7. Infectious Disease Modelling

(Ruth Baker's Notes, Chapter 5, Section 5.1)

In this presentation:

- Susceptible-Infected-Removed (SIR) model (Kermack-McKendrick)

7.1 The SIR model

Consider a disease for which the population can be placed into three compartments:

- the Susceptible compartment, S: individuals who can catch the disease;
- the Infective compartment, I: individuals who have and transmit the disease;
- the Removed compartment, R: individuals who got infected and are now either isolated themselves, have recovered and are immune to the disease, or have died due to the disease.

7.1.1 Assumptions

- The disease dynamics are on a short timescale so that there is no birth, and no death due to causes other than the disease.
- The disease has a negligible incubation period - that is, when a person becomes infect*ed*, they immediately become infect*ious*
- There are no spatial effects.

No immigration/emigration

7.1.2 Kermack-McKendrick Model, 1927

$$\frac{\mathrm{dS}}{\mathrm{dt}} = -rIS, \tag{7.1}$$

$$\frac{\mathrm{dI}}{\mathrm{dt}} = rIS - aI, \tag{7.2}$$

$$\frac{\mathrm{dR}}{\mathrm{dt}} = aI, \tag{7.3}$$

subject to

$$S(0) = S_0, \quad I(0) = I_0, \quad R(0) = 0. \tag{7.4}$$

Further assumptions:

A.1 Law of Mass Action - there is uniform mixing between S and I:

$$S + I \longrightarrow I + I \tag{7.5}$$

with a rate r (constant), which is the rate at which the infection spreads from an Infected to a Susceptible

subject to

$$S(0) = S_0, \quad I(0) = I_0, \quad R(0) = 0. \tag{7.4}$$

$$\frac{\mathrm{dS}}{\mathrm{dt}} = -rIS, \tag{7.1}$$

$$\frac{\mathrm{dI}}{\mathrm{dt}} = rIS - aI, \tag{7.2}$$

$$\frac{\mathrm{dR}}{\mathrm{dt}} = aI, \tag{7.3}$$

A.2 The removal rate from the Infected compartment to the Removed compartment

$$I \longrightarrow R \tag{7.6}$$

is a constant (a).

A.3 There is no movement out of the Removed compartment.

A.4 Initially, the Susceptible population has size $S_0 > 0$, the Infected population has size $I_0 > 0$, and there is no Removed population.

Note that, as we would expect from the assumptions, adding the equations

$$\frac{\mathrm{d}}{\mathrm{dt}}(S + I + R) = 0 \quad \Longrightarrow \quad S + I + R = S_0 + I_0 = \text{ constant } = N. \tag{7.7}$$

Summary

- Susceptible-Infected-Removed (SIR) model (Kermack-McKendrick)

End of Lecture 7-1

7. Infectious Disease Modelling

(Ruth Baker's Notes, Chapter 5, Section 5.1)

In the previous part:

- Susceptible-Infected-Removed (SIR) model (Kermack-McKendrick)

Summary of this presentation:

- “The R number”!!!!

Kermack-McKendrick:

$$\frac{\mathrm{dS}}{\mathrm{dt}} = -rIS, \tag{7.1}$$

$$\frac{\mathrm{dI}}{\mathrm{dt}} = rIS - aI, \tag{7.2}$$

$$\frac{\mathrm{dR}}{\mathrm{dt}} = aI, \tag{7.3}$$

Follow the recipe:

Non-dimensionalise; find steady states; linear stability; phase planes.

BUT!! What questions are we trying to answer?

Does the infection grow?

How many people will get the disease?

How we do we control it?

7.1.3 "The R Number" (R_0)

$$\frac{\mathrm{dS}}{\mathrm{dt}} = -rIS, \tag{7.1}$$

$$\frac{\mathrm{dI}}{\mathrm{dt}} = rIS - aI, \tag{7.2}$$

$$\frac{\mathrm{dR}}{\mathrm{dt}} = aI, \tag{7.3}$$

subject to

$$S(0) = S_0, \quad I(0) = I_0, \quad R(0) = 0. \tag{7.4}$$

From equations (7.1) - (7.2) we have that

$$\frac{\mathrm{dS}}{\mathrm{dt}} = -rIS \quad \Longrightarrow \quad S \text{ is decreasing and therefore } S \leq S_0. \tag{7.8}$$

$$\frac{\mathrm{dI}}{\mathrm{dt}} = I(rS - a) \leq I(rS_0 - a) = rI(S_0 - \rho) \text{ where } \rho = \frac{a}{r}. \tag{7.9}$$

Therefore, if $S_0 < a/r$ then $\frac{dI}{dt} \leq 0, \forall t \geq 0$.

