

Next generation matrix method for computing \mathcal{R}_0

MATH 8xyz – Lecture 08

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The University of Manitoba campuses are located on original lands of Anishinaabeg, Ininew, Anisininew, Dakota and Dene peoples, and on the National Homeland of the Red River Métis.

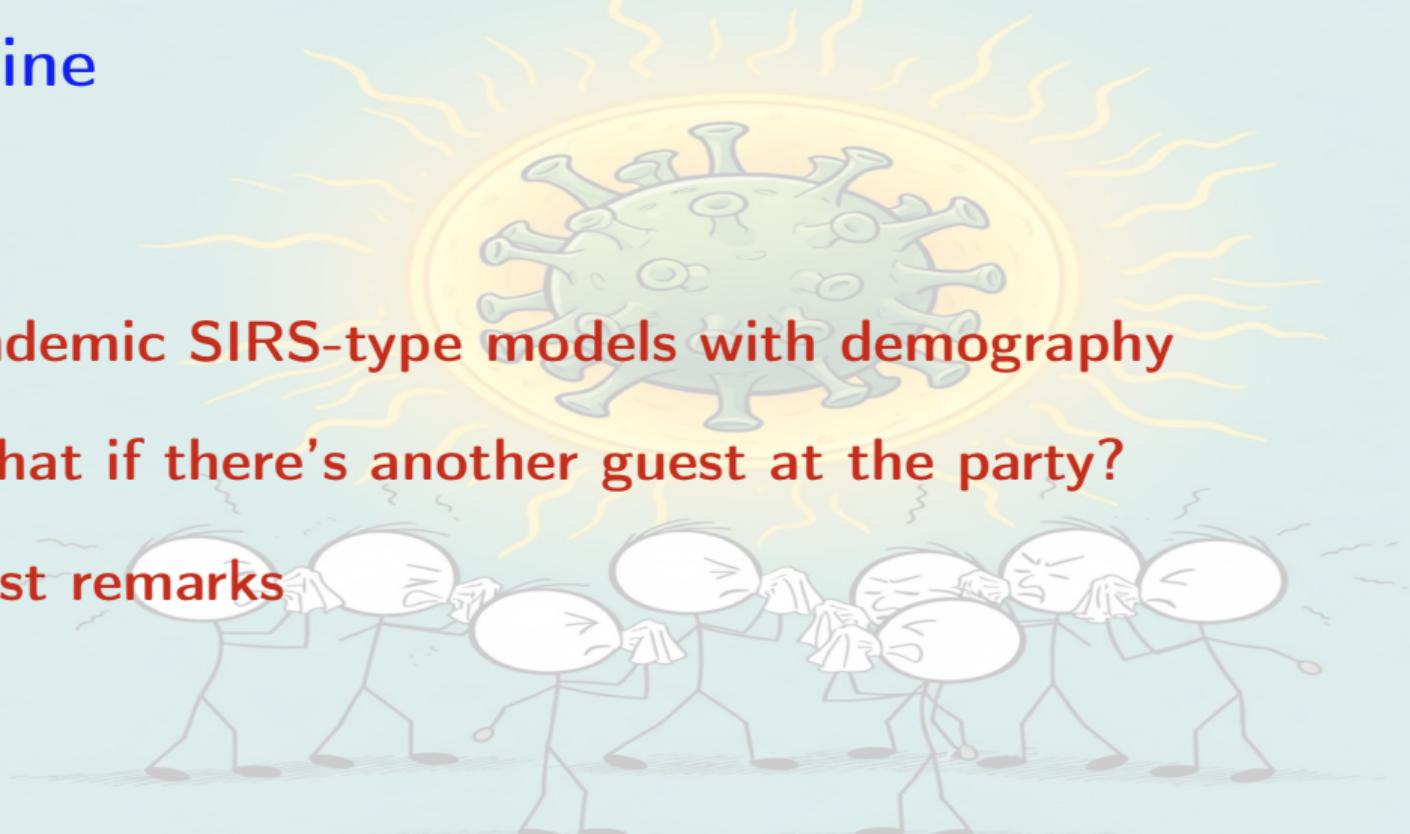
We respect the Treaties that were made on these territories, we acknowledge the harms and mistakes of the past, and we dedicate ourselves to move forward in partnership with Indigenous communities in a spirit of Reconciliation and collaboration.

Outline

Endemic SIRS-type models with demography

What if there's another guest at the party?

Last remarks



Endemic SIRS-type models with demography

What if there's another guest at the party?

Last remarks

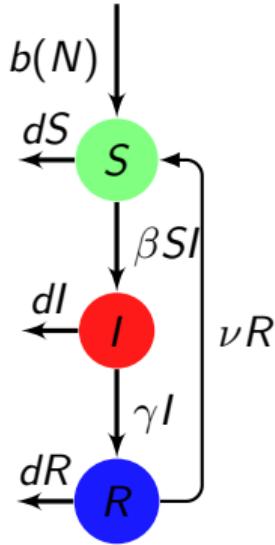
Two potential variations on the Kermack-McKendrick model

- ▶ Add *vital dynamics*, i.e., consider demographic processes
- ▶ Individuals do not die from the disease; after recovering, individuals are *immune* from infection for some time
- ▶ We can of course combine both!

Potential variations



The model



$$S' = b(N) + \nu R - dS - \beta SI \quad (1a)$$

$$I' = \beta SI - (d + \gamma)I \quad (1b)$$

$$R' = \gamma I - (d + \nu)R \quad (1c)$$

Consider the initial value problem consisting in (1) to which we adjoin initial conditions $S(0) = S_0 \geq 0$, $I(0) = I_0 \geq 0$ and $R(0) = R_0 \geq 0$

Typically, we assume $N_0 = S_0 + I_0 + R_0 > 0$ to avoid a trivial case

Birth and death are *relative*

Remark that the notions of *birth* and *death* are relative to the population under consideration

E.g., consider a model for human immunodeficiency virus (HIV) in an at-risk population of intravenous drug users. Then

- ▶ birth is the moment the at-risk behaviour starts
- ▶ death is the moment the at-risk behaviour stops, whether from “real death” or because the individual stops using drugs

Choosing a form for demography

Before we proceed with the analysis proper, we must discuss the nature of the assumptions on demography

To do this, we consider the behaviour of the total population

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

Behaviour of the total population

Summing the equations in (1)

$$N' = b(N) - dN \quad (2)$$

There are three common ways to define $b(N)$ in (2)

1. $b(N) = b$
2. $b(N) = bN$
3. $b(N) = bN - cN^2$

Case 3 leads to logistic dynamics of the total population and is not discussed here

Case of a birth rate constant *per capita*

If $b(N) = bN$, then birth in (2) satisfies $N'/N = b$; we say that birth is **constant per capita**

