MST 383/683
Homework #5

Due Date: October 29 2021

1. Malaria is a disease that can be transmitted to humans by mosquitoes and is also transmitted to mosquitoes by humans. A percentage of pregnant women who are infected with malaria give birth to malaria-infected newborns. The dynamics of the disease can be modeled as follows:

$$\begin{aligned}
\dot{S}_m &= \mu_m(I_m + S_m) - \beta_m S_m I - \mu_m S_m, \\
\dot{I}_m &= \beta_m S_m I - \mu_m I_m, \\
\dot{S} &= \mu(S + \sigma I + R) - \beta S I_m - \mu S + \gamma R, \\
\dot{I} &= (1-\sigma)\mu I + \beta S I_m - (\mu + \alpha) I, \\
\dot{R} &= \alpha I - (\mu + \gamma) R,
\end{aligned}$$

where all parameters are greater than 0 and new type of parameter σ is the fraction of newborns that are healthy.

   (a) Interpret each variable and parameter in practical terms.

   (b) Draw a flowchart of this model.

   (c) Show that this system has two quantities that are conserved in time and use this information to reduce the system to three differential equations in S_m, S, and I.

   (d) Determine the disease free equilibrium for this reduced system.

   (e) Use the Jacobian approach to compute the basic reproduction number.

   (f) Use the next-generation approach to compute the basic reproduction number.

2. pg. 119, #5.2 part (a) only.

3. pg. 119, #5.3 part (a) and (b) only.

4. pg. 199, #5.4 part (a) and (b) only.

5. pg. 120, #5.5 part (a) and (c) only.

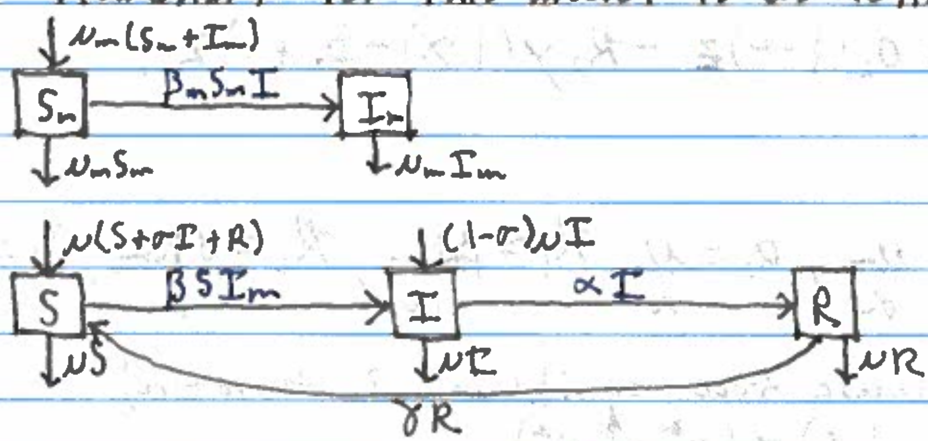
Homework #5

#1

Consider the following model for malaria:

$$\dot{S}_m = \nu_m(S_m + I_m) - \beta_m S_m I - \nu_m S_m$$
$$\dot{I}_m = \beta_m S_m I - \nu_m I_m$$
$$\dot{S} = \nu(S + \sigma I + R) - \beta S I_m - \nu S + \gamma R$$
$$\dot{I} = (1-\sigma)\nu I + \beta S I_m - (\nu + \alpha) I$$
$$\dot{R} = \alpha I - (\nu + \gamma) R.$$

The flowchart for this model is as follows



Clearly, $S_m + I_m$ and $S + I + R$ are conserved and therefore the relevant equations are:

$$\dot{S}_m = \nu_m N_m - \beta_m S_m I - \nu_m S_m$$
$$\dot{S} = \nu(N - (1-\sigma) I) - \beta S(N_m - S_m) - \nu S + \gamma(N - S - I)$$
$$\dot{I} = (1-\sigma)\nu I + \beta S (N_m - S_m) - (\nu + \alpha) I.$$

