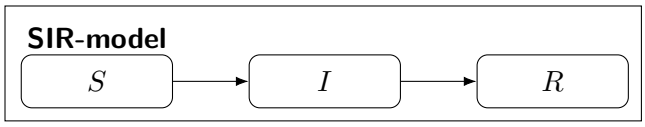
$$\dot{R} = \delta I(t). \tag{2.3}$$

The following variables and parameters are used in (2.1) - (2.3):
$S(t)$ - the number of people susceptible to get the disease;
$I(t)$ - the number of people infected with the disease;
$R(t)$ - the number of people that have had, and are now immune to the disease;
α - the transmission rate;
δ - the rate of infected leaving the infected state;

Note that since $N(0) = S(0) + I(0) + R(0) = 1$, it also means that $N(t) = S(t) + I(t) + R(t) = 1$ for all t since

$$\begin{aligned}\dot{N}(t) &= \dot{S}(t) + \dot{I}(t) + \dot{R}(t) \\ &= -\alpha I(t)S(t) + \alpha I(t)S(t) - \delta I(t) + \delta I(t) = 0.\end{aligned}$$

The following figure illustrates the SIR model:



2.3 SEIR

In this example we introduce births and deaths, both from natural causes and due to the disease itself. We also introduce a new compartment E, exposed, that simulate individuals at the initial stages of the disease who can infect others but cannot die at this stage. In this type of model we could either still

keep the population constant by equating the birth and death rates, but we will in this example assume they are different for illustrating other possibilities. Thus we no longer assume that N(t)=1. This means that terms dependent on two or more states, for instance, susceptible and infected $\alpha S(t)I(t)$ have to be rescaled. This is done by dividing by the total population, the term will then be $\alpha S(t)\frac{I(t)}{N}$. Consider the system of differential equations, studied by Carcione et al. [6]:

$$\begin{aligned}
\dot{S} &= \gamma N - \mu S - \alpha S(t)\frac{I(t)}{N}, \\
\dot{E} &= \alpha S(t)\frac{I(t)}{N} - (\mu + \epsilon)E, \\
\dot{I} &= \epsilon E(t) - (\gamma + \mu + \beta)I, \\
\dot{R} &= \gamma I(t) - \mu R(t).
\end{aligned}$$

In this model the variables and parameters are given by:

$S(t)$ - the number of people susceptible to get the disease;

$E(t)$ - the number of people exposed to the disease;

$I(t)$ - the number of people infected with the disease;

$R(t)$ - the number of people that have had, and are now immune to the disease;

α - disease transmission rate;

β - average fatality;

δ - the rate of infected recovering;

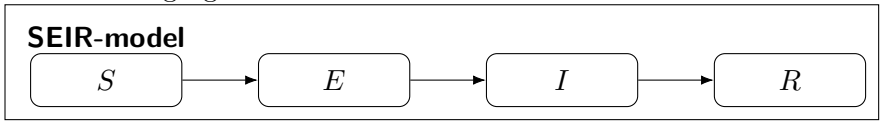
γ - birth rate;

μ - natural death rate;

ϵ - rate of progression from exposed to infected;

γ - recovery rate of infectious individuals;

The following figure illustrates the SEIR model:



Chapter 3

Introduction to DDEs

In this chapter, following Smith [4], we first define what a delay differential equation is, look at some examples and discuss different properties of DDEs. We then introduce the method of steps and the Runge-Kutta method that in combination is the method dde23 used to solve delay differential equations numerically.

3.1 Definitions of different classes of DDEs

In many cases, delayed differential equation is when the derivative of the unknown function depends on the values of the function in the past but sometimes derivative itself may contain the delayed argument. The properties of delay τ change depending on the equation. We classify the DDEs into different categories depending on the characteristics of the delay.

1. Constant delay

$$\dot{x}(t) = f(t, x(t), x(t-\tau)). \tag{3.1}$$

2. Time dependent delay

$$\dot{x}(t) = f(t, x(t), x(t-\tau(t))). \tag{3.2}$$

3. State dependent delay

$$\dot{x}(t) = f(t, x(t), x(t - \tau(t, x(t)))). \tag{3.3}$$

4. Neutral

$$\dot{x}(t) = f(t, x(t), x(t - \tau), \dot{x}(t - \tau)). \tag{3.4}$$

All of these categories assume that the derivative $\dot{x}$ at a point t is dependent on the values of the function in the past at a point shifted by the delay τ and solutions should match the initial function defined on the given interval associated with the delay. This is not always the case, as our derivative $\dot{x}$ at time t may depend on the the values of the solution over a certain finite or infinite time interval. This is called a distributed delay. The advantage of this type of a model is that for some problems it may be more realistic, but the equation becomes much harder to analyse. There are two main types of distributed delay equation:

$$\dot{x}(t) = \int_{t-\tau}^{t} f(s, x(s))\, ds \tag{3.5}$$

and

$$\dot{x}(t) = \int_{-\infty}^{t} f(s, x(t - s))\, ds. \tag{3.6}$$

It is important to note that in all of the cases we are required to know the function between $t_0 - \tau$ and t_0 in comparison to normal ODEs where we only require our initial condition at a single point.

Example 3.1.1. Let us consider the delayed negative feedback equation defined as:

$$\dot{x}(t) = -x(t - \tau). \tag{3.7}$$

Note that putting $\tau = 0$ gives us the ODE

$$\dot{x}(t) = -x(t) \tag{3.8}$$

where the solution would be of the form $x(t) = x(0)e^{-t}$. To solve equation (3.7) we can use the method of steps discussed in the next section.

3.2 Methods for solving DDEs

One of the methods for solving DDEs is the method of steps. We illustrate the method of steps for solving DDEs with constant delays. Consider a DDE of the form

$$\dot{x}(t) = f(t, x(t), x(t-\tau_1), x(t-\tau_2), ..., x(t-\tau_n)). \tag{3.9}$$

We want to solve the equation on the interval $(t_0,\ t_1)$. Denote $d_1 = \max(\tau_1, \tau_2, ..., \tau_n)$ and denote $d_2 = GCD(\tau_1, \tau_2, ..., \tau_n)$, where $GCD(\cdot)$ denotes the greatest common divisor. Meaning the largest rational number α for which there are positive integers $k_1, k_2, \ldots, k_n \in \mathbb{N}$ such that $\tau_i = k_i \cdot \alpha$ for $i = 1, 2, \ldots, n$. Our initial condition is given by an initial function $g(t)$,

$$x(t) = g(t), \qquad t_0 - d_1 \leq t \leq t_0.$$

We start by calculating the derivative on the interval $(t_0, t_0 + d_2)$, and then integrate to obtain the solution on that interval. Using the same procedure we can now calculate the solution on the next interval $(t_0 + d_2, t_0 + 2d_2)$. We then repeat this procedure until we reach t_1. Using the method of steps we therefore reduce solving a delay differential equation to solving a sequence of ordinary differential equations on a sequence of intervals. In the case when the $GCD(\cdot)$ of the delays does not exist, which means that the delays are non-commensurate, we need to use another approach to calculate the intervals to solve the equation on, see e.g. [7].

In some special cases we are able to solve the equation analytically. However it is not always possible and then we use numerical methods to estimate the values of the function that would be a solution to the equation (3.9). The

most common way to do this is using the Runge-Kutta methods, which is the main method used by the program dde23 to solve DDE's.

Example 3.2.1. Consider equation (3.7) with $\tau = 1$,

$$\dot{x}(t) = -x(t-1),$$

and assume

$$x(t) = 1, \qquad -1 \leq t \leq 0.$$

Using the initial condition we calculate the derivative of the function $x(t)$ on the interval $0 \leq t \leq 1$,

$$\dot{x}(t) = -x(t-1) = -1.$$

We then integrate the equation on $0 \leq t \leq 1$ to obtain

$$x(t) = \int -1 \ dt = C - t.$$

Since $x(0) = 1 \implies C = 1$, we have that

$$x(t) = 1 - t, \qquad 0 \leq t \leq 1.$$

We then redo the same procedure calculating the right hand side of the differential equation on $1 \leq t \leq 2$ using our new function

$$\dot{x}(t) = -x(t-1) = -(1-(t-1)) = -(2-t) = t - 2.$$

Integrating with respect to t, we obtain

$$x(t) = \int (t-2) \ dt = \frac{t^2}{2} - 2t + C,$$

Since $x(1) = 0 \implies C = \frac{3}{2}$ we have that

$$x(t) = \frac{t^2}{2} - 2t + \frac{3}{2}, \qquad 1 \le t \le 2,$$

and so on.

Example 3.2.2. Now let us consider the equation

$$\dot{x}(t) = -2x(t-1) + x(t-2),$$

and assume that

$$x(t) = t, \qquad -2 \le t \le 0$$

Using the initial condition, we calculate the right hand side of the differential equation, and integrate it on the interval $0 \le t \le 1$:

$$\dot{x}(t) = -2(t-1) + (t-2) = -t, \qquad 0 \le t \le 1.$$

and

$$x(t) = \int -t \ dt = -\frac{t^2}{2} + C.$$

Since $x(0) = 0 \implies C = 0$ we have

$$x(t) = -\frac{t^2}{2}, \qquad 0 \le t \le 1.$$

As above we calculate the right hand side of the differential equation, and integrate on the interval $1 \le t \le 2$:

$$\dot{x}(t) = 2\frac{(t-1)^2}{2} - \frac{(t-2)^2}{2} \quad \Rightarrow \quad x(t) = \int \frac{t^2}{2} - 1 \ dt = \frac{t^3}{6} - t + C.$$

Since $x(1) = \frac{1}{2} \implies C = \frac{8}{6}$, we have

$$x(t) = \frac{t^3}{6} - t + \frac{8}{6}, \qquad 1 \leq t \leq 2.$$

3.3 Solution of DDEs in Matlab and the Runge-Kutta method

To solve DDEs we have chosen to use the package dde23 for Matlab, and the inspiration for the examples is taken from [9]. This package uses numerical methods to solve DDEs, where a Runge-Kutta type method is applied to the method of steps to solve equations. Below is a short description of the family of explicit Runge-Kutta methods.

Consider the initial value problem

$$\frac{dx}{dt} = f(t, x), \qquad x(t_0) = x_0$$

where the initial conditions t_0 and $x(t_0)$ are given. The next step y_{n+1} is defined by

$$y_{n+1} = y_n + h \sum_{i=1}^{s} b_i k_i$$

where

$$\begin{aligned}
k_1 &= f(t_n, y_n), \\
k_2 &= f(t_n + c_2 h, y_n + h(a_{21} k_1)), \\
k_3 &= f(t_n + c_3 h, y_n + h(a_{31} k_1 + a_{32} k_2)), \\
&\vdots \\
k_s &= f(t_n + c_s h, y_n + h(a_{s1} k_1 + a_{s2} k_2 + \cdots + a_{s,s-1} k_{s-1}).
\end{aligned}$$

Here s is the number of stages. For instance $s = 4$ is the most common value in which case it is called the RK4 method. The coefficients are defined as b_i for $i = (1, 2, \ldots, s)$, c_i for $i = (1, 2, \ldots, s)$ and a_{ij} for $(1 \leq j < i \leq s)$, where b_i are the weights, and c_i are the nodes. The method is shown to be consistent if the weights add up to 1:

$$\sum_{i=1}^{s} b_i = 1.$$

The following two examples use dde23, and the code is given in the Appendix with explanations.

Example 3.3.1. We start with an illustrative example of the system of the form (3.1). Consider the system

$$\begin{aligned} \dot{x}_1(t) &= -x_1(t - 0.5) + x_3(t - 1), \\ \dot{x}_2(t) &= x_1(t - 0.5) - x_2(t - 2), \\ \dot{x}_3(t) &= x_2(t - 2) - x_3(t - 1), \end{aligned} \tag{3.10}$$

with the initial conditions $x_1(t) = 1$, $x_2(t) = 0$, $x_3(t) = 0$, for all $t < 0$. The solution on the interval [0,20] is plotted in Figure 3.1.

