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MATHEMATICS OF INFECTIOUS DISEASES

A project to be submitted by

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Reg. No. 210011014835

Dissertation submitted in partial fulfilment of the requirement for the

MASTER'S DEGREE

IN

MATHEMATICS

Under the Guidance of

Prof Aleena

DEPARTMENT OF MATHEMATICS

BHARATA MATA COLLEGE,THRIKKAKARA

(Affiliated to Mahatma Gandhi University, Kottayam)

2021-2022

DECLARATION

I Aleena Theresa Varghese hereby declare that this project entitled **'MATHEMATICS OF INFECTIOUS DISEASES'** is a bonafide record of work done by me under the guidance of .and this work has not previously formed by the basis for the award of any academic qualification,fellowship or other similar title od any other University or Board.

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CERTIFICATE

This is to certify that the project entitled **'MATHEMATICS OF INFECTIOUS DISEASES'** submitted for the partial fulfilment requirement of Master's Degree in mathematics is the original work done by Aleena Theresa Varghese during the period of the study in the Department of Mathematics, Bharata Mata College, Thrikkakara under my guidance and has not been included in any other project submitted previously for the award of any degree.

Prof. Aleena
Supervisor

Place: Thrikkakara
Date:

ACKNOWLEDGEMENT

First and foremost I express my sincere gratitude towards the abiding presence and grace of God Almighty. I sincerely express my gratitude to Prof.Aleena,Department of Mathematics, Bharata Mata College, Thrikkakara for guiding and helping me to complete my work. I also express my profound gratitude to Dr.Lakshmi, Head of the Department of Mathematics for her wholehearted cooperation and valuable guidance. Finally, I am obliged to all our teachers of the Mathematics Department, Bharata Mata College for the encouragement for completing this work.

Aleena Theresa Varghese

ABSTRACT

The aim of mathematical model of infectious disease is to report the transference procedure of the disease.In chapter 1 we just introduced what a math model.In chapter 2,we discussed the history of mathematical model and its issues and approaches.Using that model Bernoulli found out the efficiency of vaccination in healthy citizen to prevent them from smallpox.We also discussed some other history of math model also.

In chapter 3,we discussed about the famous SIR Model which is the most discussed model for infectious disease.We also see the analytic solution.In chapter 4,we came to know about the Basic reproductive number and also the threshold theorem.

In chapter 5,we discussed the final size relation of SIR model and some of its examples.In chapter 6 we came to know about the SIR Model with vital dynamics and force of action and its qualitative solution.In Chapter 7, we discussed the SEIR model and in chapter 8 we came to know about SIRS Model without demographic effect and we find its fixed point.

Contents

Chapter 1

INTRODUCTION

Infectious diseases are diseases that are caused by infectious agents like bacteria,fungi,viruses etc.This will spread through air, water, or by physical contact.Over the past years the mankind has been suffering from various kinds of infectious diseases.Many nations and people has been wiped out due to this diseases.Observing and predicting the effect of infectious diseases on the welfare of a society is the basis of distinguishing productive ways to manage the disease spread [4] .

There may be questions arrived that why mathematical method is used.The answer is very simple.The aim of mathematical model of infectious disease is to report the transference procedure of the disease.When a disease spread to large population there is a urgent need to find method to prevent the disease from further spread.

Chapter 2

MATHEMATICAL MODELING

The use of a mathematical model is to how a disease is transmitted from one to the other as follows: when infected person comes into a group of susceptible, and that person after some time become infected.If the number of infected person increase above expected short span of time, a disease outbreak occurs [5]. When the infection spreads quickly to many people, it is an epidemic [5].Infected persons recover from the disease, either due to treatment or due their immunity , and they gain immunity against the infection to occur again [5].

When the epidemic persist and the disease remain in the community over a period of time than expected then the disease is said to be an endemic in the community [5].If a disease spreads globally to more countries and continents then a pandemic occurs.

1 History of Mathematical Model

In the 1500s smallpox was affected the Caribbean by the Spanish army led by Cortez, from there it spreads to Mexico, Peru and

Brazil [7]. Population of Mexico was lessen from 30 million to 2 million over a period of 50 years after the Spanish takeover.In 1760, Bernoulli used mathematical model for smallpox using deterministic mathematical model.In 1906, Hamer developed a discrete-time model in the spread of measles.In 1911, Dr. Ross a physician used differential equation model to show the spread of malaria between humans and mosquitoes and set on that there exist a sill of the size of mosquitoes under which the growth of malaria can be managed [7]. Because of his marvellous contributions in the field of the transmission of malaria so Dr. Ross was awarded Nobel Prize in medicine [3] .

