ASSIGNMENT 3

JASON THOMAS

Note: the code for Q4 is on last page

A simple SI model for chlamydia bacteria infection in Australian koala populations is,

intrinsic rate of increase

μ – additional mortality due to infection

$$\frac{dS_f}{dt} = r(S_f + \alpha I_f) - rNS_f - \beta_{fm}\frac{S_f I_m}{N}$$
$$\frac{dI_f}{dt} = \beta_{fm}\frac{S_f I_m}{N} - rNI_f - \mu I_f$$
$$\frac{dS_m}{dt} = r(S_f + \alpha I_f) - rNS_m - \beta_{mf}\frac{S_m I_f}{N}$$
$$\frac{dI_m}{dt} = \beta_{mf}\frac{S_m I_f}{N} - rNI_m - \mu I_m$$

$0 < \alpha \leq 1$

(the impact of chlamydia infection on female koalas

where male and female koalas are indicated by subscripts m and f, and where

$$N = S_f + I_f + S_m + I_m\,,$$

is the total number of koalas per square kilometre. At the disease-free equilibrium we have $N = 1$ and we assume that the sex-ratio is 1:1 such that $S_m = S_f = \frac{1}{2}$.

Q1: ① If we make the assumption that the disease is transmitted only via female-male intercourse, then a multihost system is necessary to account for inability for female-female, and male-male transmission to occur.

② A multihost disease model will help represent biological reality, since chlamydia affects the ability of female koalas to have offspring

③ A multihost disease system has the added benefit that modellers can use a next-generation-matrix, which is sometimes preferable to a system of DEs when there is little data available.

④ The above-mentioned NGM can be used to derive a system of DEs, and vice-versa. This allows researchers to check their results (by deriving the system of DEs by another method, this increases confidence).

⑤ From the NGM, we can determine the Typer Reproduction Number, and this is useful as:

a) a measure of the required control effort $\nu_c = 1 - \frac{1}{T_1}$

b) a confirmation that R_0 is correct, since

$$T_1 < 1 \Rightarrow R_0 < 1, \quad T_1 > 1 \Rightarrow R_0 > 1$$

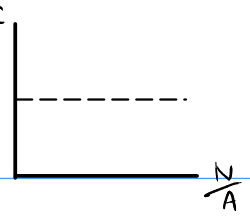
Q2. We require $K = \begin{bmatrix} 0 & k_{mf} \\ k_{fm} & 0 \end{bmatrix}$ $k_{ij} = P_r(\text{koala } j \text{ survives incubation}) \cdot$ contact rate $\cdot$ infectious period $\cdot$ $P_r(\text{transmission} \mid \text{contact})$

let:

$1/\sigma$ be the (average) incubation period

$1/\mu_j$ be the (average) lifespan of koala type j

c_{ij} is the contact rate between sexes i and j

- frequency dependent transmission implies 

so $c = \frac{N}{A}$

- in $\frac{dI_f}{dt}$, $rNI_f - \mu I_f = (rN - \mu)I_f$ (and similar for I_m)

this looks similar to γI, and if I is exp. distributed then $\frac{1}{\gamma}$ is the average inf. period. So, $\frac{1}{rN-\mu}$ is the average infectious period

- Without a separate E compartment, probability of surviving incubation is assumed to be 1.

so $k_{ij} = 1 \cdot c_{ij} \cdot v \cdot$ inf. period

$= \beta_{ij} \cdot \frac{1}{rN-\mu}$

$= \frac{\beta_{ij}}{rN-\mu}$

and

$$K = \begin{bmatrix} 0 & \frac{\beta_{12}}{rN^*+\mu} \\ \frac{\beta_{21}}{rN^*+\mu} & 0 \end{bmatrix}$$