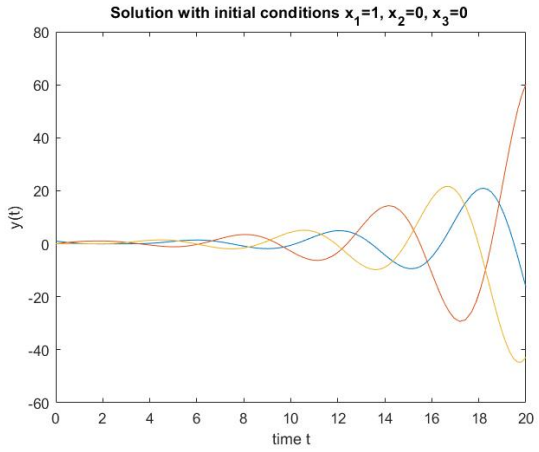


Figure 3.1: Solutions of the system (3.10)

Using another set of initial conditions $x_1(t) = t$, $x_2(t) = t^2$, $x_3(t) = t^3$, for all

$t < 0$ we obtain solutions plotted in Figure 3.2.

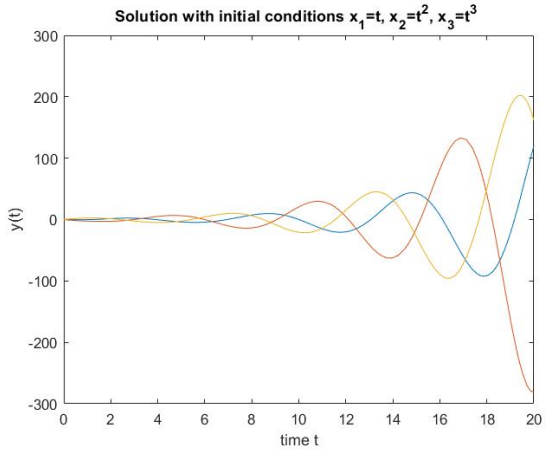
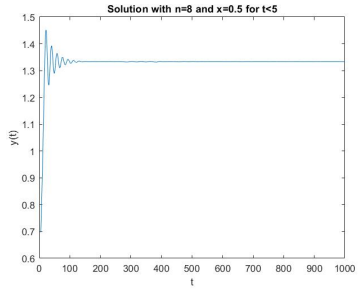


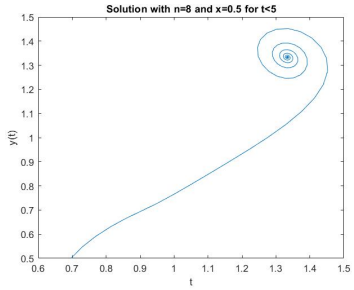
Figure 3.2: Solutions of the system (3.10) with modified initial conditions

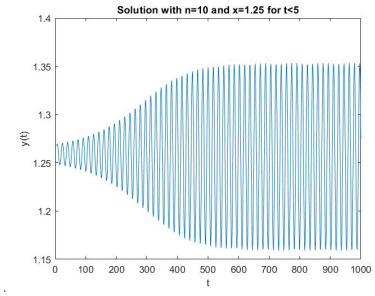
Example 3.3.2. The second example, called the Mackey-Glass equation, is used in biology. It mimics healthy and pathological behaviour in some biological models, it is for instance used to analyse relative quantity of mature cells in the blood. Consider for example DDE

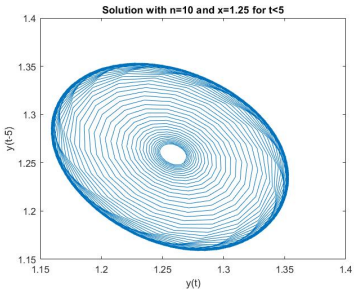
$$\dot{x}(t) = \frac{2x(t-5)}{x(t-5)^n + 10} - 0.1x(t) \tag{3.11}$$

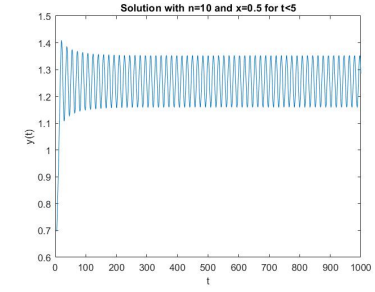
with the initial condition $x(t) = 0.1$ for all $t < 0$. We solve the equation on the interval [0,1000] plotting solutions for different values of n and different initial conditions in the following figures.

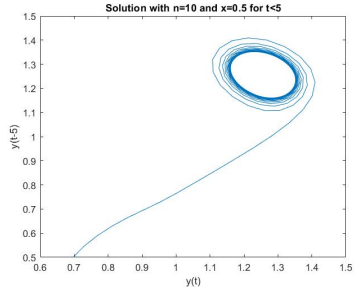





Solution with n=10 and x=1.25 for t<5
y(t)
t


Solution with n=10 and x=1.25 for t<5
y(t-5)
y(t)


Solution with n=10 and x=0.5 for t<5
y(t)
t


Solution with n=10 and x=0.5 for t<5
y(t-5)
y(t)

Chapter 4

Impact of travel on the spread of infection

In this chapter we introduce the design of the models with and without delay. We start by proving positivity of all solutions with positive initial data. We will then find the disease-free and endemic equilibria and study their stability properties, before we compute the basic reproduction number. In the final part of this chapter we introduce the delay into our model.

4.1 Design of the model without delay

In our model, we assume that all susceptible individuals S are divided into two subgroups, S_1 and S_2, in accordance with their travel patterns. The former, larger group, includes less frequent travellers and the latter, smaller group, accounts for those who travel more often. We assume that both business and leisure travels are included. Our starting conditions will be given by

$$S_1 = (1-q)S, \qquad S_2 = qS$$

where the coefficient q corresponds to the proportion of active travellers among all susceptible. Our model is a modification of the SIR [2] model and with

the spilt of susceptible in two groups we have equations for S_1 and S_2. To the best of our knowledge, there are no similar models in the literature yet. The system in our case assumes the form

$$\dot{S_1} = -\alpha I(t)S_1(t) - \gamma S_1(t) + \omega S_2(t) + \theta(1-\xi)R(t), \tag{4.1}$$

$$\dot{S_2} = -\beta I(t)S_2(t) + \gamma S_1(t) - \omega S_2(t) + \xi\theta R(t), \tag{4.2}$$

$$\dot{I} = \alpha I(t)S_1(t) + \beta I(t)S_2(t) - \delta I(t), \tag{4.3}$$

$$\dot{R} = \delta I(t) - \theta R(t) \tag{4.4}$$

where

$$N(t) = S_1(t) + S_2(t) + I(t) + R(t) \tag{4.5}$$

and

$$N(0) = S_1(0) + S_2(0) + I(0) + R(0) = 1. \tag{4.6}$$

We have the following variables and parameters:

$S(t)$ - the number of people susceptible to get the disease;

$S_1(t)$ - the number of people susceptible being non-mobile;

$S_2(t)$ - the number of people susceptible being mobile;

$I(t)$ - the number of people infected with the disease;

$R(t)$ - the number of people that have had, and are now immune to the disease;

$N(t)$ - the number of all individuals in the equation;

α - the transmission rate for people in the non-mobile state;

β - the transmission rate for people in the mobile state;

γ - the rate of people moving from non-mobile to mobile;

ω - the rate of people moving from mobile to non-mobile;

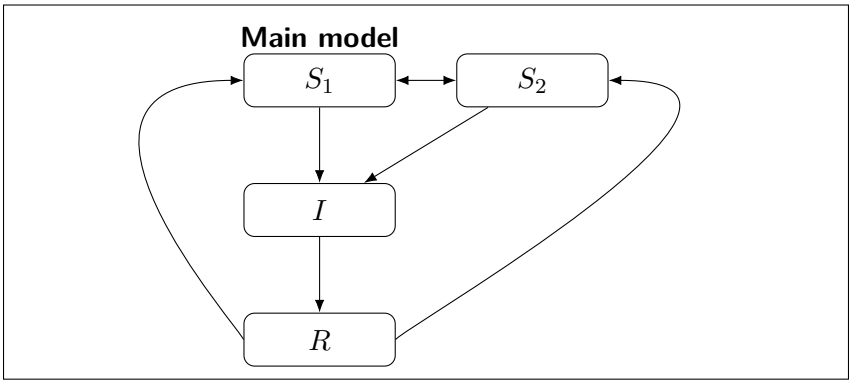
δ - the rate of infected leaving the infected state;

θ - the rate of people that can get infected again;

ξ - the rate of people going into the mobile group from recovered;

q - the proportion of people being mobile at $t = 0$.

The diagram describing the model is presented in the following figure.



In what follows, we explain the meaning of each term in our model.

1. $\alpha I(t)S_1(t)$ The number of people being non-mobile that get infected. It depends both on how many are already infected and how many are susceptible. If we have few infected or few susceptible then there will be fewer new people infected.

2. $\beta I(t)S_2(t)$ The number of people being mobile that gets infected. It depends both on how many are already infected and how many are susceptible. If we only have a few infected or few susceptible then there will be fewer new people infected. In general, we assume that he value of β will be higher than α as traveling gives you a higher chance of getting infected. However, it would be in principle possible to stud the travel to areas with a lower infection rate, if needed.

3. $\theta(1-\xi)S_1(t)$ Number of people that move from recovered state to the non-mobile state.

4. $\theta\xi S_2(t)$ Number of people that move from recovered state to the mobile state.

5. $\gamma S_1(t)$ The number of people that move from the mobile state to the non-mobile state.

6. $\omega S_2(t)$ The number of people that move from the non-mobile state to the mobile state.

7. $\delta I(t)$ The number of people that move from the infected to recovered state and remain immune to infection afterwards.

4.2 Positivity of solutions

Theorem 4.2.1. *Assume that* $S_{1_0}, S_{2_0}, I_0, R_0 \geq 0$*, then the solution* $\vec{x}(t) = (S_1(t), S_2(t), I(t), R(t))^{\mathrm{T}}$ *to the system (4.1) - (4.4) with the initial conditions*

$$(S_1(0), S_2(0), I(0), R(0))^{\mathrm{T}} = (S_{1_0}, S_{2_0}, I_0, R_0)^{\mathrm{T}}$$

is non-negative for all $t > 0$*.*

Proof. Let $\vec{x}(t) = (S_1(t), S_2(t), I(t), R(t))^{\mathrm{T}}$ be the solution to the system (4.1) - (4.4) with initial condition $\vec{x}(0) = (S_{1_0}, S_{2_0}, I_0, R_0)^{\mathrm{T}}$ where S_{1_0},S_{2_0},I_0,$R_0 \geq 0$. If $S(t_1) = 0$ for $t_1 > 0$ and all the other components $S_2(t_1), I(t_1), R(t_1)$ are positive, then the derivative of S_1 will be positive:

$$\begin{aligned}\dot{S}_1(t_1) &= -\alpha I(t_1)S_1(t_1) - \gamma S_1(t_1) + \omega S_2(t_1) + \theta(1-\xi)R(t_1) \\ &= \omega S_2(t_1) + \theta(1-\xi)R(t_1) > 0.\end{aligned}$$

This means that if $S_1(t_1) = 0$, the function $S_1(t)$ is increasing afterwards and cannot become negative as long as other components are positive. Similarly, assuming $S_2(t_1) = 0$ we get

$$\dot{S}_2(t_1) = -\beta I(t_1)S_2(t_1) + \gamma S_1(t_1) - \omega S_2(t_1) + \xi\theta R(t_1) = \gamma S_1(t_1) + \xi\theta R(t_1) > 0.$$

Assume now that $I(t_1) = 0$, then

$$\dot{I}(t_1) = \alpha I(t_1)S_1(t_1) + \beta I(t_1)S_2(t_1) - \delta I(t_1) = 0,$$

and this is not enough since the derivative can change the sign at t_1 and become negative. Therefore, we study the component $I(t)$. Integrating equation (4.3),

we conclude that its solution is

$$I(t) = Ce^{\int(\alpha S_1(u)+\beta S_2(u)-\delta)du}.$$

and since the initial condition $I(0) \geq 0$, $I(t) \geq 0$ for all $t > 0$. Assuming now that $R(t_1) = 0$, we get

$$\dot{R} = \delta I(t_1) - \theta R(t_1) = \delta I(t_1) > 0.$$

Therefore, if the initial conditions are non-negative $S_{1_0}, S_{2_0}, I_0, R_0 \geq 0$, solution to the system (4.1) - (4.4) cannot become negative eventually. □

Corollary 4.2.2. *Let* $0 \leq S_{1_0}, S_{2_0}, I_0, R_0 \leq 1$. *Then* $0 \leq S_1(t) \leq 1$, $0 \leq S_2(t) \leq 1$, $0 \leq I(t) \leq 1$ *and* $0 \leq R(t) \leq 1$ *for all* $t \geq 0$.