In 1926 Kermack and McKendrick formulate a well-known and most recognised SIR compartmental model, to study the breakout of Black Death in London over the period 1665–1666, and also for the study of plague in Mumbai during 1906 [7].In the mid 1800's Louis Pasteur established experimentally the germ theory of infection and he also discovered the first vaccine to treat rabies.Infection are not the punishment of god or by black magic. The science can explain "why" and mathematics explains "how" [7] .

2 Mathematical Model:Issues And Approaches

In the new era when there is more easy forms to travel around the world, many emerging and reemerging infections have a great chance to become an global pandemic.Facing an impending epidemic, World Health Organization were looking for answers these

questions:

(a) How intense can the epidemic be? The intensity can be check in two different methods [7] :

(1) Total number of disease-ridden people who can get medical treatment.

(2) Maximum disease-ridden people at a given time.

(b) How long will it sustain? When infection peak? What will its time span ? [7]

(c) How powerful will quarantine or vaccination be ? [7]

(d) Amount of vaccine or anti-virus drugs should be stocked ? [7]

(e) What are useful measures to control, destroy an endemic ? [7]

Mathematical modeling proved to be the most important tool in guiding WHO to make correct decisions.There will arise a question that why mathematical modeling useful? Answer is that the orthodox methods using statistical and experimental approaches may not be sufficient for several reasons [7] :

(a) Infections may affect a large community of citizens over a vast area. Experiments that are conducting in laboratories are not sufficient simply due to the large variation in scale.

(b) The infections in humans, vast-scale experiments is impractical or deceitful.

(c) The data the are existing about the disease is not complete or precise for the analysis for been reliable. There cannot be accurate data available about the people who are affected but asymptotic. Mathematical modeling gives an understanding about fundamental

structure of disease transportation and spread.It helps to identify important factors in the disease spread,and suggest an efficient method to control and prevent the disease spread and provides the severity of the epidemic. Mathematical modeling becomes an important part for the Health organization in decision-making [7]. Describe the general method of mathematical modeling? There involves the next six steps:

(a) Make a guess about the disease spread process with the available biological knowledge on pathogens of the infection and sanitation of disease.

(b) Build mathematical models for the disease transmission with respect to the assumptions. This starts by sketching the transfer diagram and deriving the math equations.

(c) Executing mathematical examination on the model to know all available qualitatively various model outcomes.This is done by using the existing mathematical methods on consistency and branched in association with the numerical simulations [7].

(d) Interpreting the math observations enclosed by the the model circumstance.

(e) Gather the available infection data from Health organizations and from research. Confirm the model using data.

(f) By comparing the model with the existing idea or information about the infection we can able to use the model to check various assumption about the infection. Compared to experimental method, the advantage of modeling method is that it is saving

plenty of time and capability [7].

The issues while using a Mathematical model is that:

(a) Because of our limited understanding about infectious disease, realistic guessing about its spreading process is not that much possible. Various levels of simplifications we need. Our assumptions are simply assumptions. When deriving findings from model, we need to keep these restrictions in mind [7].

(b) Model authentication using infection data is really useful because that provides a trial of our modeling assumption. This is not possible or may be hard to do due to the availability data [7].

Chapter 3

SIR MODEL

"As a matter of fact, all epidemiology, concerned as it is with the variation of disease from time to time or from place to place, must be considered mathematically, however many variables as implicated, if it is to be considered scientifically at all"
[8].

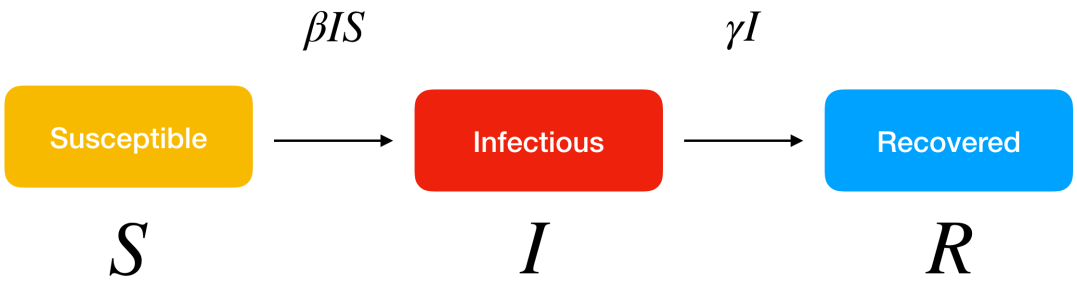
Sir Ronald Ross, MD [8]

We introduce and study the most basic transferring model for directly transmitted disease generated by bacteria, virus, fungi [8]. Direct transmissions happens through one-to-one contact: through sneeze or cold, through skin-skin connection, or by exchange of body 2 The SIR model and the Foundations of Public Health fluids [8]. Examples are the H7N9 flu, whooping cough, tuberculosis [8].
The SIR model, developed by Ronald Ross, William Hamer, in the early twenties consist of system of three connected non-linear ordinary differential equation, which does not group an precise formula solution [8].The simple tool from calculus allows us to

derive a great understanding of knowledge about the solution [8]. We demonstrate how this easy model support us to set a theoretical footing for public health mediation and how different foundations of community health needed a same model to discover [8].The SIR disease transfer model is formulated by assuming different powerful assumptions [8] .
Let N be the total population and we can divide N into 3 subgroups: susceptible , infected , and recovered(removed) and denote these by subgroup at time t by S(t), I(t), R(t) [8] .