Definitions: The parameter ρ is called **relative removal rate**;

$\sigma = \frac{1}{\rho}$ is the infection's **contact rate**

and $R_0 = \sigma S_0 = rS_0/a$ is the **basic reproduction number**

(it is dimensionless).

$$\frac{dS}{dt} = -rIS, \tag{7.1}$$

$$\frac{dI}{dt} = rIS - aI, \tag{7.2}$$

$$\frac{dR}{dt} = aI, \tag{7.3}$$

and $R_0 = \sigma S_0 = rS_0/a$ is the **basic reproduction number**

Note that, at $t = 0$:

a (r/a S – 1)I

$$\frac{dI}{dt} = a(\sigma S_0 - 1)I_0 = a(R_0 - 1)I_0.$$

Therefore, if $R_0 > 1$ then I initially increases

(this is an **epidemic** - epidemic means that $I(t) > I_0$ for some $t > 0$).

Now, R_0 is rS_0 multiplied by $\frac{1}{a}$.

The first term is the number of infections a single infected individual produces in a wholly susceptible population of size S_0 per unit time.

The second term is the average time an infected individual remains infected.

So, R_0 is *the average number of secondary infections produced by one primary infected individual in a wholly susceptible population.*

From our analysis, we see that if $R_0 > 1$ then an epidemic occurs.

Makes sense – if, on average, the number of secondary infections produced by an infected is greater than 1, then the disease will grow

$$R_0 = \sigma S_0 = rS_0/a$$

To control the disease:
Decrease the Susceptible population -- vaccination

Decrease r – the rate of spread – face, space, hands

Increase a – self-isolation

Summary

- We introduced R_o
- Showed that for R_0 > 1 is the condition for an epidemic

End of Lecture 7-2

7. Infectious Disease Modelling

(Ruth Baker's Notes, Chapter 5, Section 5.1)

In the previous part:

Introduced R_o

In this presentation:

- What is the maximum number of Infectives?
- How many people get the disease?

$$\frac{\mathrm{dS}}{\mathrm{dt}} = -rIS, \tag{7.1}$$
$$\frac{\mathrm{dI}}{\mathrm{dt}} = rIS - aI, \tag{7.2}$$
$$\frac{\mathrm{dR}}{\mathrm{dt}} = aI, \tag{7.3}$$

7.1.4 What will be the maximum number of Infectives?

From Equation (7.2), I has a turning point at $S = \rho$ and this is a maximum.

From equations (7.1) - (7.2):

$$\frac{\mathrm{dI}}{\mathrm{dS}} = -\frac{(rS - a)}{rS} = -1 + \frac{\rho}{S}.$$

Therefore I increases for $S < \rho$ and decreases for $S > \rho$.

Furthermore, integrating gives

$$I + S - \rho \ln S = I_0 + S_0 - \rho \ln S_0,$$

Hence:

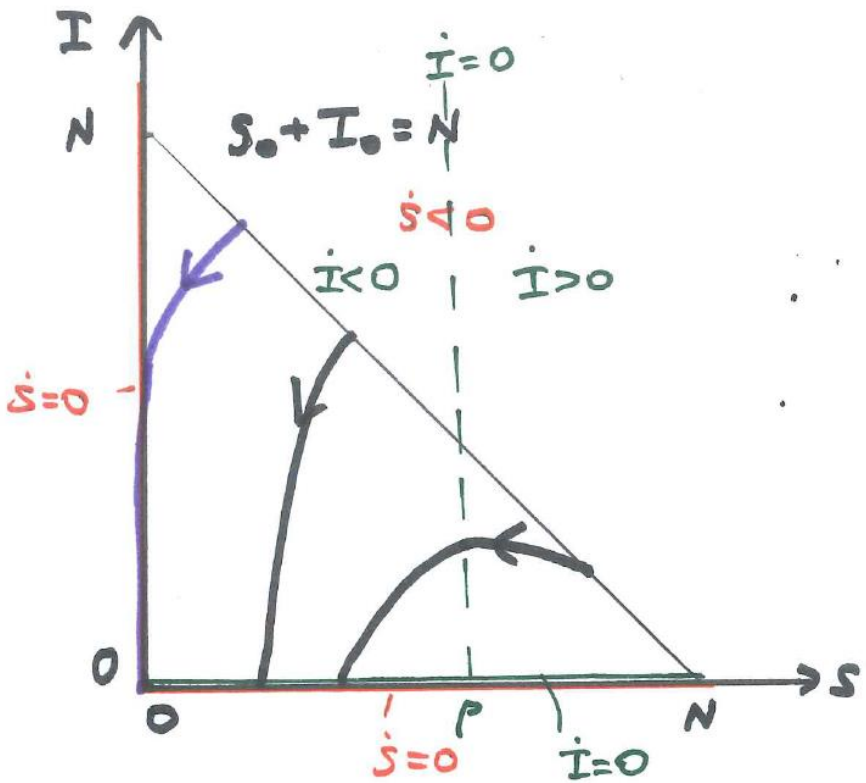
$$I_{max} = \begin{cases} I_0 & S_0 \leq \rho \\ I_0 + S_0 - \rho \ln S_0 + \rho \ln \rho - \rho & S_0 > \rho \end{cases}.$$