Proof. It follows from the Theorem 4.2.1 that $S_1(t), S_2(t), I(t), R(t) \geq 0$ for all $t \geq 0$. It can be concluded from (4.5) that for all t we have

$$\dot{N}(t) = \dot{S}_1(t) + \dot{S}_2(t) + \dot{I}(t) + \dot{R}(t) = 0.$$

Taking into account (4.6), we deduce that for all t>0

$$1 = N(t) = S_1(t) + S_2(t) + I(t) + R(t). \tag{4.7}$$

This concludes the proof. □

4.3 Equilibria

To find equilibria, we solve the system of nonlinear algebraic equations at the equilibrium $\dot{S}_1$, $\dot{S}_2$, $\dot{I}$ and $\dot{R}$ equal to zero.

$$0 = -\alpha I(t)S_1(t) - \gamma S_1(t) + \omega S_2(t) + \theta(1-\xi)R(t), \tag{4.8}$$

$$0 = -\beta I(t)S_2(t) + \gamma S_1(t) - \omega S_2(t) + \xi\theta R(t), \tag{4.9}$$

$$0 = \alpha I(t)S_1(t) + \beta I(t)S_2(t) - \delta I(t), \tag{4.10}$$

$$0 = \delta I(t) - \theta R(t). \tag{4.11}$$

We start by finding the disease free equilibrium denoted E_0 by assuming that $I = 0$. Using (4.11) we get

$$R = \frac{\delta}{\theta} I = \frac{\delta}{\theta} \cdot 0 = 0.$$

Substituting $I = 0$ and $R = 0$ into equation (4.8), we obtain first

$$S_1 = \frac{\omega}{\gamma} S_2,$$

and then, substituting in (4.7), we get

$$S_1 = \frac{\omega}{\gamma + \omega}, \qquad S_2 = \frac{\gamma}{\gamma + \omega}.$$

The disease free equilibrium E_0 is therefore given by

$$E_0 = \left(\frac{\omega}{\gamma + \omega}, \frac{\gamma}{\gamma + \omega}, 0, 0 \right).$$

We now find the endemic equilibrium E_* assuming that $I(0) \neq 0$ and using (4.10), we get

$$I(\alpha S_1 + \beta S_2 - \delta) = 0 \quad \Rightarrow \quad S_1 = \frac{\delta}{\alpha} - \frac{\beta}{\alpha} S_2.$$

From (4.11) we get

$$R = \frac{\delta}{\theta} I.$$

Then substituting expressions for S_1 and R into (4.7) we can calculate S_2 in terms of I

$$S_2 = 1 - R - I - S_1 = 1 - \frac{\delta}{\theta} I - I - \frac{\delta}{\alpha} + \frac{\beta}{\alpha} S_2.$$

Simplifying we get

$$S_2 = \frac{\alpha}{\alpha - \beta} - \frac{\alpha\delta}{\alpha^2 - \alpha\beta} - \frac{\alpha\theta + \alpha\delta}{\alpha\theta - \beta\theta} I.$$

We can now plug in for S_2 to express S_1 in terms of I

$$S_1 = \frac{\delta}{\alpha} - \frac{\beta}{\alpha - \beta} + \frac{\beta\delta}{\alpha^2 - \alpha\beta} + \frac{\beta\theta + \beta\delta}{\alpha\theta - \beta\theta} I.$$

We substitute the expressions for S_1, S_2 and R into (4.9) and solve it for I , provided that $\alpha - \beta \neq 0$, $\alpha \neq 0$, $\beta \neq 0$ and $\theta \neq 0$:

$$\begin{aligned} -\beta I\Big(\frac{\alpha}{\alpha - \beta} - \frac{\alpha\delta}{\alpha^2 - \alpha\beta} - \frac{\alpha\theta + \alpha\delta}{\alpha\theta - \beta\theta} I\Big) + \\ \gamma\Big(\frac{\delta}{\alpha} - \frac{\beta}{\alpha - \beta} + \frac{\beta\delta}{\alpha^2 - \alpha\beta} + \frac{\beta\theta + \beta\delta}{\alpha\theta - \beta\theta} I\Big) - \\ \omega\Big(\frac{\alpha}{\alpha - \beta} - \frac{\alpha\delta}{\alpha^2 - \alpha\beta} - \frac{\alpha\theta + \alpha\delta}{\alpha\theta - \beta\theta} I\Big) + \xi\delta I = 0. \end{aligned}$$

Collecting the terms, we obtain

$$\begin{aligned} \alpha\beta\Big(\frac{\theta + \delta}{\alpha\theta - \beta\theta}\Big) I^2 + \\ \Big(\frac{\alpha\beta\delta}{\alpha^2 - \alpha\beta} - \frac{\alpha\beta}{\alpha - \beta} + \frac{\gamma\beta\theta + \gamma\beta\delta}{\alpha\theta - \beta\theta} + \frac{\alpha\omega\theta + \alpha\omega\delta}{\alpha\theta - \beta\theta} + \xi\delta\Big) I + \\ \Big(\frac{\alpha\omega\delta + \gamma\beta\delta}{\alpha^2 - \alpha\beta} - \frac{\gamma\beta + \alpha\omega}{\alpha - \beta} + \frac{\gamma\delta}{\alpha}\Big) = 0 \end{aligned}$$

and

$$\alpha\beta\Big(\frac{\theta+\delta}{\theta(\alpha-\beta)}\Big)I^2+ \\ \Big(\frac{\alpha\beta\delta\theta-\alpha^2\beta\theta+\alpha\beta\gamma\theta+\alpha\beta\gamma\delta+\alpha^2\omega\theta+\alpha^2\omega\delta+\alpha^2\delta\theta\xi-\alpha\beta\delta\theta\xi}{\alpha\theta(\alpha-\beta)}\Big)I+ \\ \Big(\frac{\alpha\omega\delta+\gamma\beta\delta-\alpha\gamma\beta-\alpha^2\omega+\alpha\gamma\delta-\beta\gamma\delta}{\alpha(\alpha-\beta)}\Big)=0.$$

Simplifying the second and the third terms, we arrive at

$$\alpha\beta\Big(\frac{\theta+\delta}{\theta(\alpha-\beta)}\Big)I^2+ \\ \Big(\frac{\beta\delta\theta-\alpha\beta\theta+\beta\gamma\theta+\beta\gamma\delta+\alpha\omega\theta+\alpha\omega\delta+\alpha\delta\theta\xi-\beta\delta\theta\xi}{\theta(\alpha-\beta)}\Big)I+ \\ \Big(\frac{\omega\delta-\gamma\beta-\alpha\omega+\gamma\delta}{(\alpha-\beta)}\Big)=0.$$

Multiplying by $\theta(\alpha-\beta)$ and collecting terms, we have

$$\alpha\beta\Big(\theta+\delta\Big)I^2+ \\ \Big(\beta(\delta\theta-\delta\theta\xi+\gamma\theta+\gamma\delta)+\alpha(\omega\theta+\omega\delta+\delta\theta\xi-\beta\theta)\Big)I+ \\ \theta\Big(\omega(\delta-\alpha)+\gamma(\delta-\beta)\Big)=0.$$

We write the quadratic equation for I in the form

$$A_1I^2+A_2I+A_3=0, \tag{4.12}$$

where we define A_1, A_2 and A_3 as follows:

$$\begin{aligned} A_1&=\alpha\beta\Big(\theta+\delta\Big), \\ A_2&=\beta(\delta\theta-\delta\theta\xi+\gamma\theta+\gamma\delta)+\alpha(\omega\theta+\omega\delta+\delta\theta\xi-\beta\theta), \\ A_3&=\theta\Big(\omega(\delta-\alpha)+\gamma(\delta-\beta)\Big). \end{aligned} \tag{4.13}$$

The solutions of equations (4.12) are

$$I_{1,2} = \frac{-A_2 \pm \sqrt{A_2^2 - 4A_1A_3}}{2A_1}. \tag{4.14}$$

Substituting (4.14) into the terms of S_1, S_2 and R we get

$$\begin{aligned}
S_{1_{1,2}} &= \frac{\delta}{\alpha} - \frac{\beta}{\alpha-\beta} + \frac{\beta\delta}{\alpha(\alpha-\beta} + \frac{-A_2 \pm \sqrt{A_2^2 - 4A_1A_3}}{2\alpha\theta(\alpha-\beta)}, \\
S_{2_{1,2}} &= \frac{\alpha}{\alpha-\beta} - \frac{\alpha\delta}{\alpha^2-\alpha\beta} - \frac{-A_2 \pm \sqrt{A_2^2 - 4A_1A_3}}{2\beta\theta(\alpha-\beta)}, \\
R_{1,2} &= \theta\frac{-A_2 \pm \sqrt{A_2^2 - 4A_1A_3}}{2\delta A_1}.
\end{aligned}$$

Lemma 4.3.1. *Assume that $\delta < \alpha < \beta$. Then the quadratic equation (4.12) has one positive and one negative solution.*

Proof. Note that A_1 is always positive. Since the first factor θ in the expression for A_3 is always positive, the sign of A_3 is determined by the sign of the second factor $\omega(\delta-\alpha)+\gamma(\delta-\beta)$. Note that if $\delta < \alpha < \beta$, then A_3 is less than zero since:

$$A_3 = \omega\underbrace{(\delta-\alpha)}_{<0} + \gamma\underbrace{(\delta-\beta)}_{<0} < 0$$

In that case by Vieta's theorem the quadratic equation (4.12) must have one positive and one negative root. The proof is complete. □

The following simple biological argument explains why the quadratic equations can have two positive solutions. The roots of quadratic equation (4.14) depend continuously on the parameters α, β and δ. Therefore, by increasing the value of δ we can make one root zero and another negative for some $\alpha < \delta_\star < \beta$ which corresponds to asymptotically stable disease free equilibrium. Increasing further δ does not generate new equilibria with positive value of I. This argument is illustrated in Figure 4.1 (a)-(c).

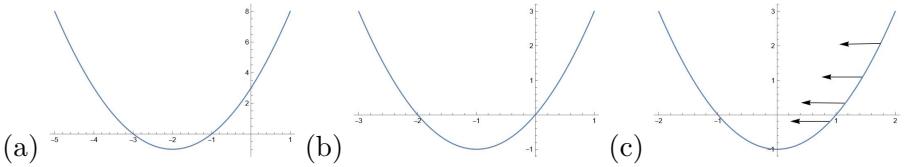


Figure 4.1: (a) $\alpha < \beta \leq \delta$; (b) $\delta_\star$; (c) $\delta < \alpha < \beta$.

4.4 Stability

We now rewrite our system as a system of three equations, using the condition (4.7). This is done because condition (4.7) relates all four variables thus making one of the differential equations in our system redundant. The system assumes the form

$$\begin{aligned}
\dot{I} &= \alpha I(t)S_1(t) + \beta I(t)S_2(t) - \delta I(t),\\
\dot{S_1} &= -\alpha I(t)S_1(t) - \gamma S_1(t) + \omega S_2(t) + \theta(1-\xi)(1 - I - S_1 - S_2),\\
\dot{S_2} &= -\beta I(t)S_2(t) + \gamma S_1(t) - \omega S_2(t) + \theta\xi(1 - I - S_1 - S_2).
\end{aligned}$$

We calculate the Jacobian to study the stability of the equilibria:

$$\begin{pmatrix}
\alpha S_1 + \beta S_2 - \delta & \alpha \cdot I & \beta \cdot I \\
-\alpha \cdot S_1 - \theta \cdot (1-\xi) & -\gamma - \theta \cdot (1-\xi) - \alpha \cdot I & \omega - \theta \cdot (1-\xi) \\
-\beta \cdot S_2 - \xi \cdot \theta & \gamma - \theta \cdot \xi & -\omega - \theta \cdot \xi - \beta \cdot I
\end{pmatrix}.$$

We start with the stability for the disease free equilibrium E_0:

$$\begin{pmatrix}
\alpha \cdot \frac{\omega}{\gamma+\omega} + \beta \cdot \frac{\gamma}{\gamma+\omega} - \delta & 0 & 0 \\
-\alpha \cdot \frac{\omega}{\gamma+\omega} - \theta \cdot (1-\xi) & -\gamma - \theta \cdot (1-\xi) & \omega - \theta \cdot (1-\xi) \\
-\beta \cdot \frac{\gamma}{\gamma+\omega} - \xi \cdot \theta & \gamma - \theta \cdot \xi & -\omega - \theta \cdot \xi
\end{pmatrix}.$$

The eigenvalues of this matrix are

$$\lambda_1 = -\omega - \gamma, \quad \lambda_2 = \frac{\alpha\omega + \beta\gamma - \delta(\omega+\gamma)}{\omega+\gamma}, \quad \lambda_3 = -t.$$

The equilibrium is asymptotically stable when the real parts of all eigenvalues are negative. Observe that λ_1 and λ_3 are always negative, but λ_2 is negative only if

$$\frac{\alpha\omega + \beta\gamma}{\delta(\omega + \gamma)} < 1.$$

The expression on the left hand side of the latter inequality will be used in Section 4.5 to define the basic reproduction number $\mathscr{R}_0$ of the system. The disease free equilibrium is asymptotically stable if $\mathscr{R}_0 < 1$.