A person from **susceptible** have not contacted infectious disease but the person has contact an infected one [1].
A person from the **infected group** directly in contacted the disease and they transmit the disease to the other [1].
A person in the **recovery(removed) class** is the one who is recovered permanently from the disease [1].

Some assumptions made by Kermack-McKendrick for he SIR Model without Vital Dymanics.
(a). Population is always constant [6].
(b). We just ignored the incubation period of disease. [6]
(c). People mixed uniformly [6] .
(d). The total amount of diseased person available at the time is directly proportional to rate at which people is diseased [6].



where β is the transmission rate and γ is the recovery rate [1].

The SIR Model is the system of ordinary differential equation:

$$\frac{dS}{dt} = -\beta SI \tag{3.1}$$

$$\frac{dI}{dt} = \beta SI - \gamma I \tag{3.2}$$

$$\frac{dR}{dt} = \gamma I \tag{3.3}$$

where the initial conditions are:

$S(0) = S_0 > 0, I(0) = I_0 > 0$ and $R(0) = 0$ [1]

Theorem 1. *Prove that population is constant [7].*

Proof:

Consider,

$N = S(t) + I(t) + R(t)$

Add (3.1),(3.2) and (3.3),

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = -\beta SI + \beta SI - \gamma I + \gamma I$$

$$\frac{d}{dt}[S + I + R] = 0$$

$$\frac{d}{dt}[N] = 0$$

$$N'(t) = N_0 \ \forall t$$

1 Analytic Solution

1.1 To find number of infected person at a given time

First we divide equation (3.2) by (3.1),

$$\frac{dI/dt}{dS/dt} = \frac{\beta SI - \gamma I}{-\beta SI}$$

$$\frac{dI}{dS} = \frac{\beta SI}{-\beta SI} - \frac{\gamma I}{-\beta SI}$$

$$\frac{dI}{dS} = -1 + \frac{\gamma}{\beta S}$$

Multiply both side by dS, we get,

$$dI = (-1 + \frac{\gamma}{\beta} \cdot \frac{1}{S})dS$$

Next integrate both the sides,

$$I(t) = -S(t) + \frac{\gamma}{\beta} In \mid S(t) \mid + C$$

Where e $= \frac{\gamma}{\beta}$ and e is the relative recovery rate.