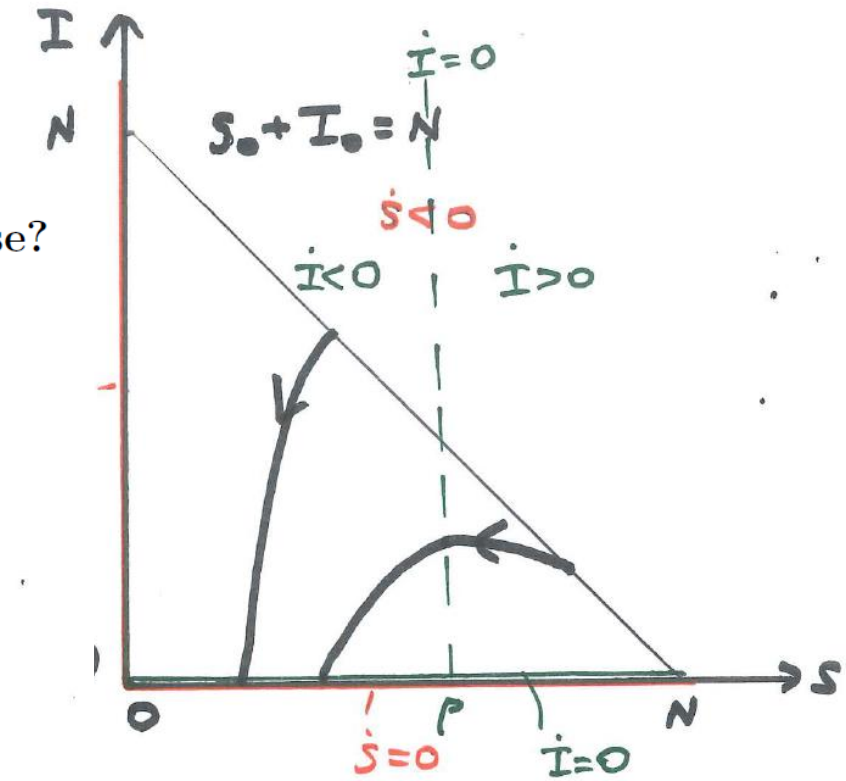
$$\frac{dS}{dt} = -rIS, \tag{7.1}$$

$$\frac{dI}{dt} = rIS - aI, \tag{7.2}$$

$$\frac{dR}{dt} = aI, \tag{7.3}$$

7.1.5 How many people will catch the disease?





Assume $\rho < N$

S nullclines
$S=0$, $I=0$

I nullclines
$I=0$, $S=\rho$

$$\frac{\mathrm{dS}}{\mathrm{dt}} = -rIS, \tag{7.1}$$
$$\frac{\mathrm{dI}}{\mathrm{dt}} = rIS - aI, \tag{7.2}$$
$$\frac{\mathrm{dR}}{\mathrm{dt}} = aI, \tag{7.3}$$

From the $S - I$ phase plane, we know that $I \to 0$ as $t \to \infty$.