For the endemic equilibrium E_*, we need to find the characteristic polynomial for the Jacobian matrix at E_*. Note that for the endemic equilibrium $\alpha S_1 + \beta S_2 - \delta = 0$ and our Jacobian matrix then becomes.

$$\begin{pmatrix} 0 & \alpha \cdot I & \beta \cdot I \\ -\alpha \cdot S_1 - \theta \cdot (1-\xi) & -\gamma - \theta \cdot (1-\xi) - \alpha \cdot I & \omega - \theta \cdot (1-\xi) \\ -\beta \cdot S_2 - \xi \cdot \theta & \gamma - \theta \cdot \xi & -\omega - \theta \cdot \xi - \beta \cdot I \end{pmatrix}.$$

Note that for the endemic equilibrium $\alpha S_1 + \beta S_2 - \delta = 0$. The characteristic polynomial is given by:

$$\begin{aligned} &\lambda^3 + (\gamma + \omega + \theta\xi + \alpha I + \beta I - \theta(\xi - 1))\lambda^2 \\ &\quad ((\gamma + \alpha I - \theta(\xi - 1))(\omega + \theta\xi + \beta I) - (\gamma - \theta\xi)(\omega + \theta(\xi - 1)))\lambda \\ &\quad + (\alpha I(\alpha S_1 - \theta(\xi - 1)) + \beta I(\theta\xi + \beta S_2))\lambda \\ &I\left(\theta\beta^2 S_2 + \beta^2\gamma S_2 + \alpha^2\omega S_1 + \theta\beta\gamma + \theta\alpha\omega + \theta\alpha^2\xi S_1 - \theta\beta^2\xi S_2 + \alpha^2\beta I S_1\right) \\ &+ I\left(\alpha\beta^2 I S_2 + \theta\alpha\beta I - \theta\alpha\beta S_2 + \alpha\beta\gamma S_1 + \alpha\beta\omega S_2 - \theta\alpha\beta\xi S_1 + \theta\alpha\beta\xi S_2\right). \end{aligned}$$

We do not try to solve this equation as it is too complex, but we use the Routh–Hurwitz criterion to derive the stability conditions.

Theorem 4.4.1. *The third-order polynomial $P(s) = s^3 + b_2 b^2 + b_1 s + b_0$ has all roots with negative real parts if and only if b_2, b_1, and b_0 are positive and $b_2 b_1 > b_0$.*

Denote the coefficient for λ^2 in our characteristic polynomial as B_2, the coef-

ficient for λ as B_1 and the free term as B_0.

Theorem 4.4.2. *The endemic equilibrium for the system (4.1) - (4.4) is asymptotically stable if and only if B_2, B_1, and B_0 are positive and $B_2B_1 > B_0$.*

For the simulation we verify the asymptotic stability for all the plots used in the thesis by inserting the specific values and verifying the negative eigenvalues.

4.5 Basic reproduction number

The basic reproduction number $\mathscr{R}_0$ is the expected number of cases generated by one case in a population. It is important for the analysis of the spread of infection because it gives us an indication of the development of the disease. An increasing basic reproduction number might indicate a outbreak, affecting decisions made by a government. We can obtain $\mathscr{R}_0$ by using the next generation method described by van den Driessche and Watmough's [10]. We define m as the number of states in our system, and n as the number of infected states. In this section it is convenient to rewrite our system so that we can apply the theory described in [10]:

$$\begin{aligned}
\dot{I} &= \alpha I(t)S_1(t) + \beta I(t)S_2(t) - \delta I(t),\\
\dot{S_1} &= -\alpha I(t)S_1(t) - \gamma S_1(t) + \omega S_2(t) + \theta(1-\xi)(1-I-S_1-S_2),\\
\dot{S_2} &= -\beta I(t)S_2(t) + \gamma S_1(t) - \omega S_2(t) + \theta\xi(1-I-S_1-S_2).
\end{aligned}$$

We use the following notation

$x = (I, S_1, S_2)^{\mathrm{T}}$

$\mathscr{F}_i(x),\ i = 1, ..., n$ - the rate of appearance of new infections in compartment i;

$\mathscr{V}_i^+(x),\ i = 1, ..., n$ - the rate of transfer of individuals into compartment i by all other means;

$\mathscr{V}_i^-(x),\ i = 1, ..., n$ - the rate of transfer of individuals out of compartment i;

$\mathscr{V}_i = \mathscr{V}_i^- - \mathscr{V}_i^+$;

$X_s = \{x \geq 0 \mid x_i = 0,\ i = 1, ..., m\}$ - the set of all disease free states.

To use [10, Lemma 1] we write our system in the form

$$\dot{x}_i = f_i(x) = \mathscr{F}_i(x) - \mathscr{V}_i(x) \qquad i = 1, ..., n \tag{4.15}$$

and check that it satisfies the following conditions:

$$\text{If } x \geq 0 \text{ then } \mathscr{F}_i, \mathscr{V}_i^-, \mathscr{V}_i^+ \geq 0 \quad i = 1, ..., n \tag{4.16}$$

$$\text{If } x_i = 0 \text{ then } \mathscr{V}_i^- = 0 \ i = 1, ..., m, \tag{4.17}$$

$$\mathscr{F}_i = 0 \qquad \forall\ i > m \tag{4.18}$$

$$\text{If } \ x \in X_s \text{ then } \mathscr{F}_i(x) = 0 \text{ and } \mathscr{V}_i^+(x) = 0 \ \forall\ i = 1, ..., m \tag{4.19}$$

$$\text{If } \ \mathscr{F}(x) \text{ is set to zero, then all eigenvalues of } Df(x_0) \text{ have negative real parts} \tag{4.20}$$

where x_0 is the disease free equilibrium.

Lemma 4.5.1. *The system (4.1) - (4.4) is of the form (4.15) and satisfies the conditions (4.16) - (4.20).*

Proof. We start by defining the vectors describing the generation of new infected and the flow between the states:

$$\mathscr{F}(x) = \begin{bmatrix} \alpha I S_1 + \beta I S_2 & 0 & 0 \end{bmatrix}^T,$$

$$\mathscr{V}(x) = \begin{bmatrix} \delta I \\ \alpha I(t) S_1(t) + \gamma S_1 - \omega S_2 - \theta(1-\xi)(1 - I - S_1 - S_2) \\ \beta I(t) S_2(t) - \gamma S_1 + \omega S_2 - \theta\xi(1 - I - S_1 - S_2) \end{bmatrix},$$

$$\mathscr{V}^+(x) = \begin{bmatrix} 0 \\ \omega S_2 + \theta + \theta\xi(I + S_1 + S_2) \\ \gamma S_1 + \theta\xi \end{bmatrix},$$

$$\mathscr{V}^-(x) = \begin{bmatrix} \delta I \\ \alpha I S_1 + \gamma S_1 + \theta(I + S_1 + S_2) + \theta\xi \\ \beta I S_2 + \omega S_2 + \theta\xi(I + S_1 + S_2) \end{bmatrix}.$$

The system can then be described as in (4.15). Since our parameters are always positive then we observe that if $x \geq 0$, then $\mathscr{V}_i^+, \mathscr{V}_i^-$ and $\mathscr{F}_i$ as defined above is greater than zero for $i = 1, 2, 3, 4$. Therefore, condition (4.16) holds. The verification of condition (4.17) follows immediately, as when $I = 0$ then $\mathscr{V}_1^-(x) = \delta I = 0$. For when $i > 1$, $\mathscr{F}_i = 0$ and thus (4.18) holds. When we are in the disease free state and I is equal to zero, $\mathscr{F}_1 = 0$. This implies that (4.19) holds. To prove (4.20), we calculate the Jacobian matrix of the system when $\mathscr{F}(x)$ is equal to zero:

$$Df(x) = D(\mathscr{F}(x) - \mathscr{V}(x)) = D(-\mathscr{V}(x)).$$

and

$$Df(x) = \begin{bmatrix} -\delta & 0 & 0 \\ -\alpha S_1 - \theta(1-\xi) & -\alpha I - \gamma - \theta(1-\xi) & \omega - \theta(1-\xi) \\ -\beta S_2 - \xi\theta & \gamma - \xi\theta & -\omega - \omega - \xi\theta) \end{bmatrix}.$$

Substituting the disease free equilibrium, we get:

$$Df(x_0) = \begin{bmatrix} -\delta & 0 & 0 \\ -\alpha\frac{\omega}{\gamma+\omega} - \theta(1-\xi) & -\gamma - \theta(1-\xi) & \omega - \theta(1-\xi) \\ -\beta\frac{\gamma}{\gamma+\omega} - \xi\theta & \gamma - \xi\theta & -\omega - \xi\theta \end{bmatrix}.$$

The eigenvalues $\lambda = (-\delta, -\theta, -\omega - \gamma)$ are all negative. All conditions in [10,

Lemma 1] are verified. □

Following [10], we can find the basic reproduction number.

Theorem 4.5.2. *The basic reproduction number of the system (4.1) - (4.4) is given by*

$$\mathscr{R}_0 = \frac{\alpha\omega + \beta\gamma}{\delta(\gamma + \omega)}. \tag{4.21}$$

Proof. To calculate, we need the equilibrium point for the disease free equilibrium, $\mathscr{F}(x)$ and $\mathscr{V}(x)$. These are given by

$$x_0 = \begin{bmatrix} 0 & \frac{\omega}{\gamma+\omega} & \frac{\gamma}{\gamma+\omega} \end{bmatrix}^T,$$

$$\mathscr{F}(x) = \begin{bmatrix} (\alpha I S_1 + \beta I S_2) & 0 & 0 \end{bmatrix}^T,$$

$$\mathscr{V} = \begin{bmatrix} \delta I \\ \alpha I(t) S_1(t) + \gamma S_1 - \omega S_2 - \theta(1-\xi)(1 - I - S_1 - S_2) \\ \beta I(t) S_2(t) - \gamma S_1 + \omega S_2 - \theta\xi(1 - I - S_1 - S_2) \end{bmatrix}.$$

We need two Jacobian matrices

$$F = \left[\frac{\partial \mathscr{F}_i}{\partial x_j}(x_0)\right], \qquad V = \left[\frac{\partial \mathscr{V}_i}{\partial x_j}(x_0)\right], \quad \text{where } 1 \leq i, j \leq m$$

which in our case simplify to

$$F = \frac{\alpha\omega}{\gamma + \omega} + \frac{\beta\gamma}{\gamma + \omega} = \frac{\alpha\omega + \beta\gamma}{\gamma + \omega}$$

and

$$V = \delta \Rightarrow V^{-1} = \frac{1}{\delta}.$$

Multiplying F and V^{-1}, we obtain the reproduction number (4.21). □

Theorem 4.5.3 ([10], Theorem 2)**.** *Consider the disease transmission model given by (4.15) with $f(x)$ satisfying conditions (4.16) - (4.20). If x_0 is a disease free equilibrium of the model, then x_0 is locally asymptotically stable if $\mathscr{R}_0 < 1$, but unstable if $\mathscr{R}_0 > 1$, where $\mathscr{R}_0$ is defined by (4.21)*

The next result follows from Theorem 4.5.3.