$$I(t) = -S(t) + eIn \mid S(t) \mid + C \tag{3.4}$$

But we have I(0) $= I_0$ and S(0) $= S_0$

So to find C,

$$\mathrm{I}(0) = -S(0) + eIn \mid S(0) \mid + C$$

$$I_0 = -S_0 + eInS_0 + C$$

But we have,

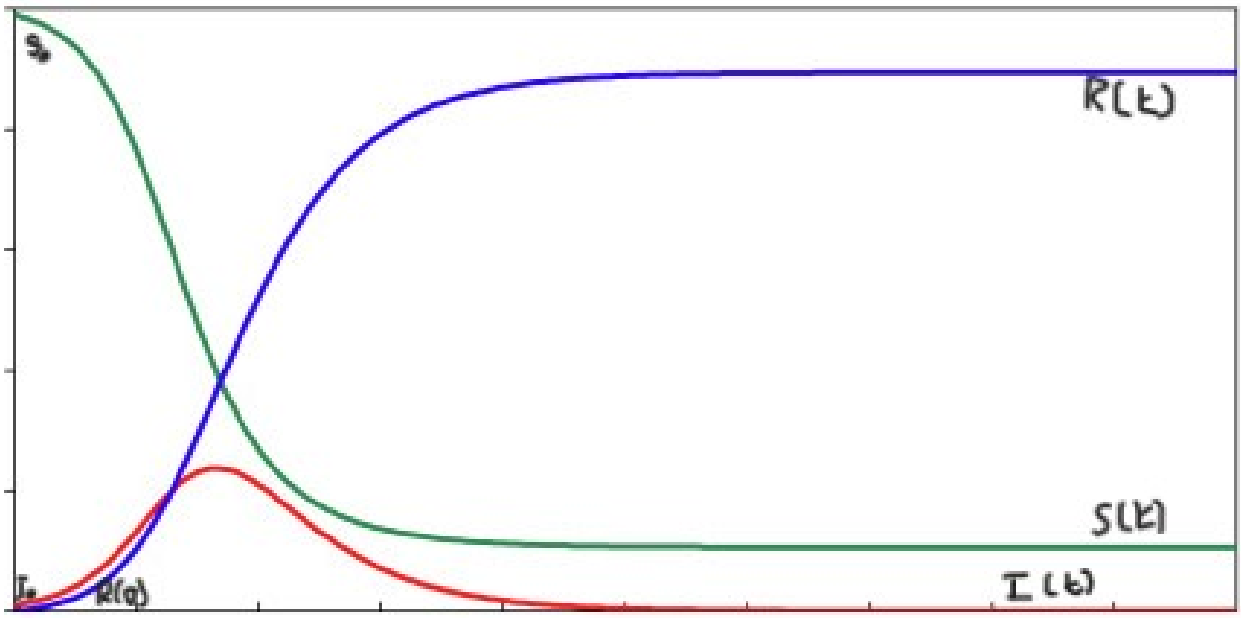
$$C = I_0 + S_0 - eInS_0 \tag{3.5}$$

Substitute (3.5) in (3.4),

$$I(t) = -S(t) + eIn \mid S(t) \mid + I_0 + S_0 - eInS_0$$

$$I(t) = I_0 + S_0 - S(t) + eIn(S(t)/S_0) \text{ [1]}$$

1.2 To find number of maximum infection.



Where we get maximum at S = e also $\frac{dI}{dt} = 0$

We have, $I(t) = I_0 + S_0 - S(t) + eIn(S(t)/S_0)$ [1]

So,

$$I_{max} = I_0 + S_0 - e + eIn(e/S_0)$$

But we have, $I_0 + S_0 = N$ [1]

Therefore we get,

$$I_{max} = N - e + eIn(e/S_0)$$ [1]

1.3 To find S(t)

To find out the remaining number of suspecptible persons [1].

Divide equation (3.1) and (3.3)

$$\frac{dS/dt}{dR/dt} = \frac{-\beta SI}{\gamma I}$$

$$\frac{dS}{dR} = \frac{-\beta S}{\gamma}$$

$$\frac{dS}{dR} = \frac{-\beta}{\gamma} \cdot S$$

$$\frac{dS}{S} = \frac{-\beta}{\gamma} dR$$

$$\frac{1}{S} dS = \frac{-\beta}{\gamma} dR$$

$$In \mid S(t) \mid = \frac{-\beta}{\gamma} \cdot R + C$$

But we have,

e $= \frac{\gamma}{\beta}$ so we get, $\frac{1}{e} = \frac{\beta}{\gamma}$

$$In \mid S(t) \mid = -\frac{R(t)}{e} + C \tag{3.6}$$

So at time t = 0 we can find C, we also have $S(0) = S_0$ and R(0) = 0

So we get,

$$\text{In}S_0 = \frac{-R(0)}{e} + \text{C}$$

which implies that,

$$InS_0 = \frac{0}{e} + C \implies C = InS_0 \tag{3.7}$$

Substitute (3.7) in (3.6),

$$In \mid S(t) \mid = \frac{-R(t)}{e} + InS_0$$

$$In(S(t)/S_0) = \frac{-R(t)}{e}$$

Take exponential on each of the side,

$$\text{S(t)} = S_0 e^{\frac{-R(t)}{e}} \text{ [1]}$$

1.4 To find R(t)

Consider (3.3),

$$R(t) = \frac{\beta}{S_0}[(\frac{S_0}{e} - 1) + \alpha \tanh(\frac{\alpha\gamma t}{2} - \phi)] \text{ [1]}$$

Given that,

$$\alpha = [(\frac{S_0}{e} - 1)^2 + \frac{2S_0(N - S_0)}{e^2}]^{1/2} \text{ [1]}$$

$$\phi = \frac{\tanh^{-1}(S_0/e - 1)}{\alpha} \text{ [1]}$$

Here R(t) is really hard to find that is why we made such assumptions,so that we get the value for R(t) [1].

Chapter 4

BASIC REPRODUCTIVE NUMBER

Let R_0 denotes the *Basic Reproductive Number* [6].
It is defined as the expected number of secondary cases produced by single infection in a completely susceptible population [6].

1 Threshold Theorem

Theorem 2. *(1). If $R_0 > 1$ then the epidemic get started unless the basic number of susceptible exceeds a certain threshold value [1].*
(2). If $R_0 \geq 1$, then disease spread among the susceptible group or if $R_0 < 1$ infection dies in S(t) [1].