If we let $x = S_m/N_m$, $y = S/N$, $z = I/N$ and $\tau = \alpha t$ it follows that

$$\frac{dx}{d\tau} = \frac{\nu_m}{\alpha} - \frac{\beta_m N}{\alpha} xz - \frac{\nu_m}{\alpha} x$$

$$\frac{dy}{d\tau} = \frac{\nu}{\alpha}(1-(1-\sigma)z) - \frac{\beta N_m}{\alpha} y(1-x) - \frac{\nu}{\alpha} y + \frac{\gamma}{\alpha}(1-x-y)$$

$$\frac{dz}{d\tau} = \frac{(1-\sigma)\nu}{\alpha} z + \frac{\beta N_m}{\alpha} y(1-x) - \left(\frac{\nu}{\alpha}+1\right) z$$

$$\Rightarrow \frac{dx}{d\tau} = a_1 - R_1 xz - a_1 x,$$

$$\frac{dy}{d\tau} = a_2(1-(1-\sigma)z) - R_2 y(1-x) - a_2 y + b(1-x-y),$$

$$\frac{dz}{d\tau} = a_2(1-\sigma)z + R_2 y(1-x) - (a_2+1)z,$$

where

$$a_1 = \frac{\nu_m}{\alpha}, \quad a_2 = \frac{\nu}{\alpha}, \quad R_1 = \frac{\beta N}{\alpha}, \quad R_2 = \frac{\beta N_m}{\alpha}, \quad b = \frac{\gamma}{\alpha}.$$

The disease free equilibrium is therefore;

$$(1,1,0) = (x^*, y^*, z^*).$$

The Jacobian is given by:

$$J = \begin{bmatrix} -R_1 z - a_1 & 0 & -R_1 x \\ R_2 y - b & -R_2(1-x) - b & -a_2(1-\sigma) \\ -R_2 y & R_2(1-x) & -a_2\sigma - 1 \end{bmatrix}$$

$$\Rightarrow J(1,1,0) = \begin{bmatrix} -a_1 & 0 & -R_1 \\ R_2 - b & -b & -a_2(1-\sigma) \\ -R_2 & 0 & -a_2\sigma - 1 \end{bmatrix}$$

#2.

The SEIR model with an asymptomatic stage is given by:

$$\dot{S} = \Lambda - \beta S(I+qA) - \nu S$$
$$\dot{E} = \beta S(I+qA) - (\eta+\nu)E$$
$$\dot{I} = p\eta E - (\alpha+\nu)I$$
$$\dot{A} = (1-p)\eta E - (\gamma+\nu)A$$
$$\dot{R} = \alpha I + \gamma A - \nu R.$$

The disease free equilibrium is given by

$$(S^*, E^*, I^*, A^*, R^*) = (\Lambda/\nu, 0, 0, 0, 0).$$

The infected compartments are E, I, A and have a coorespponding Jacobian:

$$\bar{J} = \begin{bmatrix} -(\eta+\nu) & \beta S & q\beta S \\ p\eta & -(\alpha+\nu) & 0 \\ (1-p)\eta & 0 & -(\gamma+\nu) \end{bmatrix}$$

$$\Rightarrow \bar{J}(\Lambda/\nu, 0, 0, 0, 0) = \begin{bmatrix} 0 & \beta \Lambda/\nu & q\beta \Lambda/\nu \\ p\eta & 0 & 0 \\ (1-p)\eta & 0 & 0 \end{bmatrix} - \begin{bmatrix} \eta+\nu & 0 & 0 \\ 0 & \alpha+\nu & 0 \\ 0 & 0 & \gamma+\nu \end{bmatrix}$$

$$= F - V.$$

Therefore,

$$FV^{-1} = \begin{bmatrix} 0 & \beta \Lambda/\nu(\alpha+\nu) & q\beta \Lambda/\nu(\gamma+\nu) \\ p\eta(\eta+\nu) & 0 & 0 \\ (1-p)\eta(\eta+\nu) & 0 & 0 \end{bmatrix}$$