In this case, (2) takes the form

$$N' = bN - dN = (b - d)N$$

with initial condition $N(0) = N_0$

The solution to this scalar autonomous ODE is easy

$$N(t) = N_0 e^{(b-d)t}, \quad t \geq 0$$

Thus there are 3 possibilities:

- ▶ if $b > d$, $N(t) \rightarrow \infty$, the total population explodes
- ▶ if $b = d$, $N(t) \equiv N_0$, the total population remains constant
- ▶ if $b < d$, $N(t) \rightarrow 0$, the total population collapses

From now on, assume $b(N) = b$

- We want a reasonable case, we could therefore suppose that $b(N) = d$, which would lead to a constant total population
- However, this is a little reductive, so we choose instead $b(N) = b$, which, we will see, works as well even though it can initially be thought of as not being very realistic

The model (for good this time)



$$S' = b + \nu R - dS - \beta SI \quad (3a)$$

$$I' = \beta SI - (d + \gamma)I \quad (3b)$$

$$R' = \gamma I - (d + \nu)R \quad (3c)$$

Consider the initial value problem consisting in (3) to which we adjoin initial conditions $S(0) = S_0 \geq 0$, $I(0) = I_0 \geq 0$ and $R(0) = R_0 \geq 0$

Typically, we assume $N_0 = S_0 + I_0 + R_0 > 0$ to avoid a trivial case

Endemic SIRS-type models with demography

The SIRS model(s)

Mathematical analysis of the SIRS model

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A better vaccination model?

Is the system well-posed?

For an ODE epidemiological model

- ▶ Do solutions to (3) exist and are they unique?
- ▶ Is the positive cone invariant under the flow of (3)?
- ▶ Are solutions to (3) bounded? Some models have unbounded solutions but they are rare and will need to be considered specifically

Solutions exist and are unique

- The vector field is always C^1 , implying that solutions exist and are unique

If we had instead considered an incidence of the form $f(S, I, N) = \beta SI/N$ and, say, demography with $b(N) = bN$, then some discussion might have been needed if $b < d$

Invariance of \mathbb{R}_+^3 under the flow (1)

Let us start by assuming that $I(0) = I_0 = 0$. Then (3b) remains $I' = 0$, meaning that the SR -plane (i.e., the set $\{I = 0\}$) is positively invariant under the flow of (3)

On that plane, (3) reduce to

$$S' = b + \nu R - dS \quad (4a)$$

$$R' = -(d + \nu)R \quad (4b)$$

\implies a solution with $I_0 > 0$ cannot enter the plane $\{I = 0\}$. Indeed, suppose that $I_0 > 0$ but $\exists t_* > 0$ such that $I(t_*) = 0$. Then at $(S(t_*), I(t_*) = 0, R(t_*))$, there are two solutions to (3): the one we just generated as well as the one governed by (4)

This contradicts uniqueness of solutions to (3)

Invariance of \mathbb{R}_+^3 under the flow (2)

We saw that $I(t) > 0$ if $I(0) > 0$

Suppose now that $S = 0$. Equation (3a) is then

$$S' = b + \nu R > 0$$

So if $S(0) = S_0 > 0$, then $S(t) > 0$ for all t . If, on the other hand, $S_0 = 0$, then $S(t) > 0$ for $t > 0$ small; from what we just saw, this is then also true for all $t > 0$

We say the vector field points *inward*

$\implies S$ cannot become zero

Do the same for R

To summarise, for invariance

For simplicity, denote $\mathbb{R}^* = \mathbb{R} \setminus \{0\}$

- If $(S(0), I(0), R(0)) \in \mathbb{R}_+ \times \mathbb{R}_+^* \times \mathbb{R}_+$, then $\forall t > 0$,

$$(S(t), I(t), R(t)) \in (\mathbb{R}_+^*)^3$$

- If $(S(0), I(0), R(0)) \in \mathbb{R}_+ \times \{0\} \times \mathbb{R}_+$, then $\forall t \geq 0$,

$$(S(t), I(t), R(t)) \in \mathbb{R}_+^* \times \{0\} \times \mathbb{R}_+$$

The model is therefore satisfactory in that it does not allow solutions to become negative

Remark – Know your audience

This reasoning has its place in an MSc or PhD manuscript: you need to demonstrate that you know what to do and how to do it

In a research paper, this is not really necessary and actually often superfluous; the statement *it is easy to show that solutions exist uniquely and that the positive orthant is invariant under the flow of the system* is typically sufficient

(However, be sure to cover your bases: don't show the proof in the paper but have it in your notes.. *it is easy to show* can be a dangerous statement if it is not easy...)

The total population is asymptotically constant

Since $b(N) = b$, the total population equation (2) takes the form

$$N' = b - dN$$

This equation has a unique equilibrium $N^* = b/d$ and it is very easy to check that this equilibrium is GAS: this is a scalar autonomous equation, so solutions are monotone; they increase to N^* if $N_0 < N^*$ and decrease to N^* if $N_0 > N^*$

So we can work at the limit N^* where $R = N^* - (S + I)$ and thus drop the equation for R

Boundedness

It follows from what we just saw that the positive cone \mathbb{R}_+^3 is (positively) invariant under the flow of (3)

Since $N(t) \rightarrow N^*$, we deduce that solutions of (3) are bounded

Seeking equilibria

We seek $S = S^*, I = I^*, R = R^*$ such that

$$0 = b + \nu R - dS - \beta SI \quad (5a)$$

$$0 = \beta SI - (d + \gamma)I \quad (5b)$$

$$0 = \gamma I - (d + \nu)R \quad (5c)$$

From (5b), either $I^* = 0$ or $\beta S - (d + \gamma) = 0$, i.e., $S^* = (d + \gamma)/\beta$

When $I^* = 0$, substituting $I^* = 0$ into (5c) implies that $R^* = 0$ and, in turn, substituting $I^* = R^* = 0$ into (5c) gives $S^* = b/d$. This gives the disease-free equilibrium (DFE)

$$\mathbf{E}_0 := (S^*, I^*, R^*) = \left(\frac{b}{d}, 0, 0 \right) \quad (6)$$

We return to $S^* = (d + \gamma)/\beta$ in a while

Classic method for computing \mathcal{R}_0

\mathcal{R}_0 is the surface in parameter space where the DFE loses its LAS

To find \mathcal{R}_0 , we therefore study the LAS of the DFE

In an arbitrary (S, I, R) , the Jacobian matrix of (3) takes the form

$$J_{(S,I,R)} = \begin{pmatrix} -d - \beta I & -\beta S & \nu \\ \beta I & \beta S - (d + \gamma) & 0 \\ 0 & \gamma & -(d + \nu) \end{pmatrix} \quad (7)$$