2 Derive Formula For R_0

Given, $\frac{dI}{dt} \geq 0$

$$\implies \beta SI - \gamma I \geq 0$$

$$\implies \beta SI \geq \gamma I$$

Divide by γI,

$$\frac{\beta SI}{\gamma I} \geq \frac{\gamma I}{\gamma I}$$

We get,

$$\frac{\beta S}{\gamma} \geq 1 \tag{4.1}$$

We have,

$$R_0 \geq 1 \tag{4.2}$$

From (4.1) and (4.2) we get,

$$R_0 = \frac{\beta S_0}{\gamma} \text{ [1]}$$

Suppose that the visitor transmit the disease the we take the suscptible as the total community [1].

Consider $S_0 = N$

$$\therefore R_0 = \frac{\beta N}{\gamma} \text{ [1]}$$

This is the Basic Reproductive number.

Chapter 5

FINAL SIZE RELATION FOR SIR MODEL

Consider the SIR model,

So add equation (3.1) and (3.2),

$$\frac{dS}{dt} + \frac{dI}{dt} = -\beta SI + \beta SI - \gamma I$$

$$\frac{d}{dt} = -\gamma I$$

$$\frac{d}{dt}[S + I] = -\gamma I dt$$

$$d[S(t) + I(t)] = -\gamma I(t) dt$$

Integrate both sides from 0 to ∞ implies,

$$lim_{m\to\infty} = \int_0^m d[S(t) + I(t)] = lim_{m\to\infty} \int_0^m -\gamma I(S) dS$$

$$lim_{m\to\infty}[S(m) + I(m) - S(0) - I(0)] = -\gamma lim_{m\to\infty} \int_0^m I(S) dS$$

By expanding this we get,

$lim_{m\to\infty}S(m)+lim_{m\to\infty}I(m)-lim_{m\to\infty}S(0)-lim_{m\to\infty}I(0) = -\gamma\int_0^m I(S)dS$

We know that I_0 and S_0 are constant values also we know that the limit of a constant is constant. [1]

So the end of infection is,

$lim_{m\to\infty}S(m) = S_\infty$ [1]

$lim_{m\to\infty}I(m) = 0$ [1]

So we get,

$S_\infty + 0 - S_0 - I_0 = -\gamma lim_{m\to\infty}\int_0^m I(S)dS$

$S_\infty - (I_0 + S_0) = -\gamma lim_{m\to\infty}\int_0^m I(S)dS$

We know that at the start of epidemic, $I_0 + S_0 = N$ [1]

$S_\infty - N = -\gamma lim_{m\to\infty}\int_0^m I(S)dS$ [1]

Divide by $-\gamma$ we get that,

$$\frac{S_\infty - N}{-\gamma} = lim_{m\to\infty} \int_0^m I(S)dS$$

We get,

$$\frac{N - S_\infty}{\gamma} = lim_{m\to\infty} \int_0^m I(S)dS \tag{5.1}$$

We have,

$$\frac{dS}{dt} = -\beta SIdt$$

Seperating the variables we get,

$$\frac{dS}{S} = -\beta Idt$$

Integrate the terms from 0 to ∞ wwe get,

$$lim_{m\to\infty} \int_0^m \frac{1}{S} dS = lim_{m\to\infty} \int_0^m -\beta I(s)ds$$

$$lim_{m\to\infty}[InS(m) - InS(0)] = -\beta lim_{m\to\infty} \int_0^m I(S)dS$$

$$lim_{m\to\infty} InS(m) - lim_{m\to\infty} InS_0 = -\beta lim_{m\to\infty} \int_0^m I(S)dS$$

Divide the whole equation by $-\beta$ we get,

$$\frac{InS_\infty - InS_0}{-\beta} = -\beta lim_{m\to\infty} \int_0^m I(S)dS \text{ [1]}$$

we get,

$$\frac{InS_0 - InS_\infty}{\beta} = lim_{m\to\infty} \int_0^m I(S)dS \tag{5.2}$$

So from (5.1) and (5.2) we have,

$$\frac{N - S_\infty}{\gamma} = \frac{1}{\beta} In(S_0/S_\infty) \tag{5.3}$$

We know that $R_0 = \dfrac{\beta N}{\gamma}$ [1]

$$\implies \frac{R_0}{N} = \frac{\beta}{\gamma}$$

Multiply (5.3) by β we get,

$$\frac{\beta}{\gamma}(N - S_\infty) = In(S_0/S_\infty)$$

Substitute,

$$\frac{R_0}{N}(N - S_\infty) = In(S_0/S_\infty)$$

We get,

$$R_0(\frac{N}{N} - \frac{S_\infty}{N}) = In(S_0/S_\infty)$$

$\therefore$ we get,

$$R_0(1 - \frac{S_\infty}{N}) = In(S_0/S_\infty) \tag{5.4}$$

$\therefore$ (5.4) is known as the **Final Size Relation**. [1]

1 Some Examples

EXAMPLE 1: A study of Yale University freshmen described an influenza epidemic with $S_0 = 0.911$ and $S_\infty = 0.513$ [1]. Here we are measuring the number of susceptible as a fraction of the total population size [1] . Compute R_0.