Theorem 4.5.4. *Consider the system (4.1) - (4.4). Then the disease free equilibrium x_0 is locally asymptotically stable if $\mathscr{R}_0 < 1$, but unstable if $\mathscr{R}_0 > 1$ where $\mathscr{R}_0$ is defined by (4.21).*

4.6 Introducing delay

Now we introduce the delay into the system. The reason for doing this is that the delay allows us to transfer infected to recovered after τ days, where τ is the duration of the disease, which makes the system more realistic. In addition we introduce a cosine function, $\phi(t)$, dependent on time that simulates the change in travel throughout the week. This cyclic behavior can be observed, for example, in the Transportation Security Administration data [14] plotted in Figure 4.2, with Saturdays being outliers we do not account for. Note that we assume here that everyone takes the exact same amount of time to recover and become susceptible to the disease again. Consider now the system:

$$\frac{dS_1}{dt} = -\alpha I(t)S_1(t) - \Delta\gamma S_1(t) + \omega S_2(t) + (1-\xi)\phi(t-\tau-\eta)I(t-\tau-\eta), \tag{4.22}$$

$$\frac{dS_2}{dt} = -\beta I(t)S_2(t) + \Delta\gamma S_1(t) - \omega S_2(t) + \xi\phi(t-\tau-\eta)I(t-\tau-\eta), \tag{4.23}$$

$$\frac{dI}{dt} = \alpha I(t)S_1(t) + \beta I(t)S_2(t) - \Phi(t-\tau)I(t-\tau), \tag{4.24}$$

$$\frac{dR}{dt} = \Phi(t-\tau)I(t-\tau) - \phi(t-\tau-\eta)I(t-\tau-\eta), \tag{4.25}$$

with initial condition:

$$N(0) = S_1(0) + S_2(0) + I(0) + R(0) = 1, \tag{4.26}$$

where

$S_1(t)$ - is the number of people susceptible being non-mobile;

$S_2(t)$ - is the number of people susceptible being mobile;

$I(t)$ - is the number of people infected with the disease;

$R(t)$ - is the number of people that have had, and are now immune to the disease;

$\Phi(t-\tau) = \alpha S_1(t-\tau) + \beta S_2(t-\tau)$;

$\phi(t-\tau-\eta) = \alpha S_1(t-\tau-\eta) + \beta S_2(t-\tau-\eta)$;

$\Delta(t) = \theta \cos(\frac{2\pi t}{\kappa}) + 1$;

θ - is the scaling factor for how large is the difference between periods of more and less travel;

κ - is the number of days between two periods where the population travels a lot;

τ - is the time it takes to recover from the disease;

η - is the time from when one have recovered until one can catch the disease again;

α - is the transmission rate for people in the non-mobile state;

β - is the transmission rate for people in the mobile state.

We have the following terms in the system.

1. $\alpha I(t) S_1(t)$ The number of people being non-mobile that gets infected. It depends both on how many are already infected and how many are susceptible. If we have a few infected or a few susceptible then there will be fewer new people infected.

2. $\beta I(t) S_2(t)$ The number of people being mobile that get infected. It depends both on how many are already infected and how many are susceptible. If we have a few infected or a few susceptible then there will be fewer new people

infected.

3. $\Phi(t-\tau)$ The number of people infected τ days ago and is now recovering.

4. $\gamma S_1(t)$ The number of people that move from the mobile state to the non-mobile state

5. $\omega S_2(t)$ The number of people that move from the non-mobile state to the mobile state

6. Δ The function describing cyclic changes in the travel pattern during the week

7. $\phi(t-\tau-\eta)$ The number of people infected $\tau+\eta$ days ago and is now becoming susceptible the distribution between the two susceptible states is given by η

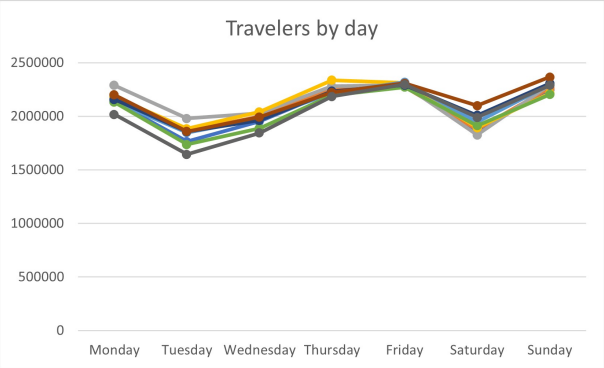


Figure 4.2: Travel patterns on different weekdays. Data is taken from 3/7/22 to 09/05/22 from [14]

Analytical analysis of the system (4.22) - (4.25) with delayed arguments and cyclic travel patterns is much more challenging. Therefore, we provide only numerical simulations that illustrate the possible scenario in Chapter 5.

Chapter 5

Simulation and discussion

In this chapter we will first look at how the different parameters are determined. We will then introduce data we will use to calculate the parameters, before we simulate and show how the different parameters affect the simulation. Finally we discuss the impact of travel restrictions on the spread of infection.

5.1 Parameters

One of the difficulties arising during the model developments is the need to "convert" proportions of quantities into the rate of change of quantities. That is we need to move from a discrete model to a continuous model. To give an example let us assume the average amount of days to recover from the disease to be 10 days. This means that in a continuous model we want $\frac{1}{10} = 0.1 = 10\%$ to be removed from the infected state $x(t)$ in one day. Consider the differential equation, where we assume that the "rate of change", that is, the coefficient of removal is 0.1:

$$\dot{x}(t) = \alpha x(t) = -0.1x(t)$$

Note that there is a minus sign in the equation because we remove people from the infected population. The solution to this equation is given by $x(t) =$

$e^{-0.1t}$, where $x(1) = e^{-0.1} = 0.9048$. This estimation is quite good considering our target after one day is $1 - 0.1 = 0.9$, but note that the accuracy of the estimation decreases with higher values of α. Now consider another equation

$$\dot{x}(t) = -0.33x(t).$$

In this case the solution is $x(t) = e^{-0.33t}$, where $x(1) = 0.7189$ with 0.66 being our target. The discrepancy becomes even more striking when looking at $x(10) = 0.03688$ where our target is $0.66^{10} = 0.0156833688$. To "correct" this we know that $x(1) = 0.66$, and we want to find an α that better fits our target which is one third of the quantity being removed in one day. We find α by solving the following equation

$$1 - 0.33 = 0.66 = x(1) = e^{-\alpha} \Rightarrow \alpha = -\ln(0.66) = 0.41551544396.$$

Recalculating the solution to the differential equation with the value of $\alpha = 0.41551544396$, we get $x(1) = 0.66$ and $x(10) = 0.0156833688$ compared to our targets of $0.66^1 = 0.66$ and $0.66^{10} = 0.0156833688$. The general formula for finding the "adjustment" for a single differential equation is therefore given by

$$\alpha = -\ln(1 - p), \tag{5.1}$$

where p is the target proportion we want to remove from the quantity x in one time unit (day, month, year, etc.).

However, this does not solve the problem for higher dimensional systems. Let us take a look at what happens when we consider two dimensions, in our case S_1 and S_2. To find the exact values of parameters γ and ω in our model, we use an algorithm suggested by one of the supervisors. Consider the following

discrete system

$$\begin{aligned} s_1(n+1) &= as_1(n) + bs_2(n), \\ s_2(n+1) &= (1-a)s_1(n) + (1-b)s_2(n), \end{aligned} \tag{5.2}$$

which describes evolution of a population consisting of two groups $s_1(n)$ and $s_2(n)$ day by day ($n = 0, 1, \ldots$). Here a is the proportion of s_1 that remains in s_1 and b is the proportion of s_1 moving from s_2 to s_1 in one time unit. We assume that $b \leq a$ and the sum of the two population adds up to one:

$$s_1(n) + s_2(n) = 1.$$

We can find the equilibrium $[s_1, s_2]$ of the system for $s_1(n)$ and $s_2(n)$ by assuming that $s_1(n) = s_1(n+1)$ and $s_2(n) = s_2(n+1)$

$$s_1 = as_1 + b(1 - s_1) \Rightarrow s_1 = \frac{b}{1 - a + b}, \tag{5.3}$$

and:

$$(1 - s_2) = a(1 - s_2) + bs_2 \Rightarrow s_2 = \frac{1 - a}{1 - a + b}. \tag{5.4}$$

We assume that we are given real constants s_1 and b, and we need to calculate the value of a. We find the corresponding value of a using the formula (5.3):

$$s_1 = \frac{b}{1 - a + b} \Rightarrow a = 1 + b - \frac{b}{s_1}.$$

Now we can write the discrete system (5.2) in a matrix form:

$$X_{n+1} = \begin{bmatrix} a & b \\ 1-a & 1-b \end{bmatrix} X_n$$

or

$$X_{n+1} = AX_n \tag{5.5}$$

where $X_n = [s_1(n), s_2(n)]^{\mathrm{T}}$. Recall that $b \leq a$, which will guarantee positive eigenvalues. The characteristic equation is

$$\begin{vmatrix} a-\lambda & b \\ 1-a & 1-a-\lambda \end{vmatrix} = \lambda^2 + (b-1-a)\lambda + (a-b) = 0.$$

We calculate the eigenvalues $\lambda_1 = 1$, $\lambda_2 = a - b$. The corresponding eigenvectors are found by solving the linear systems

$$\begin{bmatrix} a-\lambda_1 & b \\ 1-a & 1-b-\lambda_1 \end{bmatrix} = \begin{bmatrix} a-1 & b \\ 1-a & -b \end{bmatrix} \Rightarrow \vec{v_1} = \begin{bmatrix} 1 \\ \frac{1-a}{b} \end{bmatrix},$$

$$\begin{bmatrix} a-\lambda_2 & b \\ 1-a & 1-b-\lambda_2 \end{bmatrix} = \begin{bmatrix} b & b \\ 1-a & 1-a \end{bmatrix} \Rightarrow \vec{v_2} = \begin{bmatrix} -1 \\ 1 \end{bmatrix}.$$

Using the eigenvalues and eigenvectors we have obtained, we can write the general solution to the system (5.5) as

$$X_n = \begin{bmatrix} s_1(n) \\ s_2(n) \end{bmatrix} = c_1 v_1 \lambda_1^n + c_2 v_2 \lambda_2^n.$$

Now we use X_n for constructing the fundamental matrix of the continuous system that will have the same general solution. Our aim is to find the matrix B of the continuous system

$$\dot{x}(s) = Bx(s) \tag{5.6}$$

where $x(s) = [x_1(s), x_2(s)]^{\mathrm{T}}$ represents a continuous vector function. The first step is to convert the general solution X_n into the general solution to the

system (5.6):

$$x(s) = \begin{bmatrix} x_1(s) \\ x_2(s) \end{bmatrix} = c_1 v_1 \lambda_1^s + c_2 v_2 \lambda_2^s.$$

Because $x(s)$ is the general solution, we can write the fundamental matrix of (5.6) as

$$X(s) = \begin{bmatrix} v_{11}\lambda_1 & v_{12}\lambda_2^s \\ v_{21}\lambda_1 & v_{22}\lambda_2^s \end{bmatrix} = \begin{bmatrix} v_{11} & v_{12}\lambda_2^s \\ v_{21} & v_{22}\lambda_2^s \end{bmatrix}.$$

Recall that λ_1=1. Moreover, $0 \leq \lambda_2 \leq 1$ because $\lambda_2 = a - b$ and both a and b are between 0 and 1. The fundamental matrix $X(s)$ must satisfy the equation

$$\dot{X}(s) = BX(s). \tag{5.7}$$

We need to calculate the derivative of $X(s)$:

$$\dot{X}(s) = \begin{bmatrix} 0 & v_{12}\lambda_2^s \ln(\lambda_2) \\ 0 & v_{22}\lambda_2^s \ln(\lambda_2) \end{bmatrix}.$$

Taking into account that the fundamental matrix $X(s)$ is regular, we can calculate the matrix B as

$$B = \dot{X}(s)X^{-1}(s).$$

Using the above described algorithm we find the parameters γ and ω determining the transitions between S_1 and S_2. We might also consider using similar algorithm to calculate the parameters α, β δ and θ, but the transition from S_1 and S_2 to I is represented by nonlinear terms and it is therefore not possible to apply the algorithm that works for linear systems. We therefore use an approach based on (5.1) instead.

5.2 Selection of parameters

When we want to simulate, it is important to find reliable parameter values to make the simulations as accurate as possible. The difficulties with finding right values for the parameters vary a lot. According to [5], the average time of the infectious period of Covid-19 is 15.2 days, this gives a $\delta = -\ln\left(1 - \frac{1}{15.2}\right) = 0.06805346324$ using our method for estimating (5.1). Note that the average time of infections period has a high standard deviation of 10.3 days so the value of δ might vary quite a lot.