The LAS of the DFE depends on the sign of the real parts of the eigenvalues of (7) at that equilibrium point, so we evaluate

$$J_{E_0} = \begin{pmatrix} -d & -\beta S^* & \nu \\ 0 & \beta S^* - (d + \gamma) & 0 \\ 0 & \gamma & -(d + \nu) \end{pmatrix} \quad (8)$$

Block upper triangular matrix \implies eigenvalues are $-d < 0$, $-(d + \nu) < 0$ and $\beta S^* - (d + \gamma)$

\implies LAS of the DFE determined by sign of $\beta S^* - (d + \gamma)$

Sign of $\beta S^* - (d + \gamma)$

Recall that at the DFE (6), $S^* = b/d$, so

$$\text{sign}(\beta S^* - (d + \gamma)) = \text{sign}\left(\beta \frac{b}{d} - (d + \gamma)\right)$$

So the DFE is LAS if

$$\beta \frac{b}{d} < d + \gamma \iff \frac{\beta}{d + \gamma} \frac{b}{d} < 1$$

Denote

$$\mathcal{R}_0 = \frac{\beta}{d + \gamma} \frac{b}{d} \tag{9}$$

(We sometimes emphasise that $b/d = N^*$, the total population, and thus write $\mathcal{R}_0 = \beta N^*/(d + \gamma)$)

Seeking equilibria (2)

Now consider the second EP where $S^* = (d + \gamma)/\beta = N^*/\mathcal{R}_0$

Write (5c) as $R^* = \gamma I^*/(d + \nu)$

Since $S^* + I^* + R^* = N^*$, this means that

$$N^* - S^* - I^* = \gamma I^*/(d + \nu)$$

so substituting $S^* = N^*/\mathcal{R}_0$,

$$\left(1 + \frac{\gamma}{d + \nu}\right) I^* = \left(1 - \frac{1}{\mathcal{R}_0}\right) N^*$$

So finally

$$I^* = \left(1 - \frac{1}{\mathcal{R}_0}\right) \frac{d + \nu}{d + \nu + \gamma} N^*$$

The EEP

The **endemic equilibrium** (EEP) of (3) is

$$\begin{aligned} \mathcal{E}_* := (S^*, I^*, R^*) = \\ \left(\frac{1}{\mathcal{R}_0} N^*, \left(1 - \frac{1}{\mathcal{R}_0}\right) \frac{d + \nu}{d + \nu + \gamma} N^*, N^* - (S^* + I^*) \right) \quad (10) \end{aligned}$$

Remark that \mathcal{E}_* is **not biologically relevant** when $\mathcal{R}_0 \leq 1$

Theorem 1

Let the basic reproduction number be

$$\mathcal{R}_0 = \frac{\beta}{d + \gamma} N^* \quad (9)$$

and consider the EP of (3): the DFE

$$\mathbf{E}_0 = \left(\frac{b}{d}, 0, 0 \right) \quad (6)$$

and the EEP

$$\mathbf{E}_* = \left(\frac{1}{\mathcal{R}_0} N^*, \left(1 - \frac{1}{\mathcal{R}_0} \right) \frac{d + \nu}{d + \nu + \gamma} N^*, N^* - (S^* + I^*) \right) \quad (10)$$

- ▶ If $\mathcal{R}_0 < 1$, then \mathbf{E}_0 is LAS and \mathbf{E}_* is not biologically relevant
- ▶ If $\mathcal{R}_0 > 1$, then \mathbf{E}_0 is unstable and \mathbf{E}_* is biologically relevant

As you can probably guess, if $\mathcal{R}_0 > 1$, then E_* is not only biologically relevant but actually also LAS

Recall the Jacobian

$$\begin{aligned} J_{(S,I,R)} &= \begin{pmatrix} -d - \beta I & -\beta S & \nu \\ \beta I & \beta S - (d + \gamma) & 0 \\ 0 & \gamma & -(d + \nu) \end{pmatrix} \\ &= \begin{pmatrix} -\beta I & -\beta S & \nu \\ \beta I & \beta S - \gamma & 0 \\ 0 & \gamma & -\nu \end{pmatrix} - d\mathbb{I} \end{aligned} \tag{7}$$

From this, we get that $-d$ is an eigenvalue of J

- ▶ there is a theorem that tells us that if $\lambda \in \sigma(M)$, then $\lambda + k \in \sigma(M + k\mathbb{I})$
 $(\sigma(M)$ is the spectrum of M , the set of eigenvalues of M)
- ▶ the first matrix on the second line has all column sums zero so has a zero eigenvalue

We could continue and after some blood, sweat and tears, get that J_{E_*} has its eigenvalues with negative real parts when E_* is biologically relevant, i.e., when $\mathcal{R}_0 > 1$

With even more blood, sweat and tears, we can actually show that the result is *global*

We express that on the next slide

Theorem 2

Let the basic reproduction number be defined by (9) and consider the DFE (6) and the EEP (10)

- ▶ If $\mathcal{R}_0 < 1$, then E_0 is globally asymptotically stable (GAS) and E_* is not biologically relevant
- ▶ If $\mathcal{R}_0 > 1$, then E_0 is unstable and E_* is GAS

In other words

- ▶ when $\mathcal{R}_0 < 1$, then all solutions go to the DFE, the disease goes **extinct**
- ▶ when $\mathcal{R}_0 > 1$, then all solutions go to the EEP, the disease becomes **endemic**

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```

library(deSolve)
rhs_SIRS <- function(t, x, p) {
  with(as.list(c(x, p)), {
    dS = b + nu * R - d * S - beta * S * I
    dI = beta * S * I - (d + gamma) * I
    dR = gamma * I - (d + nu) * R
    return(list(c(dS, dI, dR)))
  })
}
# Initial conditions
NO = 1000
IO = 1
RO = 0
IC = c(S = NO-(IO+RO), I = IO, R = RO)
# "Known" parameters
d = 1/(80*365.25)
b = NO * d

```