Solution:

From final size formula,

$$R_0(1 - \frac{S_\infty}{N}) = In(S_0/S_\infty)$$

Given that, $S_0 = 0.911, S_\infty = 0.513$ and N =1

$$R_0(1 - 0.513) = In(0.911/0.513)$$

$\therefore R_0 = 1.18$

Since $R_0 \geq 1$ .The disease is an epidemic.

EXAMPLE 2: A disease is introduced by two visitors into a town with 1200 inhabitants. An average infective is in contact with 0.4 inhabitants per day [1]. The average duration of the infective period is 6 days, and recovered infectives are immune against reinfection [1]. How many inhabitants would have to be immunized to avoid an epidemic [1].

Solution :

Let N $= 1200$, $\gamma = 1/6$, $\beta N = 0.4$, $_0 = 2$, $S_0 = N = 1200$

Let $R_0 = \dfrac{\beta S_0}{\gamma} = \dfrac{\beta N}{\gamma}$ [1]

Let, $\beta N = 0.4$,

$$\beta = \frac{1}{3000}$$

$$R_0 = \frac{\frac{1}{3000} \times 1200}{\frac{1}{6}}$$

$$\therefore R_0 = 2.4$$

An epidemic will take place if nothing happens.

The fraction of population who immunized to neglect epidemic is:

$$1 - \frac{1}{R_0}$$

$$1 - \frac{1}{2.4} = \frac{7}{12}$$

So the total number of inhabitants who would have to be immunized to avoid an epidemic is , [1]

$$\frac{7}{12} \times 1200 = 700$$

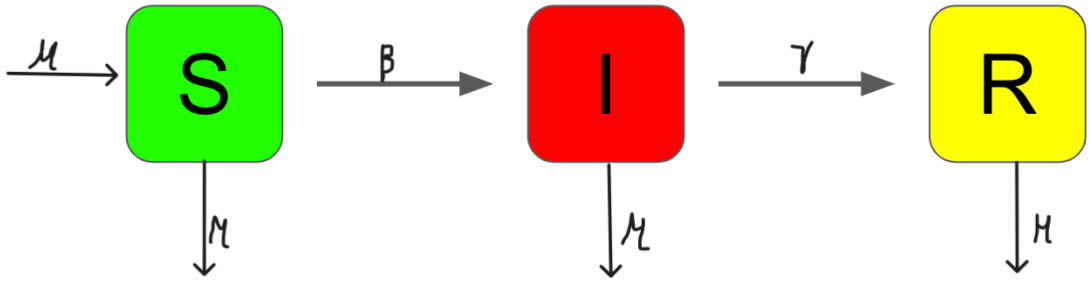
So there are 700 inhabitants.

Chapter 6

SIR MODEL WITH VITAL DYNAMICS AND FORCE OF INFECTION

FORCE OF INFECTION : It is denoted by λ and it is the rate at which susceptible person attains an infectious disease. [1]

In 1932, Kermack and McKendrick made SIR Model that includes both birth and death rate . [1]



where β is the transfer rate , γ is removed rate and μ is death

or birth rate. [1]

Consider the system of DE:

$$\frac{dS}{dt} = \mu N - \frac{\beta SI}{N} - \mu S \tag{6.1}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I - \mu I \tag{6.2}$$

$$\frac{dR}{dt} = \gamma I - \mu R \tag{6.3}$$

Let s(t) = $\frac{S(t)}{N}$, r(t) = $\frac{R(t)}{N}$, i(t) = $\frac{I(t)}{N}$ [1]

Differentiating,

$\frac{dS}{dt} = N\frac{ds}{dt}, \frac{dR}{dt} = \frac{dr}{dt}, \frac{dI}{dt} = N\frac{di}{dt}$ [1]

Substitute this into (6.1) ,(6.2) , (6.3) we get:

$$\frac{ds}{dt} = \mu - \beta si - \mu s \tag{6.4}$$

$$\frac{di}{dt} = \beta si - \gamma i - \mu i \tag{6.5}$$

$$\frac{dr}{dt} = \gamma i - \mu r \tag{6.6}$$

These are our new equation.