We also have, from equations (7.1) - (7.3) that

$$\frac{dS}{dR} = -\frac{S}{\rho}.$$

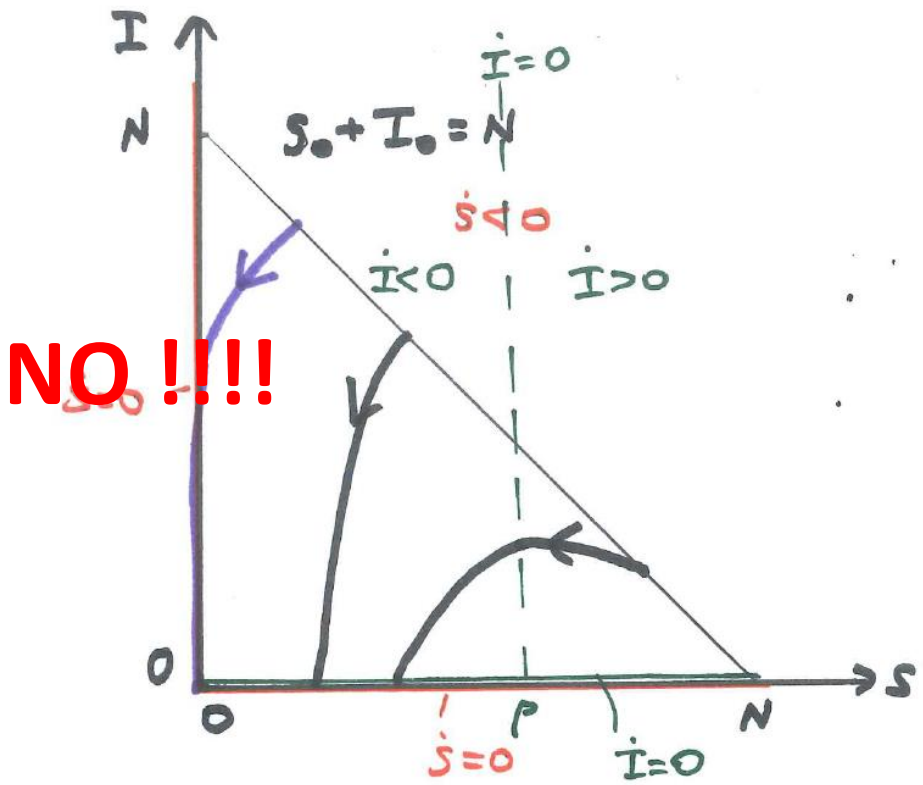
Therefore, $S = S_o e^{-\frac{R}{\rho}} \geq S_o e^{-\frac{N}{\rho}} > 0$, and this is true for all t.

Note that $S(t) + R(t) + I(t) = N$ and, since $S(t)$ and $I(t)$ can never go negative (for example, go to Equation (7.1), set $S = 0$ for contradiction).

So, it follows that $R(t) \leq N$ for all $t \geq 0$.

Hence, we have that $S(t)$ is strictly bounded below by 0, and $\frac{dS}{dt} < 0$ for $I \neq 0$ so the limit as t tends to ∞ of $S(t)$, namely, $S(\infty)$ exists and satisfies:

$$S(\infty) = S_o e^{-\frac{N - S(\infty)}{\rho}}.$$


I
N
$S_0 + I_0 = N$
$\dot{I}=0$
$\dot{S}<0$
$\dot{I}<0$
$\dot{I}>0$
NO !!!!
$\dot{S}=0$
0
0
P
N
S
$\dot{S}=0$
$\dot{I}=0$

7.2 Relaxing Some Assumptions

Suppose that the incubation period is not negligible. Then we need to introduce the "Exposed" compartment - people who have contacted the disease but do not yet pass it along. In this case we would have the so-called "SEIR" model:

$$S \longrightarrow E \longrightarrow I \longrightarrow R$$

Or, maybe there is no immunity so that after infection, you are susceptible again - we have the SIS model:

$$S \longrightarrow I \longrightarrow S$$

Or, maybe the population is not isolated, but each population S_i, I_i (in the case of an SIS system) in town ("node") i is connected to those in other towns:

$$\frac{dS_i}{dt} = -\beta S_i I_i + \sum_{j \neq i} (m_{ij} S_j - m_{ji} S_i) + \gamma I_i$$

$$\frac{dI_i}{dt} = \beta S_i I_i + \sum_{j \neq i} (\hat{m}_{ij} I_j - \hat{m}_{ji} I_i) - \gamma I_i$$

m_{ij} is migration rate from j to i for Susceptibles, etc.

effect of local lockdown?

We can make the model increasingly complicated.

Within-host modelling, linking with population-level modelling ...

Summary

- We studied how the disease spread (maximum infection)
- Disease dies out due to infection going to zero, leaving behind a non-zero susceptible population.

End of Lecture 7-3