```
gamma = 1/14
nu = 1/365.25
# Set beta s.t. R_0 = 1.5
R_0 = 1.5
beta = R_0 * (d + gamma) / (N0-I0-R0)
params = list(b = b, d = d, gamma = gamma, beta = beta, nu = nu)
times = seq(0, 500, 1)
# Call the numerical integrator
sol_SIRS <- ode(y = IC, times = times, func = rhs_SIRS,
                  parms = params, method = "ode45")
# Plot the result
plot(sol_SIRS[, "time"], sol_SIRS[, "I"],
      type = "l", lwd = 2,
      xlab = "Time (days)", ylab = "Prevalence")
```



I just did ...

What I advise not to do: illustrate a mathematical result without adding anything to the result itself

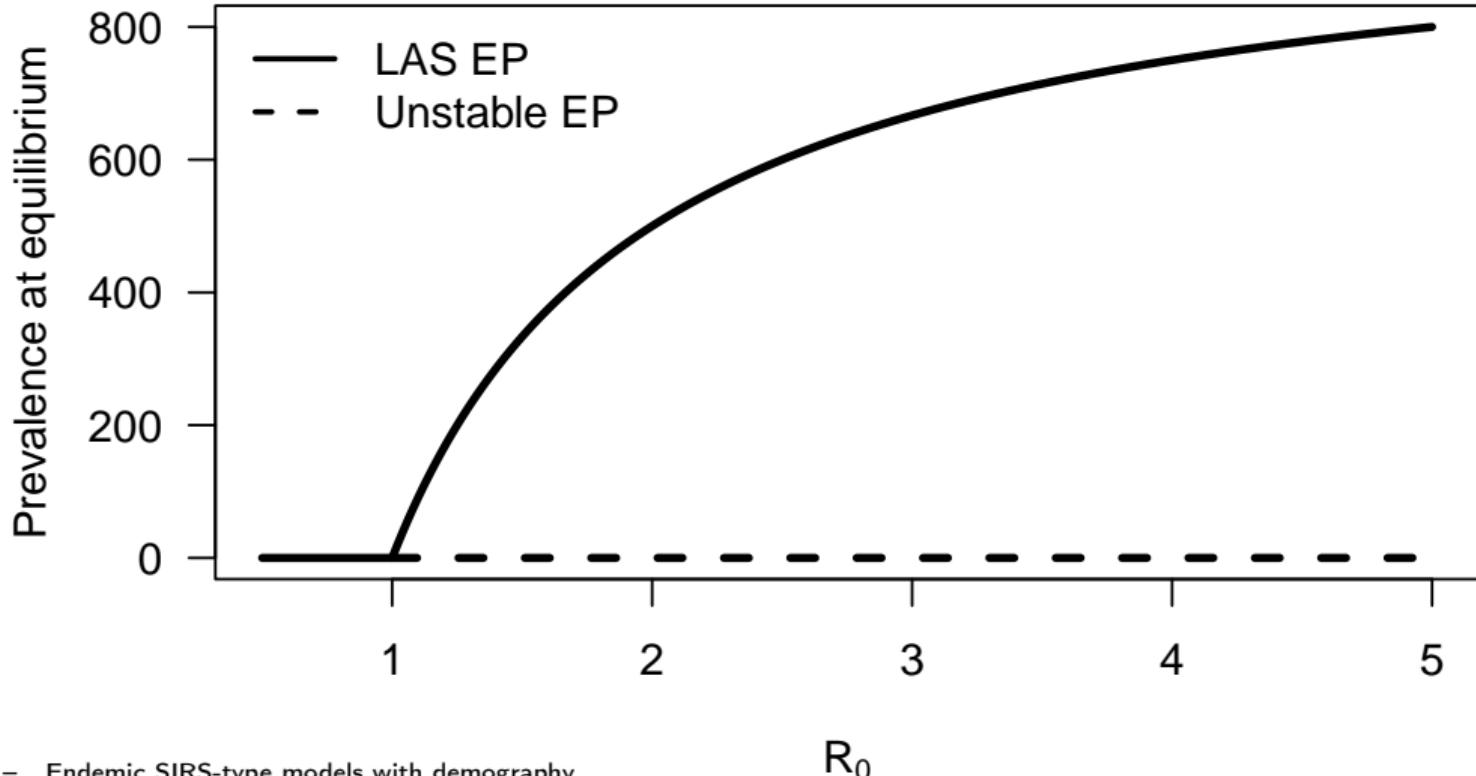
Let us make things a bit better. See the code



We could continue, but with a model this simple, there is little more to do: the 3 parameters of the system are combined within \mathcal{R}_0 and the latter summarises the dynamics well

We are going to show something important: the bifurcation diagram

We saw that when $\mathcal{R}_0 < 1$, $I \rightarrow 0$, whereas when $\mathcal{R}_0 > 1$, $I \rightarrow (1 - 1/\mathcal{R}_0)N$. Let us represent this (code)



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An SIRS model with vaccination

Take SIRS model (3) and assume the following

- ▶ Vaccination takes newborn individuals and moves them directly into the removed compartment, without them becoming infected/infectious
- ▶ A fraction p is vaccinated at birth

The model



$$S' = (1 - p)b + \nu R - dS - \beta SI \quad (11a)$$

$$I' = \beta SI - (d + \gamma)I \quad (11b)$$

$$R' = bp + \gamma I - (d + \nu)R \quad (11c)$$

Consider the initial value problem consisting in (11) to which we adjoin initial conditions $S(0) = S_0 \geq 0$, $I(0) = I_0 \geq 0$ and $R(0) = R_0 \geq 0$

Typically, we assume $N_0 = S_0 + I_0 + R_0 > 0$ to avoid a trivial case

This modification doesn't change much

Equation (2) for the total population is unchanged

The Jacobian (7) at arbitrary point is also unchanged

The DFE is affected, though; as a consequence, so is the reproduction number

The DFE for the SIRS vaccination model

Considering (11) at equilibrium and substituting $I^* = 0$ into this system gives

$$\begin{aligned} 0 &= (1 - p)b + \nu R^* - dS^* \\ 0 &= bp - (d + \nu)R^* \end{aligned}$$

which we rewrite as the linear system

$$\begin{pmatrix} d & -\nu \\ 0 & d + \nu \end{pmatrix} \begin{pmatrix} S^* \\ R^* \end{pmatrix} = \begin{pmatrix} (1 - p)b \\ bp \end{pmatrix}$$

Thus

$$\begin{aligned} \begin{pmatrix} S^* \\ R^* \end{pmatrix} &= \frac{1}{d(d + \nu)} \begin{pmatrix} d + \nu & \nu \\ 0 & d \end{pmatrix} \begin{pmatrix} (1 - p)b \\ pb \end{pmatrix} \\ &= \frac{1}{d(d + \nu)} \begin{pmatrix} (d + \nu)(1 - p)b + pb\nu \\ pbd \end{pmatrix} \end{aligned}$$

As a consequence, the DFE takes the form

$$\mathbf{E}_0^\nu := (S^*, I^*, R^*) = \left(\left(1 - p + \frac{p\nu}{d + \nu} \right) N^*, 0, \frac{pd}{d + \nu} N^* \right) \quad (12)$$

Substituting (12) into the eigenvalue that determines stability of the DFE, $\beta S^* - (d + \gamma)$, we get

$$\begin{aligned} \beta S^* - (d + \gamma) < 0 &\iff \frac{\beta}{d + \gamma} S^* < 1 \\ &\iff \frac{\beta}{d + \gamma} \left(1 - p + \frac{p\nu}{d + \nu} \right) N^* < 1 \end{aligned}$$

So we define

$$\mathcal{R}_0^\nu = \frac{\beta}{d + \gamma} \left(1 - p + \frac{p\nu}{d + \nu} \right) N^* \quad (13)$$

Herd immunity

Therefore

- ▶ $\mathcal{R}_0^v < \mathcal{R}_0$ if $p > 0$
- ▶ To control the disease, \mathcal{R}_v must take a value less than 1, i.e.,

$$\mathcal{R}_v < 1 \iff p > 1 - \frac{1}{\mathcal{R}_0} \quad (14)$$

By vaccinating a fraction $p > 1 - 1/\mathcal{R}_0$ of newborns, we thus are in a situation where the disease is eventually eradicated

This is **herd immunity** (*bis repetita*)

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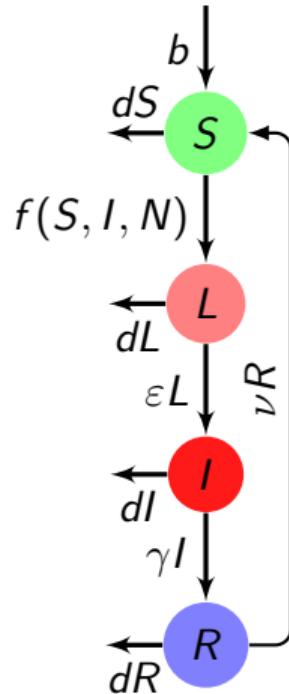
Incubation periods

- ▶ SIS and SIR: progression from S to I is instantaneous
- ▶ Several incubation periods:

| Disease | Incubation period |
|-------------------------------|-------------------|
| Yersinia Pestis | 2-6 days |
| Ebola haemorrhagic fever (HF) | 2-21 days |
| Marburg HF | 5-10 days |
| Lassa fever | 1-3 weeks |
| Tse-tse | weeks–months |
| HIV/AIDS | months–years |

Hypotheses

- ▶ There is demography
- ▶ New individuals are born at a constant rate b
- ▶ There is no vertical transmission: all “newborns” are susceptible
- ▶ The disease is non lethal, it causes no additional mortality
- ▶ New infections occur at the rate $f(S, I, N)$
- ▶ There is a period of incubation for the disease