We have that the population is constant. [1]

Here we have $R_0 = \dfrac{\beta s}{(\gamma + \mu)}$ [1]

1 Qualitative Solution

Let us consider,

$\dfrac{ds}{dt} = 0, \dfrac{di}{dt} = 0, \dfrac{dr}{dt} = 0$ [1]

From (6.5),

$\beta si - \gamma i - \mu i = 0$

i $= 0$ or $s = \dfrac{\gamma + \mu}{\beta}$ [1]

So put i $= 0$ in (6.4) we get,

$\mu - \beta si - \mu s = 0$

$\mu(1 - s) = 0$

So we get, s = 1

Substitute i = 0 in (6.6),

$\gamma i - \mu r = 0$

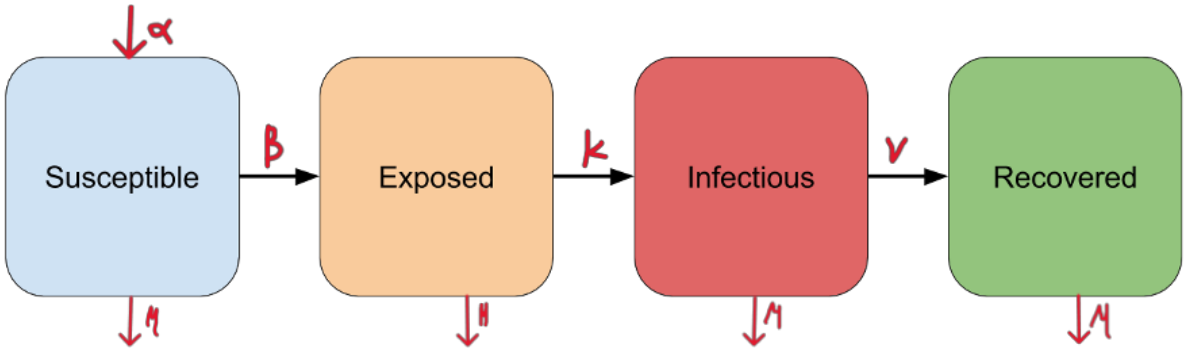
So we get, r = 0

So we get the fixed point as (s^*, i^*, r^*) = (1,0,0). [1]

Chapter 7

SEIR MODEL

In many diseases there is an exposed period the disease has been transmitted from the group of susceptible to infected group. [1] Consider the mean exposed period as $\frac{1}{\kappa}$. [1]



Given that α is birth rate ,β is transfer rate , κ is death rate and γ is recovered rate. [1]

Consider the DE:

$$\frac{dS}{dt} = \alpha N - \frac{\beta SI}{N} - \mu S \tag{7.1}$$

$$\frac{dE}{dt} = \frac{\beta SI}{N} - \kappa E - \mu E \tag{7.2}$$

$$\frac{dI}{dt} = \kappa E - \mu I \tag{7.3}$$

$$\frac{dR}{dt} = \gamma I - \mu R \tag{7.4}$$

Let s(t) = $\frac{S(t)}{N}$, e(t) = $\frac{E(t)}{N}$, i(t) = $\frac{I(t)}{N}$ and r(t) = $\frac{R(t)}{N}$ [1]

Differentiating,

$\frac{dS}{dt} = N\frac{ds}{dt}$ [1]

$\frac{dE}{dt} = N\frac{de}{dt}$ [1]

$\frac{dI}{dt} = N\frac{di}{dt}$ [1]

$\frac{dR}{dt} = N\frac{dr}{dt}$ [1]

Substitute in (7.1) we get,

$$N\frac{ds}{dt} = \alpha N - \frac{\beta s N i N}{N} - \mu s N$$

So we get ,

$$\frac{ds}{dt} = \alpha - \beta s i - \mu s \tag{7.5}$$

Similarly substitute in (7.2),(7.3) and (7.4) we get,

$$\frac{de}{dt} = \beta s i - \kappa e - \mu e \tag{7.6}$$

$$\frac{di}{dt} = \kappa e - \gamma i - \mu i \tag{7.7}$$

$$\frac{dr}{dt} = \gamma i - \mu r \tag{7.8}$$

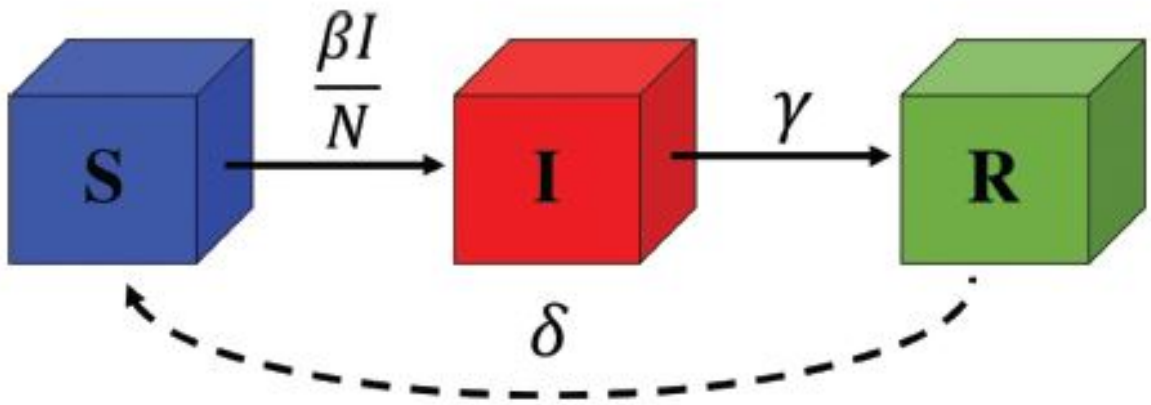
Here the population is constant. [1]

An example of SEIR Model is the Covid-19 pandemic.