We also want to know how many and how often people are traveling on average, this can be found by collecting data from the Norwegian statistics bureau [12]. To estimate the number of regular travelers, we chose a year without Covid-19, namely 2019. The data is given quarterly, and we therefore add the numbers for each quarter to get the total for 2019. There are four types of categories in the survey, short trips (1-3 days), long trips (4+ days), business trips domestic and business trips outbound. We assume that the average amount of days spent traveling on a short trip is 2 days, and average time spent on long trips is 9.5 days. Based on an article written by Travel Leaders Corporate [15], we assume that an average number of days traveled on business trips to be 3.05 for domestic, and 5.82 for outbound trips. We can then calculate the number of days traveled in millions per year, and divide it by the amount of days that would be possible to travel per year in millions, given the population of Norway was 5,348 million in 2019.

Short trips (1-3 days) in millions

3.43+2.41+2.40+2.43=10.67

$10.67 \cdot 2 = 21.34$

Long trips (4+ days) in millions 2019

1.11+2.07+2.99+1.66=7.83

$7.83 \cdot 9.5 = 74.385$

Business trips domestic in millions 2019

1.31+0.80+0.51+1.00=3.62

$3.62 \cdot 3.05 = 11.041$

Business trips outbound in millions 2019

0.36+0.36+0.42+0.34=1.48

$1.48 \cdot 5.82 = 8.6136$

In total this gives 21.34+74.385+11.041+8.6136=115.3796 million days traveled in a year. The maximum number of days the Norwegian population could travel would be $365 \cdot 5.348 = 1952.02$ in millions. This means that an average of $\frac{115.3796}{1952.02} = 0.0591 = 5.91\%$ of the Norwegian population are traveling at a given time. Note that there are a lot of assumptions made, both in the average amount of traveling days and in that we assume that the traveling is equally distributed throughout the year. Using that in our model we want the quota of travelers to be 0.0591, and one quarter of travelers daily move from mobile to non-mobile on average so that the trip is completed in four days. to move from mobile to non-mobile we can calculate what the proportion of travelers staying in S_2 as

$$a = 1 - b - \frac{b}{s_1} = 0.986565.$$

We can then set up the discrete system (5.5)

$$X_{n+1} = \begin{bmatrix} 0.986565 & 0.25 \\ 0.013435 & 0.75 \end{bmatrix} X_n.$$

Converting it into a continuous system using the algorithm introduced in Sec-

tion 5.1, we obtain

$$B = \begin{bmatrix} 0.0591\ln(1.36185) & -0.9409\ln(1.36185) \\ -0.0591\ln(1.36185) & 0.9409\ln(1.36185). \end{bmatrix}.$$

This means that

$$\gamma = 0.0591\ln(1.36185) = 0.0182526845$$

and

$$\omega = 0.9409\ln(1.36185) = 0.29059138499.$$

These parameters will be used as reference values in equations (4.1), (4.2) and (4.22), (4.23). We can also use the reproduction number from [5], it is assumed to be 4.18 for Covid-19 with a standard deviation of 2.26. Note that since the reproduction number for our model computed in Section 4.5 is

$$\mathscr{R}_0 = \frac{\alpha\omega + \beta\gamma}{\delta(\omega + \gamma)},$$

and we also know δ, ω and γ we can calculate α given β and vice versa. Unfortunately, $\mathscr{R}_0$ varies greatly during an outbreak depending on the measures taken by the government and it is therefore not a very reliable way to calculate α depending on β but it can be used to model a specific outbreak. When determining the rate at which individuals move from recovered to susceptible there is a significant variation in data and not enough arguments to support any firm conclusion; we assume 14 days in our models. It means that we set $\theta = -\ln\left(1 - \frac{1}{14}\right) = 0.07410797215$ for the model without delay.

5.3 Simulations for the model without delay

To take a look at what effect the different parameters we choose a set of initial conditions as a reference point, and then change one parameter to see the

impact of the perturbation. We use the initial conditions

$$\begin{bmatrix} S_1(0) \\ S_2(0) \\ I(0) \\ R(0) \end{bmatrix} = \begin{bmatrix} 0.999(1-q) \\ 0.999q \\ 0.001 \\ 0 \end{bmatrix} \tag{5.8}$$

where $q = 0.0591$. We set the variables to the values seen in Table 5.1. When

Parameters	Meaning	Value
α	Infection rate non-mobile	0.15
β	Infection rate mobile	0.6
γ	Transition rate to mobile	0.0182526845
ω	Transition rate to non-mobile	0.29059138499
δ	Percentage leaving infected	0.06805346324
θ	Percentage leaving recovered	0.07410797215
ξ	Distribution between S_1 and S_2 arriving from R	0.0591
q	Proportion of travelers at $t = 0$	0.0591

Table 5.1: Reference values for parameters

we want to reduce the number of travelers we have to recalculate the values for γ, ω, and change the values of ξ and q. This recalculation can be seen for γ and ω and change in parameters in Table 5.2 where σ is the change in the intensity of travel.

Percentage of travelers	Travel flow $\sigma = \xi = q$	γ	ω
0.1 %	0.001	0.00028801701	0.28772899933
1 %	0.01	0.00291056373	0.28814580936
5.91 %	0.0591	0.0182526845	0.29059138499
15 %	0.15	0.05224635708	0.29606269012

Table 5.2: Values of parameters for different traveling patterns

We also have to recalculate δ when we change the recovery rate as in Table 5.3.

Days to complete recovery	δ
8.2	0.13005312824
10.2	0.10318423623
15.2	0.06805346324
20.2	0.05077232537

Table 5.3: Values of recovery rate for different duration of recovery periods

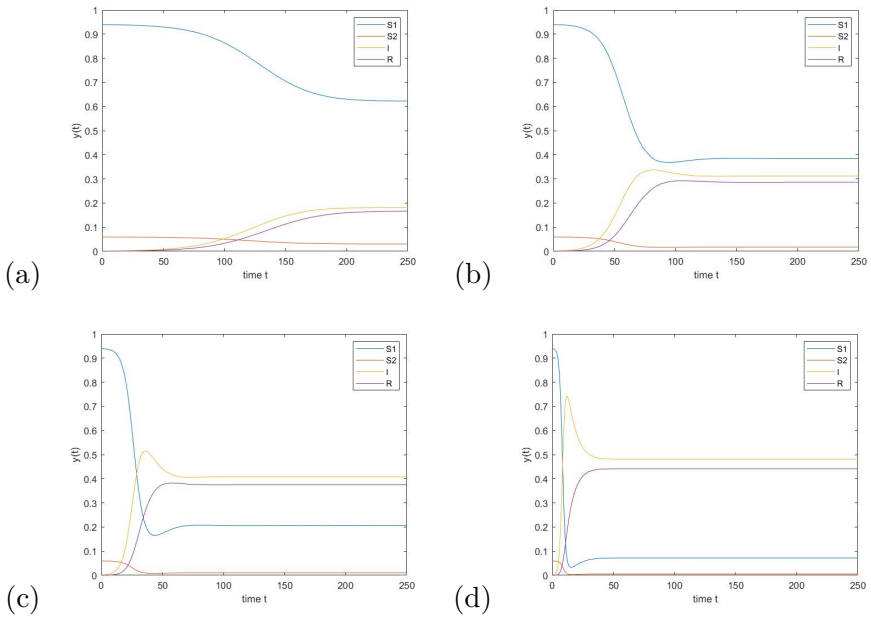


Figure 5.1: The dynamics of the system (4.1) - (4.4) for different values of α. Values for other parameters are in Table 5.1. (a) $\alpha = 0.08$; (b) $\alpha = 0.15$ (Reference); (c) $\alpha = 0.3$; (d) $\alpha = 0.9$.

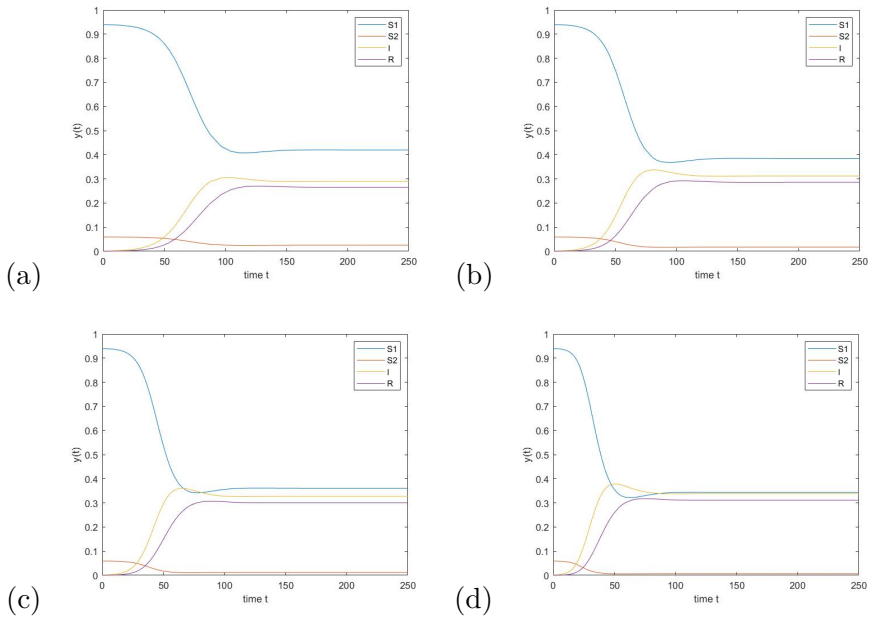


Figure 5.2: The dynamics of the system (4.1) - (4.4) for different values of β. Values for other parameters are as in Table 5.1. (a) $\beta = 0.2$; (b) $\beta = 0.6$ (Reference); (c) $\beta = 1.2$; (d) $\beta = 2.4$.

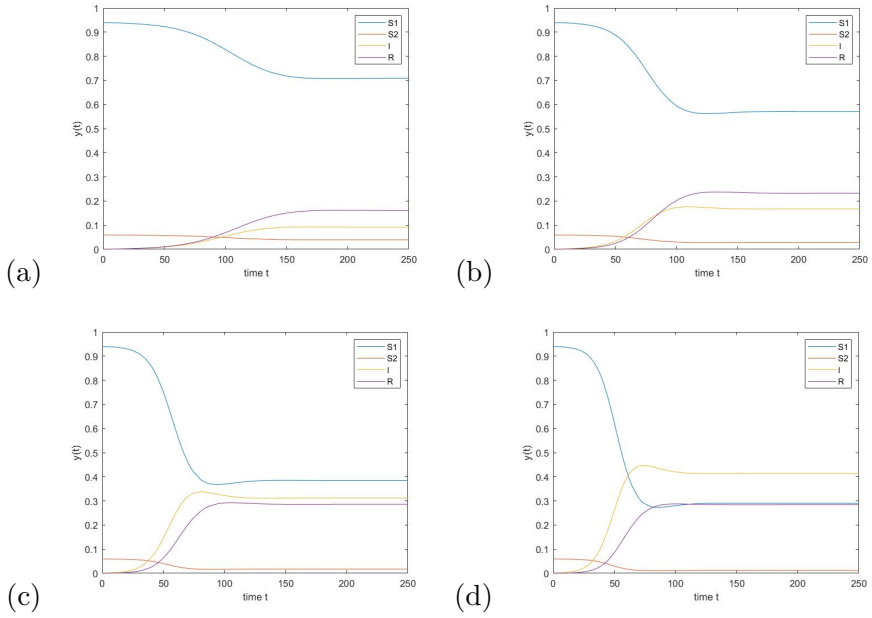


Figure 5.3: The dynamics of the system (4.1) - (4.4) for a different travel pattern given in Table 5.2. Values for other parameters are as in Table 5.1. (a) $\delta = 0.13$; (b) $\delta = 0.1$; (c) $\delta = 0.07$ (Reference); (d) $\delta = 0.05$.