- ▶ There is a period of time after recovery during which the disease confers immunity to reinfection (immune period)



The model is as follows:

$$S' = b + \nu R - dS - f(S, I, N) \quad (15a)$$

$$L' = f(S, I, N) - (d + \varepsilon)L \quad (15b)$$

$$I' = \varepsilon L - (d + \gamma)I \quad (15c)$$

$$R' = \gamma I - (d + \nu)R \quad (15d)$$

Meaning of the parameters:

- ▶ $1/\varepsilon$ average duration of the incubation period
- ▶ $1/\gamma$ average duration of infectious period
- ▶ $1/\nu$ average duration of immune period

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Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission

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Dedicated to the memory of John Jacquez

The basic reproduction number \mathcal{R}_0

Used frequently in epidemiology (not only math epi)

Definition 3 (\mathcal{R}_0)

The basic reproduction number \mathcal{R}_0 is the average number of secondary cases generated by the introduction of an infectious individual in a wholly susceptible population

- ▶ If $\mathcal{R}_0 < 1$, then on average, each infectious individual infects less than one other person, so the epidemic has chances of dying out
- ▶ If $\mathcal{R}_0 > 1$, then on average, each infectious individual infects more than one other person and the disease can become established in the population (or there will be a major epidemic)

Computation of \mathcal{R}_0

Mathematically, \mathcal{R}_0 is a bifurcation parameter aggregating some of the model parameters and such that the disease free equilibrium (DFE) loses its local asymptotic stability when $\mathcal{R}_0 = 1$ is crossed from left to right

- ▶ As a consequence, \mathcal{R}_0 is found by considering the spectrum of the Jacobian matrix of the system evaluated at the DFE
- ▶ The matrix quickly becomes hard to deal with (size and absence of “pattern”) and the form obtained is not unique, which is annoying when trying to interpret \mathcal{R}_0

Preliminary setup of PvdD & Watmough 2002

$x = (x_1, \dots, x_n)^T$, $x_i \geq 0$, with the first $m < n$ compartments the infected ones

X_s the set of all disease free states:

$$X_s = \{x \geq 0 | x_i = 0, i = 1, \dots, m\}$$

Distinguish new infections from all other changes in population

- ▶ $F_i(x)$ rate of appearance of new infections in compartment i
- ▶ $V_i^+(x)$ rate of transfer of individuals into compartment i by all other means
- ▶ $V_i^-(x)$ rate of transfer of individuals out of compartment i

Assume each function continuously differentiable at least twice in each variable

$$x'_i = f_i(x) = F_i(x) - V_i(x), \quad i = 1, \dots, n$$

where $V_i = V_i^- - V_i^+$

Some assumptions

- **(A1)** If $x \geq 0$, then $F_i, V_i^+, V_i^- \geq 0$ for $i = 1, \dots, n$

Since each function represents a directed transfer of individuals, all are non-negative

- **(A2)** If $x_i = 0$ then $V_i^- = 0$. In particular, if $x \in X_s$, then $V_i^- = 0$ for $i = 1, \dots, m$

If a compartment is empty, there can be no transfer of individuals out of the compartment by death, infection, nor any other means

- (A3) $F_i = 0$ if $i > m$

The incidence of infection for uninfected compartments is zero

- A4 If $x \in X_s$ then $F_i(x) = 0$ and $V_i^+(x) = 0$ for $i = 1, \dots, m$

Assume that if the population is free of disease then the population will remain free of disease; i.e., there is no (density independent) immigration of infectives

One last assumption for the road

Let x_0 be a DFE of the system, i.e., a (locally asymptotically) stable equilibrium solution of the disease free model, i.e., the system restricted to X_s . We need not assume that the model has a unique DFE

Let $Df(x_0)$ be the Jacobian matrix $[\partial f_i / \partial x_j]$. Some derivatives are one sided, since x_0 is on the domain boundary

(A5) If $F(x)$ is set to zero, then all eigenvalues of $Df(x_0)$ have negative real parts

Note: if the method ever fails to work, it is usually with (A5) that lies the problem

Stability of the DFE as function of \mathcal{R}_0

Theorem 4

Suppose the DFE exists. Let then

$$\mathcal{R}_0 = \rho(FV^{-1})$$

with matrices F and V obtained as indicated. Assume conditions (A1) through (A5) hold. Then

- ▶ if $\mathcal{R}_0 < 1$, then the DFE is LAS
- ▶ if $\mathcal{R}_0 > 1$, the DFE is unstable

Important to stress *local* nature of stability that is deduced from this result. We will see later that even when $\mathcal{R}_0 < 1$, there can be several positive equilibria

Direction of the bifurcation at $\mathcal{R}_0 = 1$