The characteristic polynomial is given by

$$p(\lambda) = \det(FV^{-1} - \lambda I)$$

$$= \det\left(\begin{bmatrix} -\lambda & \beta \frac{\Lambda}{\nu}(\alpha+\nu) & q\beta\frac{\Lambda}{\nu}(\gamma+\nu) \\ p\eta(\eta+\nu) & -\lambda & 0 \\ (1-p)\eta(\eta+\nu) & 0 & -\lambda \end{bmatrix}\right)$$

$$= -\lambda^3 - \beta\frac{\Lambda}{\nu}(\alpha+\nu)(-\lambda p\eta(\eta+\nu))$$

$$+ q\beta\frac{\Lambda}{\nu}(\gamma+\nu)(+\lambda(1-p)\eta(\eta+\nu)$$

Therefore $p(\lambda)=0$ implies $\lambda=0$ or

$$\lambda^2 - \beta\frac{\Lambda}{\nu}(\alpha+\nu)p\eta(\eta+\nu) - q\beta\frac{\Lambda}{\nu}(\gamma+\nu)((1-p)\eta(\eta+\nu))$$

$$\Rightarrow \lambda^2 = \beta\frac{\Lambda}{\nu}(\eta+\nu)(p(\alpha+\nu) + q(\gamma+\nu)(1-p)\eta)$$

Which implies the next generation R_0 is given by:

$$\boxed{R_0 = \beta\frac{\Lambda}{\nu}(\eta+\nu)(p(\alpha+\nu)+q(\gamma+\nu)(1-p)\eta)}$$

$\blacksquare$

#3.

The SCIR model is given by

$$\dot{S} = \Delta - \beta S(I+qC) - \nu S + \xi R$$
$$\dot{C} = \beta S(I+qC) - (\eta+\gamma+\nu)C$$
$$\dot{I} = \eta C - (\alpha+\nu)I$$
$$\dot{R} = \alpha I + \gamma C - (\nu+\xi)R.$$

The disease free equilibrium is given by

$$(S^*, C^*, I^*, R^*) = (\Delta/\nu, 0, 0, 0).$$

The Jacobian evaluated at the disease free equilibrium is therefore

$$J^* = \begin{bmatrix} -\nu & -\beta\frac{\Delta}{\nu}q & -\beta\Delta/\nu & \xi \\ 0 & \beta\frac{\Delta}{\nu}q-(\eta+\gamma+\nu) & \beta\Delta/\nu & 0 \\ 0 & \eta & -(\alpha+\nu) & 0 \\ 0 & \gamma & \alpha & -(\nu+\xi) \end{bmatrix}$$

Two of the eigenvalues are given by $-\nu, -(\nu+\xi)$.

The other two are eigenvalues of:

$$\tilde{J}^* = \begin{bmatrix} \beta\frac{\Delta}{\nu}q-(\eta+\gamma+\nu) & \beta\Delta/\nu \\ \eta & -(\alpha+\nu) \end{bmatrix}$$

To ensure stability we need

$$\frac{\beta\Delta}{\nu} < \frac{\eta+\gamma+\alpha+2\nu}{q}$$

and

$$-\left(\frac{\beta\Delta}{\nu}q-(\eta+\gamma+\nu)\right)(\alpha+\nu) - \frac{\beta\Delta}{\nu}\eta > 0$$

$$\Rightarrow \frac{\beta\Delta}{\nu}\eta < \left((\eta+\gamma+\nu) - \frac{\beta\Delta}{\nu}q\right)(\alpha+\nu)$$

The next generation approach yields

$$\dot{C} = \beta S(I + qC) - (\eta + \gamma + \nu)C$$
$$\dot{I} = \eta C - (\alpha + \nu)I$$

as the infected compartment with corresponding Jacobian at the disease free state

$$\bar{J} = \begin{bmatrix} \beta \Lambda/\nu \, q - (\eta + \gamma + \nu) & \beta \Lambda/\nu \\ \eta & -(\alpha + \nu) \end{bmatrix}$$

$$= \begin{bmatrix} \beta \Lambda/\nu \, q & \beta \Lambda/\nu \\ \eta & 0 \end{bmatrix} - \begin{bmatrix} \eta + \gamma + \nu & 0 \\ 0 & \alpha + \nu \end{bmatrix}$$

$$= \qquad F \qquad - \qquad V.$$

Therefore,

$$F \cdot V^{-1} = \begin{bmatrix} \beta \Lambda q / \nu(\eta + \gamma + \nu) & \beta \Lambda / \nu(\alpha + \nu) \\ \eta / \eta + \gamma + \nu & 0 \end{bmatrix}$$