R_0 is equal to the dominant eigenvalue of K

A matrix has eigenvalues $\lambda \iff \det(A - \lambda I) = 0$

$$\det\left(\begin{bmatrix} -\lambda & \frac{\beta_{mf}}{rN-\mu} \\ \frac{\beta_{fm}}{rN-\mu} & -\lambda \end{bmatrix}\right) = 0 \qquad (-\lambda)^2 - \beta_{mf} \cdot \beta_{fm} \cdot \left(\frac{1}{rN-\mu}\right)^2 = 0$$

$$\lambda = \pm \sqrt{\beta_{mf} \cdot \beta_{fm} \left(\frac{1}{rN-\mu}\right)^2}$$

$$\lambda = R_0 = \frac{\sqrt{\beta_{mf} \cdot \beta_{fm}}}{rN - \mu}$$

Q3 let $f=2$, $m=1$

The infectious subsystem is:

$$\frac{dI_1}{dt} = \beta_{12}^* \frac{S_1^* I_2^*}{N^*} - rN^* I_1^* - \mu I_1^*$$

$$\frac{dI_2}{dt} = \beta_{21}^* \frac{S_2 I_1}{N^*} - rN^* I_2 - \mu I_2^*$$

Now linearise at the DFE, where $S \simeq N$

$$\frac{dI_1}{dt} = \beta_{12}^* I_2^* - rN^* I_1^* - \mu I_1^* \quad \text{in } T \text{ in } \Sigma$$

$$\frac{dI_2}{dt} = \beta_{21}^* I_1^* - rN^* I_2^* - \mu I_2^*$$

So $T = \begin{bmatrix} 0 & \beta_{12} \\ \beta_{21} & 0 \end{bmatrix}$, $\Sigma = \begin{bmatrix} -rN^* - \mu & 0 \\ 0 & -rN^* - \mu \end{bmatrix}$, $\underset{\sim}{x} = \begin{bmatrix} I_1^* \\ I_2^* \end{bmatrix}$

$$\Sigma^{-1} = \frac{1}{\det(\Sigma)} = \frac{1}{(-rN^* - \mu)^2} \begin{bmatrix} rN^* + \mu & 0 \\ 0 & rN^* + \mu \end{bmatrix}$$

$$= \begin{bmatrix} \frac{-1}{rN^* + \mu} & \frac{1}{(-rN^* - r)^2} \\ \frac{1}{(-rN^* - r)^2} & \frac{-1}{rN^* + \mu} \end{bmatrix}$$

$$-T = \begin{bmatrix} 0 & -\beta_{12} \\ -\beta_{21} & 0 \end{bmatrix}$$

$$K_L = -T\Sigma^{-1} = \begin{bmatrix} 0 & -\beta_{12} \\ -\beta_{21} & 0 \end{bmatrix} \begin{bmatrix} \frac{-1}{rN^* + \mu} & \frac{1}{(-rN^* - r)^2} \\ \frac{1}{(-rN^* - r)^2} & \frac{-1}{rN^* + \mu} \end{bmatrix} = \begin{bmatrix} \frac{-\beta_{12}}{(-rN^* - r)^2} & \frac{\beta_{12}}{rN^* + \mu} \\ \frac{\beta_{21}}{rN^* + \mu} & \frac{-\beta_{12}}{(-rN^* - r)^2} \end{bmatrix}$$