μ bifurcation parameter s.t. $\mathcal{R}_0 < 1$ for $\mu < 0$ and $\mathcal{R}_0 > 1$ for $\mu > 0$ and x_0 DFE for all values of μ and consider the system

$$x' = f(x, \mu) \quad (16)$$

Write

$$D_x f(x_0, 0) = D(\mathcal{F}(x_0) - \mathcal{V}(x_0))|_{\mathcal{R}_0=1}$$

as block matrix

$$D\mathcal{F}(x_0) = \begin{pmatrix} F & 0 \\ 0 & 0 \end{pmatrix}, \quad D\mathcal{V}(x_0) = \begin{pmatrix} V & 0 \\ J_3 & J_4 \end{pmatrix}$$

Write $[\alpha_{\ell k}]$, $\ell = m+1, \dots, n$, $k = 1, \dots, m$ the $(\ell - m, k)$ entry of $-J_4^{-1} J_3$ and let v and w be left and right eigenvectors of $D_x f(x_0, 0)$ s.t. $vw = 1$

Let

$$a = \sum_{i,j,k=1}^m v_i w_j w_k \left(\frac{1}{2} \frac{\partial^2 f_i}{\partial x_j \partial x_k}(x_0, 0) + \sum_{\ell=m+1}^n \alpha_{\ell k} \frac{\partial^2 f_i}{\partial x_j \partial x_\ell}(x_0, 0) \right) \quad (17)$$

$$b = v D_{x\mu} f(x_0, 0) w = \sum_{i,j=1}^n v_i w_j \frac{\partial^2 f_i}{\partial x_j \partial \mu}(x_0, 0) \quad (18)$$

Theorem 5

Consider model (16) with $f(x, \mu)$ satisfying conditions (A1)–(A5) and μ as described above

Assume that the zero eigenvalue of $D_x f(x_0, 0)$ is simple

Define a and b by (17) and (18); assume that $b \neq 0$. Then $\exists \delta > 0$ s.t.

- ▶ if $a < 0$, then there are LAS endemic equilibria near x_0 for $0 < \mu < \delta$
- ▶ if $a > 0$, then there are unstable endemic equilibria near x_0 for $-\delta < \mu < 0$

Example of the SLIRS model (15)

Variation of the infected variables in (15) are described by

$$\begin{aligned}L' &= f(S, I, N) - (\varepsilon + d)L \\I' &= \varepsilon L - (d + \gamma)I\end{aligned}$$

Write

$$\mathcal{I}' = \begin{pmatrix} L \\ I \end{pmatrix}' = \begin{pmatrix} f(S, I, N) \\ 0 \end{pmatrix} - \begin{pmatrix} (\varepsilon + d)L \\ (d + \gamma)I - \varepsilon L \end{pmatrix} =: \mathcal{F} - \mathcal{V} \quad (19)$$

Denote

$$f_L^* := \frac{\partial}{\partial L} f \Big|_{(S,I,R)=E_0} \quad f_I^* := \frac{\partial}{\partial I} f \Big|_{(S,I,R)=E_0}$$

the values of the partials of the incidence function at the DFE E_0

Compute the Jacobian matrices of vectors \mathcal{F} and \mathcal{V} at the DFE E_0

$$\mathcal{F} = \begin{pmatrix} f_L^* & f_I^* \\ 0 & 0 \end{pmatrix} \quad \text{and} \quad \mathcal{V} = \begin{pmatrix} \varepsilon + d & 0 \\ -\varepsilon & d + \gamma \end{pmatrix} \quad (20)$$

Thus

$$V^{-1} = \frac{1}{(d + \varepsilon)(d + \gamma)} \begin{pmatrix} d + \gamma & 0 \\ \varepsilon & d + \varepsilon \end{pmatrix}$$

Also, in the case N is constant, $\partial f / \partial L = 0$ and thus

$$FV^{-1} = \frac{{f_I}^*}{(d + \varepsilon)(d + \gamma)} \begin{pmatrix} \varepsilon & d + \varepsilon \\ 0 & 0 \end{pmatrix}$$

As a consequence,

$$\mathcal{R}_0 = \varepsilon \frac{{f_I}^*}{(d + \varepsilon)(d + \gamma)}$$

Theorem 6

Let

$$\mathcal{R}_0 = \frac{\varepsilon f_I^*}{(d + \varepsilon)(d + \gamma)} \quad (21)$$

Then

- ▶ if $\mathcal{R}_0 < 1$, the DFE is LAS
- ▶ if $\mathcal{R}_0 > 1$, the DFE is unstable

It is important here to stress that the result we obtain concerns the **local** asymptotic stability. We see later that even when $\mathcal{R}_0 < 1$, there can be several locally asymptotically stable equilibria

Application

The DFE is

$$(\bar{S}, \bar{L}, \bar{I}, \bar{R}) = (N, 0, 0, 0)$$

- ▶ Mass action incidence (frequency-dependent contacts):

$$f_I^* = \beta \bar{S} \Rightarrow \mathcal{R}_0 = \frac{\epsilon \beta N}{(\epsilon + d)(\gamma + d)}$$

- ▶ Standard incidence (proportion-dependent contacts):

$$f_I^* = \frac{\beta \bar{S}}{N} \Rightarrow \mathcal{R}_0 = \frac{\epsilon \beta}{(\epsilon + d)(\gamma + d)}$$

Links between SLIRS-type models

$$S' = b + \nu R - dS - f(S, I, N)$$

$$L' = f(S, I, N) - (d + \varepsilon)L$$

$$I' = \varepsilon L - (d + \gamma)I$$

$$R' = \gamma I - (d + \nu)R$$

| | |
|------|--|
| SLIR | SLIRS where $\nu = 0$ |
| SLIS | Limit of SLIRS when $\nu \rightarrow \infty$ |
| SLI | SLIR where $\gamma = 0$ |
| SIRS | Limit of SLIRS when $\varepsilon \rightarrow \infty$ |
| SIR | SIRS where $\nu = 0$ |
| SIS | Limit of SIRS when $\nu \rightarrow \infty$ |
| | Limit SLIS when $\varepsilon \rightarrow \infty$ |
| SI | SIS where $\nu = 0$ |

Values of \mathcal{R}_0

$(\bar{S}, \bar{I}, \bar{N})$ values of S, I and N at DFE. Denote $\bar{f}_I = \partial f / \partial I(\bar{S}, \bar{I}, \bar{N})$.

| | |
|-------|---|
| SLIRS | $\frac{\varepsilon \bar{f}_I}{(d+\varepsilon)(d+\gamma)}$ |
| SLIR | $\frac{\varepsilon \bar{f}_I}{(d+\varepsilon)(d+\gamma)}$ |
| SLIS | $\frac{\varepsilon \bar{f}_I}{(d+\varepsilon)(d+\gamma)}$ |
| SLI | $\frac{\varepsilon \bar{f}_I}{(d+\varepsilon)(d+\gamma)}$ |