The largest eigenvalue is therefore

$$\frac{\dfrac{\beta \Lambda q}{\nu(\eta + \gamma + \nu)} + \sqrt{\left(\dfrac{\beta \Lambda q}{\nu(\eta + \gamma + \nu)}\right)^2 + \dfrac{4 \beta \Lambda \eta}{\nu(\eta + \gamma + \nu)(\alpha + \nu)}}}{2}$$

which yields the R_0 for the next generation approach. ∎

Expanding along the middle column it is clear that $-b$ is an eigenvalue. The remaining eigenvalues are eigenvalues of the following matrix:

$$\begin{bmatrix} -a_1 & -R_1 \\ -R_2 & -a_2\sigma - 1 \end{bmatrix} = \bar{J}$$

The trace is negative so for stability we need only ensure the determinant is positive.

$$\det(\bar{J}) = a_1(a_2\sigma + 1) - R_1 R_2 > 0$$

$$\Rightarrow R_0 = \frac{R_1 R_2}{a_1(a_2\sigma + 1)} < 1.$$

Therefore

$$R_0 = \frac{\beta_m \beta N N_m}{\alpha^2 \frac{\nu_m}{\alpha}\left(\frac{\nu}{\alpha}\sigma + 1\right)}$$

$$\Rightarrow \boxed{R_0 = \frac{\beta_m \beta N N_m}{\nu_m \nu(\sigma + \alpha/\nu)}}$$

Now, if we use the next generation approach for the original system the infected compartments are given by:

$$\dot{I}_m = \beta_m S_m I - \nu_m I_m$$

$$\dot{I} = (1-\sigma)\nu I + \beta S I_m - (\nu + \alpha) I.$$

The Jacobian with respect to the infected compartments is given by:

$$\bar{\bar{J}} = \begin{bmatrix} -\nu_m & \beta_m S_m \\ \beta S & (1-\sigma)\nu - (\nu+\alpha) \end{bmatrix}$$

Evaluating at $(N_m, N, 0)$ we obtain the splitting

$$\tilde{J}(N_m, N, 0) = \underbrace{\begin{bmatrix} 0 & \beta_m N_m \\ \beta N & 0 \end{bmatrix}}_{F} - \underbrace{\begin{bmatrix} \nu_m & 0 \\ 0 & (1+\sigma)\nu+\alpha \end{bmatrix}}_{V}.$$

Therefore,

$$FV^{-1} = \begin{bmatrix} 0 & \beta_m N_m / ((1+\sigma)\nu+\alpha) \\ \beta N / \nu_m & 0 \end{bmatrix}$$

which has a spectral radius of

$$\left(\frac{\beta_m \beta N \cdot N_m}{\nu_m((1+\sigma)\nu+\alpha)}\right)^{1/2} = \left(\frac{\beta_m \beta N \cdot N_m}{\nu_m \cdot \nu((1+\sigma)+\alpha/\nu)}\right)^{1/2}$$

This is not exactly the same as what was computed before so there is probably a mistake.

#5.4

The SIQR model is given by

$$\dot{S} = \Lambda - \frac{\beta S I}{S+I+R} - \nu S$$

$$\dot{I} = \frac{\beta S I}{S+I+R} - (\alpha+\gamma+\nu) I$$

$$\dot{Q} = \gamma I - (\eta+\nu) Q$$

$$\dot{R} = \alpha I + \eta Q - \nu R$$

The disease free equilibrium is given by $(\Lambda/\nu, 0, 0, 0)$.
The Jacobian evaluated at this point is given by:

$$\bar{J} = \begin{bmatrix} -\Lambda & -\beta & 0 & 0 \\ 0 & \beta-(\alpha+\gamma+\nu) & 0 & 0 \\ 0 & \gamma & -(\eta+\nu) & 0 \\ 0 & \alpha & \eta & -\nu \end{bmatrix}$$

The eigenvalues are therefore

$$\lambda_i = -\Lambda,\ \beta-(\alpha+\gamma+\nu),\ -(\eta+\nu),\ -\nu.$$

Consequently,

$$\mathcal{R}_0 = \frac{\beta}{\alpha+\gamma+\nu}.$$

The effect of the quarantining parameter γ is that larger values of γ lowers the value of $\mathcal{R}_0$.