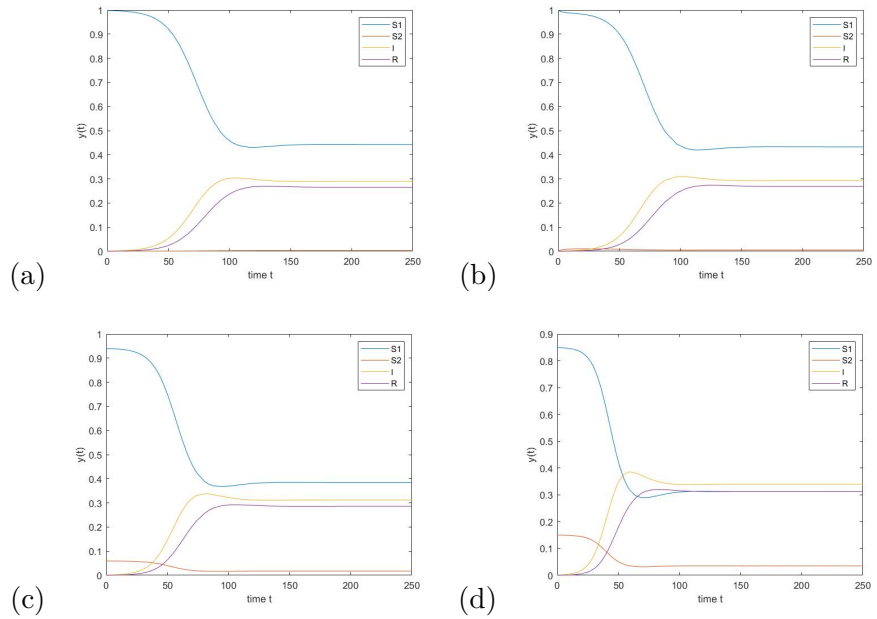


Figure 5.4: The dynamics of the system (4.1) - (4.4) for different recovery rates given in Table 5.3. Values for other parameters are as in Table 5.1 (a) $\sigma = 0.001$; (b) $\sigma = 0.01$; (c) $\sigma = 0.591$ (Reference); (d) $\sigma = 0.15$.

In Figure 5.1 we observe that in response to the change of α there is a clear change in the shape of the graph for infected individuals - the curve becomes steeper and the outbreak comes earlier. This coincides with what we would expect from the spread of infection if the transmission rate increases. Similarly, in Figure 5.2 we observe the same behavior when β changes, but the impact is not as noticeable as for the variation of α. This is natural as a change that applies to a smaller number of individuals is expected to have a lower impact. These changes are also noticeable in Figure 5.3 where δ is varied and when we increase the number of mobile travelers in Figure 5.4.

5.4 Simulation of the model with delay

We use the same initial conditions defined by equation (5.8), and set the reference values for parameters in Table 5.4.

Parameters	Meaning	Value
α	Infection rate non-mobile	0.15
β	Infection rate mobile	0.6
γ	Transition rate to mobile	0.0182526845
ω	Transition rate to non-mobile	0.29059138499
τ	Recovery in days	15.2
η	Days needed before being susceptible	14
ξ	Distribution between S_1 and S_2 arriving from R	0.0591
κ	Duration of cyclic behavior in days	7
θ	Intensity of the cycle	0.8
q	Proportion of travelers at $t = 0$	0.0591

Table 5.4: Reference values for parameters in the model with delay

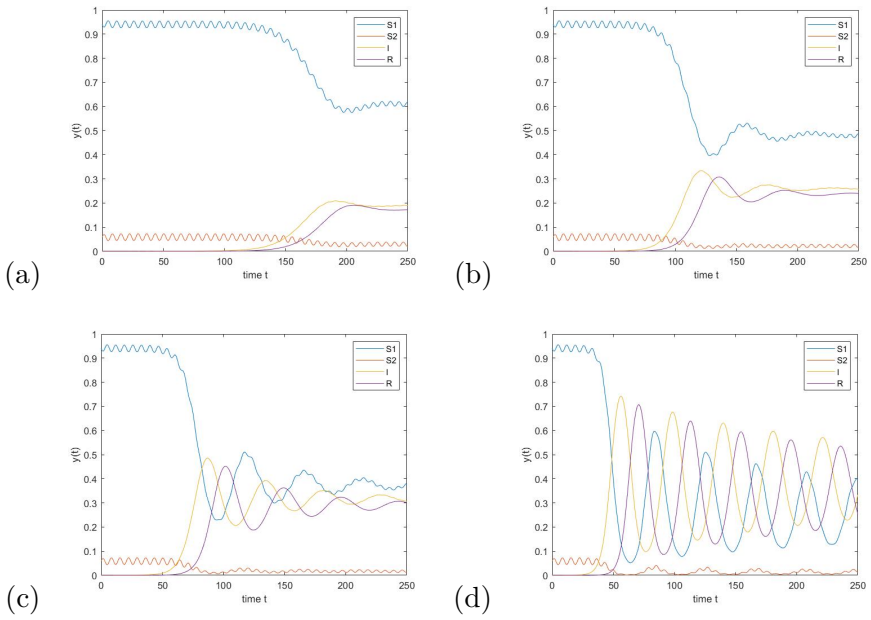


Figure 5.5: The dynamics of the system (4.22) - (4.25) for different values of α. Values for other parameters are as in Table 5.4. (a) $\alpha = 0.08$; (b) $\alpha = 0.15$ (Reference); (c) $\alpha = 0.3$; (d) $\alpha = 0.9$.

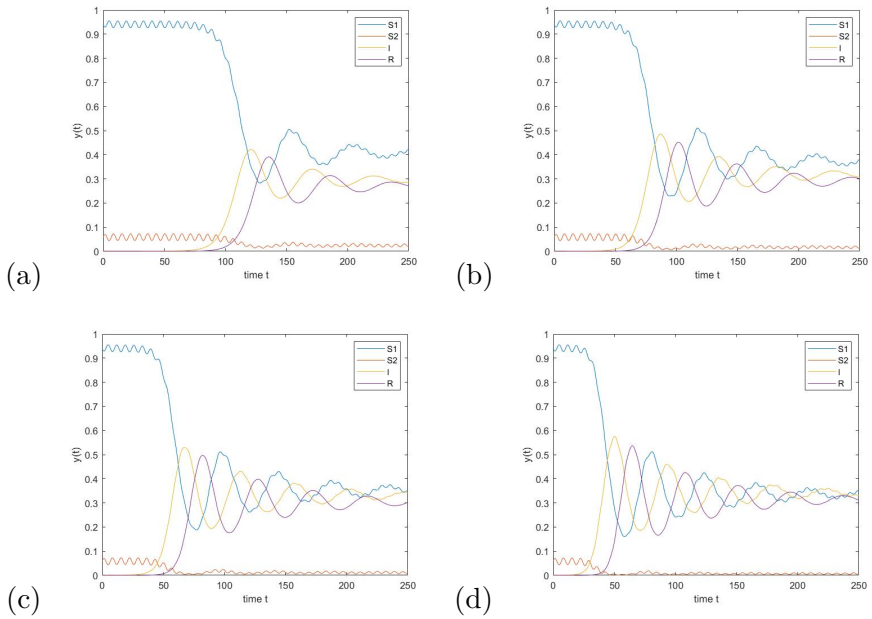


Figure 5.6: The dynamics of the system (4.22) - (4.25) for different values of β. Values for other parameters are as in Table 5.4. (a) $\beta = 0.2$; (b) $\beta = 0.6$ (Reference); (c) $\beta = 1.2$; (d) $\beta = 2.4$.

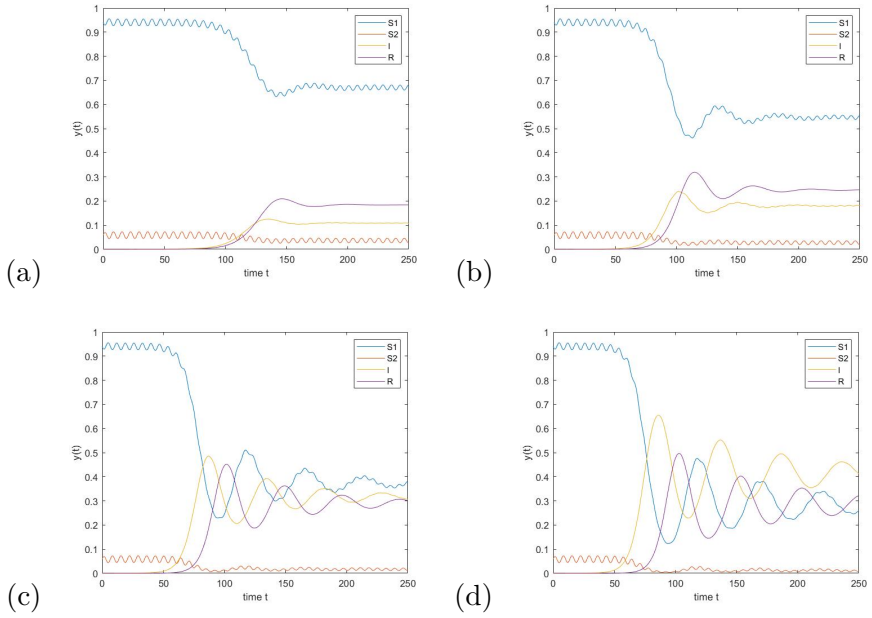


Figure 5.7: The dynamics of the system (4.22) - (4.25) for a different travel equilibrium given in Table 5.2. Values for other parameters are as in Table 5.4. (a) $\tau = 8.2$; (b) $\tau = 10.2$ (Reference); (c) $\tau = 15.2$; (d) $\tau = 20.2$.

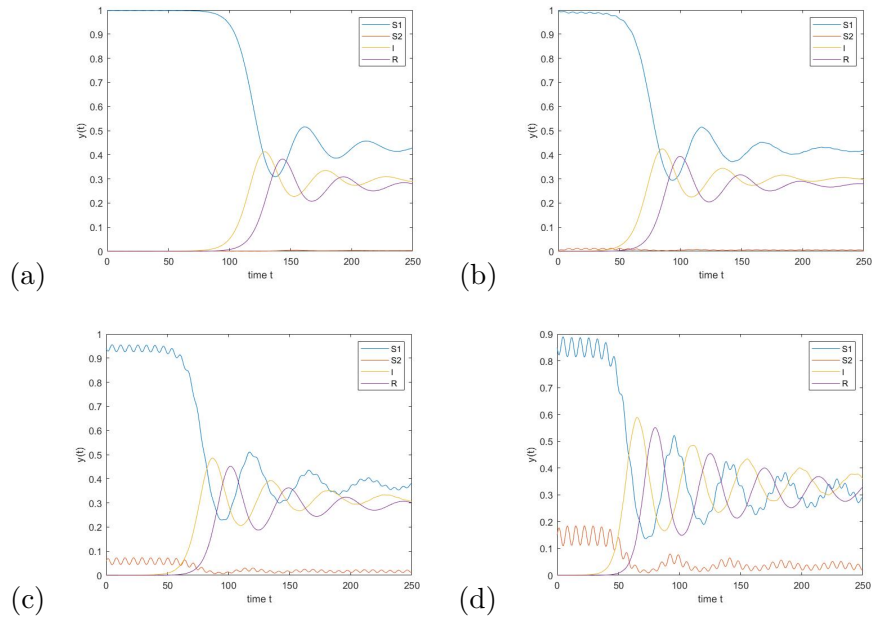


Figure 5.8: The dynamics of the system (4.22) - (4.25) for different τ. Values for other parameters are as in Table 5.4 (a) $\sigma = 0.001$; (b) $\sigma = 0.01$; (c) $\sigma = 0.591$ (Reference); (d) $\sigma = 0.15$.

Compared to the case without delay there are big differences caused by the oscillations. The solutions continue to oscillate in most cases. In Figure 5.5 we observe large differences of steepness for different values of α as well as the shifts corresponding to the start of the outbreak. The response to changes of β is more noticeable in Figure 5.6 compared to the model without delay but still not as extreme as for α. Note that the graphs of S_1 and S_2 have oscillations of a small amplitude that we do not observe in the graphs of I and R. The same observation regarding the steepness of the graph in response to change of τ in Figure 5.7 and to the increase in number of people traveling in Figure 5.8 is valid. It is important to note that the reduction in the amplitude of oscillations is natural for lower values of σ corresponding to the number of people traveling.

5.5 Discussion

At the start of the pandemic most governments adapted different strategies on how to handle the outbreak. For instance, Sweden allowed the stores and schools to stay open while most western countries opted for a lockdown [1]. It is obvious that the restrictions on travel reduce the spread of infection, but to what extent? Many studies report the research on this topic. For example,

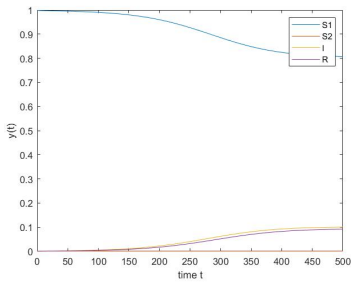
"At the international level, studies consistently estimated that the Wuhan travel measures led to a 70%–80% reduction in cases exported in the first few weeks, and likely had a smaller effect within Mainland China, where estimates of effectiveness ranged from 10% to 70%. Also, the Wuhan travel ban likely led to delays of up to a few weeks in the importation of cases to other countries. Additional travel measures, namely a reduction in the number of flights to countries, had additional effects at reducing the number of imported cases" [8, p.13].