| SIRS | $\frac{\varepsilon \bar{f}_I}{d+\gamma}$ |
| SIR | $\frac{\bar{f}_I}{d+\gamma}$ |
| SIS | $\frac{\bar{f}_I}{d+\gamma}$ |
| SI | $\frac{\bar{f}_I}{d+\gamma}$ |

Endemic SIRS-type models with demography

The SIRS model(s)

Mathematical analysis of the SIRS model

Some numerics with the SIRS model

Herd immunity in the SIRS model

SLIRS model with constant population

Computing \mathcal{R}_0 more efficiently

A better vaccination model?

GLOBAL RESULTS FOR AN EPIDEMIC MODEL WITH VACCINATION THAT EXHIBITS BACKWARD BIFURCATION*

JULIEN ARINO[†], C. CONNELL MCCLUSKEY[†], AND P. VAN DEN DRIESSCHE[†]

Abstract. Vaccination of both newborns and susceptibles is included in a transmission model for a disease that confers immunity. The interplay of the vaccination strategy together with the vaccine efficacy and waning is studied. In particular, it is shown that a backward bifurcation leading to bistability can occur. Under mild parameter constraints, compound matrices are used to show that each orbit limits to an equilibrium. In the case of bistability, this global result requires a novel approach since there is no compact absorbing set.

Key words. epidemic model, vaccination, backward bifurcation, compound matrices, global dynamics

AMS subject classifications. 92D30, 34D23

DOI. 10.1137/S0036139902413829

SLIRS with vaccination



The usual situation



What can happen with vaccination – Backward bifurcation





Endemic SIRS-type models with demography

What if there's another guest at the party?

Last remarks



What if there's another guest at the party?

Two Ross-Macdonald-type models

A little complexification of Ross-Macdonald

A model for cholera

A model for zoonotic transmission of waterborne disease

See, e.g., Simoy & Aparicio, Ross-Macdonald models: Which one should we use?, *Acta Tropica* (2020)

Ross introduced the model in 1911. Later “tweaked” by Macdonald to include mosquito latency period

Here, I show a version in the paper cited, with some notation changed



Reproduction number

$$\mathcal{R}_0 = \frac{\beta_H \beta_V}{(\gamma_H + \gamma_V) d_V} \frac{V^*}{H^*} \quad (22)$$

where H^* and V^* are the total host and vector populations, respectively



Reproduction number

$$\mathcal{R}_0 = \frac{\beta_H \beta_V}{(\gamma_H + \gamma_V) d_V} \frac{\varepsilon_V}{d_V + \varepsilon_V} \frac{\varepsilon_H}{d_H + \varepsilon_H} \frac{V^*}{H^*} \quad (23)$$

where H^* and V^* are the total host and vector populations, respectively

Here

$$f_X = \frac{\varepsilon_X}{d_X + \varepsilon_X}$$

are the fractions of latent individuals (of type $X = \{V, H\}$) who survive the latency period

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Recall this guy?



Let us add a few arrows



Arino, Ducrot & Zongo, A metapopulation model for malaria with transmission-blocking partial immunity in hosts, Journal of Mathematical Biology (2012)

Incidence functions take the form

$$\Phi_H = b_H(H, V) \sigma_{VH} \frac{I_V}{V}$$

and

$$\Phi_V = b_V(H, V) \left(\sigma_{HV} \frac{I_H}{H} + \hat{\sigma}_{HV} \frac{R_H}{H} \right)$$

where b_H and b_V are numbers per unit time of mosquito bites a human has and the number of humans a mosquito bites, respectively

Parameters of the incidence function

- ▶ σ_{HV} probability of transmission of the parasite (in gametocyte form) from an infectious human to a susceptible mosquito
- ▶ $\hat{\sigma}_{HV}$ probability of transmission of the parasite (in gametocyte form) from a semi-immune human to a susceptible mosquito
- ▶ σ_{VH} probability of transmission of the parasite (in sporozoite form) from an infectious mosquito to a susceptible human

Additional parameter that can be factored in (all per unit time)

- ▶ a_H maximum number of mosquito bites a human can receive
- ▶ a_V number of times one mosquito would “want to” bite humans
- ▶ a average number of bites given to humans by each mosquito

People to read for malaria models (IMOBO)

See also the work of

- ▶ Gideon Ngwa at the University of Buea
- ▶ Nakul Chitnis at the Swiss Tropical and Public Health Institute

Many others...

More complex models may be needed for malaria

Timing of processes is critical in malaria

Plasmodium life cycle in the mosquito is commensurate with mosquito lifetime

Need models that are able to account for that, because ODEs are not really good at this (see beginning of Stochastic systems lecture)

Mathematics becomes more complicated

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Research article

Endemic and epidemic dynamics of cholera: the role of the aquatic reservoir