Chapter 8

SIRS MODEL WITHOUT DEMOGRAPHIC EFFECT

This model has temporal immunity so that they recover after they move back to Suceptible. [1]



δ is the immunity loss.

Consider the DE:

$$\frac{dS}{dt} = -\frac{\beta SI}{N} + \delta R \tag{8.1}$$

$$\frac{dI}{dt} = \frac{\beta}{S} IN - \gamma I \tag{8.2}$$

$$\frac{dR}{dt} = \gamma I - \delta R \tag{8.3}$$

Assumptions:

(a). Population is constant. [1]

(b). $\delta \propto$ number of recovered individual at the given time. [1]

(c). No waiting period. [1]

We get,

s(t) = $\frac{S(t)}{N}$, i(t) = $\frac{I(t)}{N}$, r(t) = $\frac{R(t)}{N}$. [1]

Differentiating,

$\frac{dS}{dt} = N\frac{ds}{dt}$ [1]

$\frac{dI}{dt} = N\frac{di}{dt}$ [1]

$\frac{dR}{dt} = N\frac{dr}{dt}$ [1]

Substituting in (8.1),(8.2) and (8.3) we get,

$$\frac{ds}{dt} = -\beta si + \delta r \tag{8.4}$$

$$\frac{di}{dt} = \beta si + \gamma i \tag{8.5}$$

$$\frac{dr}{dt} = \gamma i - \delta r \tag{8.6}$$

Here the population is constant. [1]

1 Finding Fixed Point

Put $\frac{ds}{dt} = \frac{di}{dr} = \frac{dr}{dr} = 0$ in (8.4),(8.5),(8.6) we get, [1]

$$-\beta si + \delta r = 0 \tag{8.7}$$

$$\beta si - \gamma i = 0 \tag{8.8}$$

$$\gamma i - \delta r = 0 \tag{8.9}$$

$$s + i + r = 1 \tag{8.10}$$

From (8.8) we get,

$\beta si - \gamma i = 0$ [1]

$\implies i = 0$ or $s = \frac{\gamma}{\beta}$

Substitute i = 0 in (8.9),

$\gamma(0) - \delta r = 0$ [1]

$\implies r = 0$

Now substitute i =0 and r =0 in (8.10) we get,

s + 0 + 0 = 1

$\implies s = 1$

So the fixed point is (s^*, i^*, r^*) = (1,0,0) [1]

This is the non-disease fixed point. [1]

Chapter 9

CONCLUSION

Mathematics of infectious disease was used to control and guide the biologists to make the medicine and treatment plan up to the mark.If the infection spreads a large population it is really difficult to use vaccination so we use the mathematical modeling the see that how fast and in what rate the vaccination have to be done.Before the vaccination introduced to make the infection under control we have use various procedures to make the infection under control for this we have to quarantine and the other useful methods.So in order to track the individuals that the infected or suspected person has visited have to be tracked, for this purpose also we use the math model.

[2] So math is really helpful in controlling and preventing the disease from spreading.So in biology the use of math is really important.Without math this details cannot make that much impact and the outcome cannot really be obtained.So math is really a vital part in Public Health.

References

[1] Fred Brauer, Carlos Castillo-Chavez, and Carlos Castillo-Chavez. *Mathematical models in population biology and epidemiology*, volume 2. Springer, 2012.

[2] Carlos Castillo-Chavez, Sally Blower, Pauline van den Driessche, Denise Kirschner, and Abdul-Aziz Yakubu. *Mathematical approaches for emerging and reemerging infectious diseases: models, methods, and theory*, volume 126. Springer Science & Business Media, 2002.

[3] Ivo M Foppa. *A historical introduction to mathematical modeling of infectious diseases: Seminal Papers in Epidemiology*. Academic Press, 2016.

[4] Nicholas C Grassly and Christophe Fraser. Mathematical models of infectious disease transmission. *Nature Reviews Microbiology*, 6(6):477–487, 2008.

[5] Herbert W Hethcote. The mathematics of infectious diseases. *SIAM review*, 42(4):599–653, 2000.

[6] James Holland Jones. Notes on r0. *California: Department of Anthropological Sciences*, 323:1–19, 2007.

[7] Michael Y Li. *An introduction to mathematical modeling of infectious diseases*, volume 2. Springer, 2018.

[8] Howard Howie Weiss. The sir model and the foundations of public health. *Materials matematics*, pages 0001–17, 2013.

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