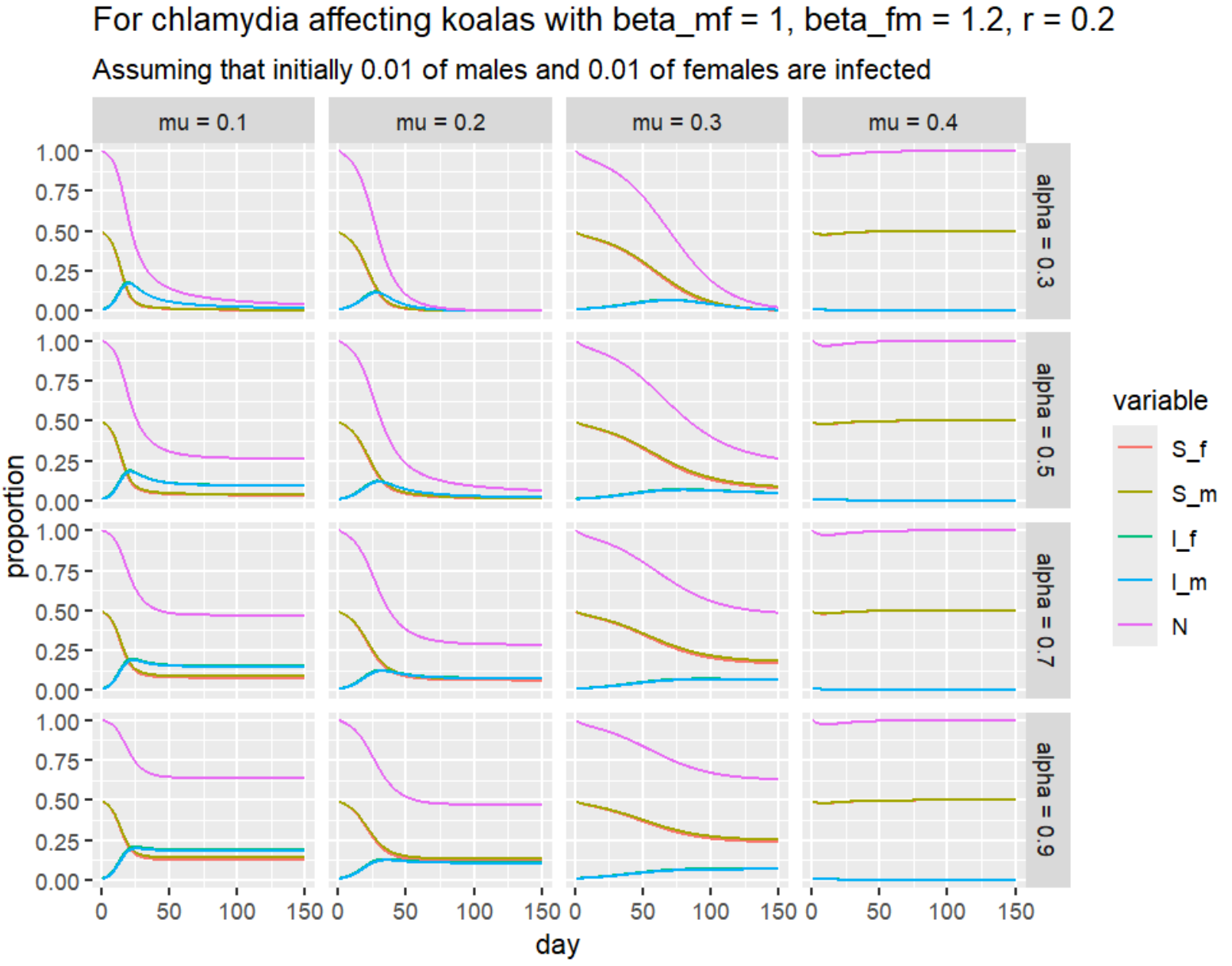
$$K = E^T K_L E \qquad E = \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}$$

Since E here is just the 2×2 identity then $K = K_L$. The result K is almost the same as the NGM by epidemiological reasoning, but not quite.

Since the diagonal of K doesn't reflect biological reality (given the assumption of transmission via male-female intercourse) then those terms are without meaning.

So, the result is the same as making the NGM via epidemiological reasoning.

Q4 This faceted chart shows how the system behaves given different values of α, μ



Observations:

- α represents female effectiveness in reproduction. A lower α means that the disease affects reproductive potential adversly. Higher values means the population can withstand the virus, as seen in the chart above.
- α behaves somewhat like a dampening component, if μ is somewhat like a forcing component.

μ represents additional mortality due to infection

The effect on this system peaks at about $\mu = 0.2$. The interpretation is that if μ gets larger, then koalas die before they can infect others.
If $\mu = 0.1$, then the drop in population is sharper than at 0.3. That's because fewer deaths leads to infectious koalas infecting more koalas, rather than dying

Based on the chart, it seems these combinations:

α	μ
0.3	0.1
0.3	0.2
0.3	0.3
0.5	0.2

lead to extinction

Conclusion

We can expect $\alpha \leq 0.3$, $\mu \simeq 0.2$ to lead to extinction