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Codeço's model



$$S' = d_H(H - S) - \beta \frac{B}{K + B} S \quad (24a)$$

$$I' = \beta \frac{B}{K + B} S - \gamma I \quad (24b)$$

$$B' = (b_B - d_B)B + \zeta I \quad (24c)$$

K concentration of cholera in water giving 50% chance of catching it

Note that the dashed arrow from I to B is not a flow: individuals do not convert into *vibrio cholerae*

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ORIGINAL ARTICLE

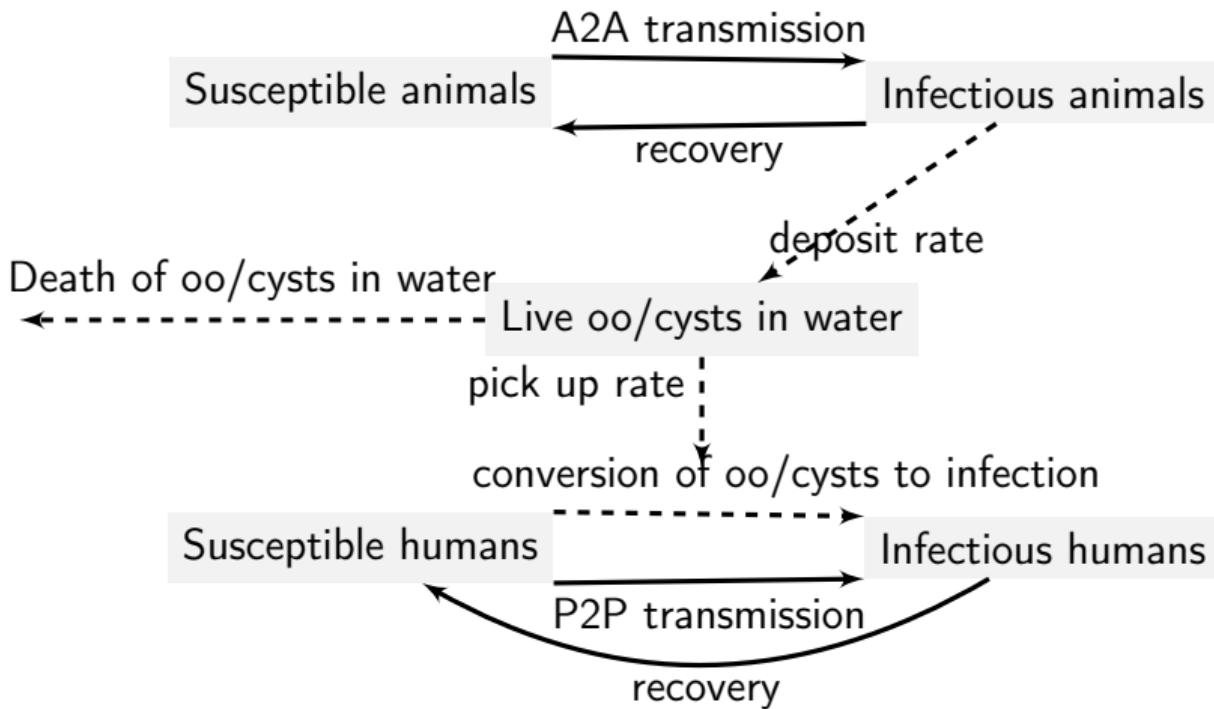
Zoonotic Transmission of Waterborne Disease: A Mathematical Model

Edward K. Waters¹  · Andrew J. Hamilton² ·
Harvinder S. Sidhu³ · Leesa A. Sidhu³ ·
Michelle Dunbar⁴

Zoonotic transmission of waterborne disease

Zoonoses are animal diseases that are transmitted to humans

Model here used for instance to model Giardia transmission from possums to humans





The full model

$$S_A' = -\beta_A S_A I_A + \gamma_A I_A \quad (25a)$$

$$I_A' = \beta_A S_A I_A - \gamma_A I_A \quad (25b)$$

$$W' = \alpha I_A - \eta W(S_H + I_H) - \mu W \quad (25c)$$

$$S_H' = -\rho \eta W S_H - \beta_H S_H I_H + \gamma_H I_H \quad (25d)$$

$$I_H' = \rho \eta W S_H + \beta_H S_H I_H - \gamma_H I_H \quad (25e)$$

Considered with $N_A = S_A + I_A$ and $N_H = S_H + I_H$ constant

Simplified model

Because N_A and N_H are constant, (25) can be simplified:

$$I_A' = \beta_A N_A I_A - \gamma_A I_A - \beta_A I_A^2 \quad (26a)$$

$$W' = \alpha I_A - \eta W N_H - \mu W \quad (26b)$$

$$I_H' = \rho \eta W (N_H - I_H) + \beta_H N_H I_H - \gamma_H I_H - \beta_H I_H^2 \quad (26c)$$

Three EP: DFE $(0, 0, 0)$; endemic disease in humans because of H2H transmission; endemic in both H and A because of W

Three EP: DFE $(0, 0, 0)$; endemic disease in humans because of H2H transmission; endemic in both H and A because of W

Let

$$\mathcal{R}_{0A} = \frac{\beta_A}{\gamma_A} N_A \quad \text{and} \quad \mathcal{R}_{0H} = \frac{\beta_H}{\gamma_H} N_H \quad (27)$$

- ▶ DFE LAS if $\mathcal{R}_{0A} < 1$ and $\mathcal{R}_{0H} < 1$, unstable if $\mathcal{R}_{0A} > 1$ or $\mathcal{R}_{0H} > 1$
- ▶ If $\mathcal{R}_{0H} > 1$ and $\mathcal{R}_{0A} < 1$, (26) goes to EP with endemicity only in humans
- ▶ Endemic EP with both A and H requires $\mathcal{R}_{0A} > 1$ and $\mathcal{R}_{0H} < 1$

Note that proof is **not** global



Endemic SIRS-type models with demography

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Last remarks

CONCLUSIONS

To simplify or not to simplify?

- ▶ In the KMK epidemic model (??) and the SIRS endemic model (3), since the total population is constant or asymptotically constant, it is possible to omit one of the state variables since $N^* = S + I + R$
- ▶ We often use $R = N^* - S - I$
- ▶ This can greatly simplify some computations
- ▶ Whether to do it or not is a matter of preference

To normalise or not to normalise?

- ▶ In the KMK epidemic model (??) and the SIRS endemic model (3), since the total population is constant or asymptotically constant, it is possible to normalise to $N = 1$
- ▶ This can greatly simplify some computations
- ▶ However, I am not a big fan: it is important to always have the “sizes” of objects in mind
- ▶ If you do normalise, at least for a paper destined to mathematical biology, always do a “return to biology”, i.e., interpret your results in a biological light, which often implies to return to original values

Where we are

- ▶ An *epidemic* SIR model (the KMK SIR) in which the presence or absence of an epidemic wave is characterised by the value of \mathcal{R}_0
- ▶ The KMK SIR has explicit solutions (in some sense). **This is an exception!**
- ▶ An *endemic* SIRS model in which the threshold $\mathcal{R}_0 = 1$ is such that, when $\mathcal{R}_0 < 1$, the disease goes extinct, whereas when $\mathcal{R}_0 > 1$, the disease becomes established in the population
- ▶ Some simple variations on these models
- ▶ A few models for vector-borne or water-borne diseases

Can I have this wrapped up to go?

To finish, we use the command `purl` to generate an R file (`course-01-introduction-math-epi.R`) in the CODE directory with all the code chunks in this Rnw file

```
# From https://stackoverflow.com/questions/36868287/purl-within-knit-duplicate
rmd_chunks_to_r_temp <- function(file){
  callr::r(function(file, temp){
    out_file = sprintf("../CODE/%s", gsub(".Rnw", ".R", file))
    knitr::purl(file, output = out_file, documentation = 1)
  }, args = list(file))
}
rmd_chunks_to_r_temp("L08-PvdD-Watmough.Rnw")
## [1] "../CODE/L08-PvdD-Watmough.R"
```

Bibliography I