We will now use the reproductive number for Corona-19, $\mathscr{R}_0 = 4.18$, to calculate β given that under our assumptions there is a four time higher chance to get infected when traveling. Recalling that

$$\mathscr{R}_0 = \frac{\alpha\omega + 4\alpha\gamma}{\delta(\omega + \gamma)}$$

for $\alpha = 0.07440240299$ we calculate β=0.29760961196. The results of modeling with different travel rates can be observed in Figure 5.9. The impact is quite noticeable as it takes a lot longer for the outbreak to start, and the curve is a lot milder. It is also important to note that even though the infection level for endemic equilibrium looks small it still corresponds to approximately 10% for (a) and 15.4% for (b) of the population being infected respectively.

It is interesting to note that there is a substantial reduction of the infection level from 0.15 to 0.1 corresponding to 33% and a increase by 80% from 250 to 450 days for the moment the outbreak settles when the intensity of travel σ is reduced to 0.001.

(a) 

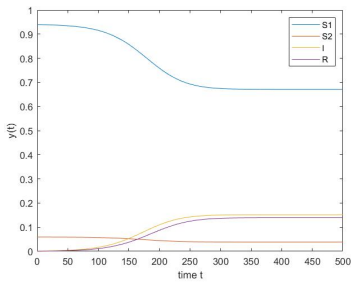
(b) 

Figure 5.9: The dynamics of the system (4.1)-(4.4) for different intensity of travel given in Table 5.2. Values for other parameters are as in Table 5.1 (a) $\sigma = 0.001$; (b) $\sigma = 0.0591$ (Reference).

Note that these calculations assume the same basic reproduction number so the figures are limited in what we can conclude, but we can still observe the importance of reducing travel which agrees with other studies in the field [8, 16].

5.6 Limitations and further work

There are many possibilities for modifying the model to include more options eliminating the limitations of the models described by (4.1) - (4.4) and (4.22) - (4.25). In our models we assume that population remains constant, but we run the simulations for a long time which means the birth and death rate should be included. Another limitation is that we combine rather dispersed real data with the parameters we introduced ourselves corresponding to the infection rate of those who travel or do not travel. Furthermore our model does not account for quarantine, hospitalization or vaccination.

What happens if we introduce a quarantine state as a prevention measure as the Norwegian government did with quarantine hotels? Would it be better to apply a home quarantine model because the risks of the infection spread in quarantine hotels can be high as reported in the media? There is also the possibility of adding an exposed compartment to describe the outbreak more accurately, or to model the effect of vaccination using the Dirac delta

function. There are many other important questions we do not answer in this thesis which we hope to address in the future.

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Matlab

Example 3.3.1

```
function l = Plot()
sol = dde23("File",[0.5, 2,1],"Initialcondition",[0, 20]);
plot(sol.x,sol.y);
title("Solution with initial conditions x_1=1, x_2=0, x_3=0")
xlabel("time t");
ylabel("y(t)");
end

function v = Initialcondition(t)
v = zeros(3,1)
v(1)= t
v(2)= t^2
v(3)= t^3

function v = File(t,y,Z)
ylag1 = Z(1,:); % The estimates for y_1 at different time delays
ylag2 = Z(2,:); % The estimates for y_2 at different time delays
ylag3 = Z(3,:); % The estimates for y_3 at different time delays
v = zeros(3,1);

```

```
% The equation we are trying to solve
v(1) = ylag3(3)-ylag1(1);
v(2) = ylag1(1) - ylag2(2);
v(3) = ylag2(2)-ylag3(3);
end
```

Example 3.3.2

```
function x = Plot2()
q=5;
%dde23(f(x),delay,x(0),Interval)
sol = dde23("Equation",q,0.5,[0, 10000]);
%creating the plot
t = linspace(q,1000,1000);
y = deval(sol,t);
ylag = deval(sol,t - q);
%Below is function to plot x(t) in relation to x(t-5)
plot(y,ylag);
%Below is function to plot x(t) against time
%plot(t,y,'-');
title("Solution with n=8 and x=0.5 for t<5")
xlabel("t");
ylabel("y(t)");
end

function v = Equation(t,y,Z)
v = 2*Z/(Z^10+10)-0.1*y;
end
```

Model without delay

```
All the values are set to their baseline settings.
function v = InitialconditionSSIR(t)
```

```
3  %We set the initial conditions, where v(1)=S_1 v(2)=S_2 ...
       v(3)=I and v(4)=R
4  v = zeros(4,1);
5  p=0.0591;
6  S=0.999;
7  v(1)= (1-p)*S;
8  v(2)= p*S;
9  v(3)= 0.001;
10 v(4)= 0;
11 end
12
13 %Note that the code is the same layout with and without ...
       delay, but in our equation we do not use ylag in the code ...
       without delay
14
15 function sol = PlotSSIR()
16 sol = dde23("SSIR",[15.2, 29.2, ...
       15.2],"InitialconditionSSIR",[0, 200]);
17 plot(sol.x,sol.y);
18 title("Reference")
19 xlabel("time t");
20 ylabel("y(t)");
21 legend({'S1','S2','I','R'},'Location','northeast')
22 end
23
24 function v = SSIR(t,y,Z)
25 ylag1 = Z(:,1); %The estimates for y_1 at different time delays
26 ylag2 = Z(:,2); %The estimates for y_2 at different time delays
27 ylag3 = Z(:,3); %The estimates for y_3 at different time delays
28 v = zeros(4,1);
29 %Value of parameters:
30 alpha=0.15;
31 beta=0.6;
32 Delta=0.06805346324;
33 gamma=0.01855134772;
34 omega=0.29063778101;
35 theta=0.07410797215;
```

```
epsilon=0.0591;
%The equation we are trying to solve,
%y(1)=S_1(t), y(2)=S_2(t), s(3)=I(t) and s(4)=R(t)
%v(1) derivative of S_1(t), v(2) derivative of S_2(t)
%v(3) derivative of I(t), v(4) derivative of R(t)
v(1)=-alpha*y(3)*y(1)-gamma*y(1)+omega*y(2)+ ...
    theta*(1-epsilon)*y(4);
v(2)=-beta*y(3)*y(2)+gamma*y(1)-omega*y(2)+epsilon*theta*y(4);
v(3)=alpha*y(3)*y(1)+beta*y(3)*y(2)-Delta*y(3);
v(4)=Delta*y(3)-theta*y(4);
end
```

Model with delay

```
function v = InitialconditionSSIR(t)
v = zeros(4,1);
p=0.0591;
S=0.999;
v(1)= (1-p)*S;
v(2)= p*S;
v(3)= 0.001;
v(4)= 0;
end


function sol = PlotSSIR()
sol = dde23("SSIRD",[15.2, 29.2, ...
    15.2],"InitialconditionSSIR",[0, 200]);
plot(sol.x,sol.y);
title("Reference")
xlabel("time t");
ylabel("y(t)");
legend({'S1','S2','I','R'},'Location','northeast')
end

```

```
function v = SSIRD(t,y,Z)
ylag1 = Z(:,1); %The estimates for y_1 at different time delays
ylag2 = Z(:,2); %The estimates for y_2 at different time delays
ylag3 = Z(:,3); %The estimates for y_3 at different time delays
v = zeros(4,1);

$\%$Parameters:
alpha=0.15;
beta=0.6;
gamma=0.0182526845;
omega=0.29059138499;
kappa=7;
theta=0.8;
xi=0.0591;
v(1)=-alpha*y(3)*y(1)-gamma*(theta*cos((2*pi*t)/kappa)+1) ...
    *y(1)+omega*y(2)+(1-xi)*alpha*ylag2(3)*ylag2(1) ...
    +(1-xi)*beta*ylag2(3)*ylag2(2);
v(2)=-beta*y(3)*y(2)+gamma*(theta*cos((2*pi*t)/kappa)+1)*y(1) ...
    -omega*y(2)+xi*alpha*ylag2(3)*ylag2(1) ...
    +xi*beta*ylag2(3)*ylag2(2);
v(3)=alpha*y(3)*y(1)+beta*y(3)*y(2) ...
    -alpha*ylag3(3)*ylag3(1)-beta*ylag3(3)*ylag3(2);
v(4)=alpha*ylag3(3)*ylag3(1)+beta*ylag3(3)*ylag3(2) ...
    -alpha*ylag2(3)*ylag2(1)-beta*ylag2(3)*ylag2(2);
end
```

Mathematica codes for analytic computations

Testing asymptotic stability

```
Clear[s1, s2, i, a1, a2, a3, u, v, n, a, b, t, e, w, y, d]
a = 0.15;
b = 0.6;
y = 0.00028801701;
w = 0.28772899933;
```

```
d = 0.06805346324;
t = 0.07410797215;
e = 0.001;
a1 = a*b*(t + d);
a2 = b*(d*t - d*t*e + y*t + y*d) + a*(w*t + w*d + d*t*e - b*t);
a3 = t*(w*d - w*a + y*d - y*b);
u = -a2 + Sqrt[a2^2 - 4*a1*a3];

s1 = d/a - (b/(a - b)) + (b*d/(a*(a - b))) + (u/(2*a*t*(a - b)));
s2 = a/(a - b) - (a*d/(a*(a - b))) - (u/(2*b*t*(a - b)));
i = (u/(2*a*b*(t + d)));

v = {{0, a*i, b*i}, {-a*s1 - t*(1 - e), -a*i - y - t*(1 - e),
    w - t*(1 - e)}, {-s2*b - e*t, y - e*t, -b*i - w - e*t}};
n = Eigenvalues[v]
m = y (b - d) + w (a - d)
```

Calculating γ and ω

```
Clear[v]
Clear[e, b, a, v, t, q, r, p, l]
e = 0.0591; %equilibrium target
b = 0.25; %transition probability from S_2 to S_1 in this ...
    case 25 percent since we want 4 days to be the average or ...
    (1/4)
a = 1 + b - b/(1 - e)
v = {{a, b}, {1 - a, 1 - b}};
t = Eigensystem[v];
q = {{0, t[[2, 2, 1]]*ln[(1/t[[1, 2]])]*(1/t[[1, 2]])^-s}, {0,
    t[[2, 2, 2]]*ln[(1/t[[1, 2]])]*(1/t[[1, 2]])^-s}};
r = {{t[[2, 1, 1]], t[[2, 2, 1]]*(1/t[[1, 2]])^-s}, {t[[2, 1, ...
    2]],
    t[[2, 2, 2]]*(1/t[[1, 2]])^-s}};
p = Inverse[r];
l = Dot[q, p]
```

Solution calculator for $I(t)$

```
Clear[a, b, t, e, d, y, w]
a = 0.15; %alpha
b = 0.6; %beta
t = 0.07410797215; %tau
d = 0.06805346324; %Delta
y = 0.00028801701; %gamma
w = 0.28772899933; %omega
e = 0.001; %xi
q = (a*b*t + a*b*d)*x^2 + (b*(d*t - d*t*e + y*t + y*d) + ...
    a*(w*t + w*d + d*t*e - b*t))*x + t*(y*d - y*b + d*w - a*w)
v = Solve[q == 0, x]
Simplify[v]
```

Calculating eigenvalues at the disease-free equilibrium

```
Clear[s, z, i, o, p, u, q, v, n, l, a, b, t, e, w, y, d]
v = {{a*(w/(y + w)) + b*(y/(y + w)) - d, 0,
    0}, {-a*(w/(y + w)) - t*(1 - e), -y - t*(1 - e),
    w - t*(1 - e)}, {-b*(y/(y + w)) - e*t, y - e*t, -w - e*t}};
n = Eigenvalues[v];
q = Simplify[n]
```

Calculating eigenvalues at the endemic equilibrium

```
Clear[s, z, i, o, p, u, q, v, n, l, a, b, t, e, w, y, d]
v = {{-d, 0, 0}, {-a*(w/(y + w)) - t*(1 - e), -y - t*(1 - e),
    w - t*(1 - e)}, {-b*(y/(y + w)) - e*t, y - e*t, -w - e*t}};
n = Eigenvalues[v];
q = Simplify[n]
```