If we now look at the basic reproduction number we have that the infected compartments are:

$$\dot{I} = \frac{\beta S I}{S+I+R} - (\alpha+\gamma+\nu)I$$

$$\dot{Q} = \gamma I - (\eta+\nu)Q$$

The Jacobian with respect to the infected compartments evaluated at the disease free equilibrium is given by:

$$\tilde{J} = \begin{bmatrix} \beta-(\alpha+\gamma+\nu) & 0 \\ \gamma & -(\eta+\nu) \end{bmatrix}$$

which has the splitting

$$\tilde{J} = F - V = \begin{bmatrix} \beta & 0 \\ \gamma & 0 \end{bmatrix} - \begin{bmatrix} \alpha+\gamma+\nu & 0 \\ 0 & \eta+\nu \end{bmatrix}$$

$$\Rightarrow F\cdot V^{-1} = \begin{bmatrix} \beta/\alpha+\gamma+\nu & 0 \\ \gamma/\alpha+\gamma+\nu & 0 \end{bmatrix}$$

which has the largest eigenvalue

$$\mathcal{R}_0 = \frac{\beta}{\alpha+\gamma+\nu}$$

#5.5

A two strain model for is given by:

$$\dot{S}_w = \Delta_w - \beta_{11} S_w I_w - \beta_{12} S_w I_d - \mu_w S_w$$
$$\dot{I}_w = \beta_{11} S_w I_w + \beta_{12} S_w I_d - (\mu_w + \alpha_w) I_w$$
$$\dot{S}_d = \Delta_d - \beta_{21} S_d I_w - \beta_{22} S_d I_d - \mu_d S_d$$
$$\dot{I}_d = \beta_{21} S_d I_w + \beta_{22} S_d I_d - (\mu_d + \alpha_d) I_d.$$

The disease free equilibrium is given by:

$$(\Delta_w/\mu_w, 0, \Delta_d/\mu_d, 0).$$

The Jacobian evaluated at this point is given by:

$$\bar{J} = \begin{bmatrix} -\Delta_w & -\beta_{11}\Delta_w/\mu_w & 0 & -\beta_{12}\Delta_w/\mu_w \\ 0 & \beta_{11}\Delta_w/\mu_w - \mu_w - \alpha_w & 0 & \beta_{12}\Delta_w/\mu_w \\ 0 & -\beta_{21}\Delta_d/\mu_d & -\Delta_d & -\beta_{22}\Delta_d/\mu_d \\ 0 & \beta_{21}\Delta_d/\mu_d & 0 & \beta_{22}\Delta_d/\mu_d - (\mu_d + \alpha_d) \end{bmatrix}$$

Expanding $\det(\bar{J} - \lambda I)$ we have that

$$\det(\bar{J} - \lambda I) = (-\Delta_w - \lambda)(-\Delta_d - \lambda)\det\begin{pmatrix} \beta_{11}\Delta_w/\mu_w - \mu_w - \alpha_w - \lambda & \beta_{12}\Delta_w/\mu_w \\ \beta_{21}\Delta_d/\mu_d & \beta_{22}\Delta_d/\mu_d - \mu_d + \alpha_d - \lambda \end{pmatrix}$$

Consequently, letting $R_{11} = \beta_{11}\Delta_w/\mu_w$, $R_{12} = \beta_{12}\Delta_w/\mu_w$, $R_{21} = \beta_{21}\Delta_d/\mu_d$, $R_{22} = \beta_{22}\Delta_d/\mu_d$, $r_1 = \mu_w + \alpha_w$ and $r_2 = \mu_d + \alpha_d$ it follows that the eigenvalues are given by:

$$\lambda_{1,2} = \frac{R_{11} + R_{22} - r_1 - r_2 \pm \sqrt{(R_{11} + R_{22} - r_1 - r_2)^2 - 4((R_{11} - r_1)(R_{22} - r_2) - R_{12}R_{21}}}{2}$$

The conditions for stability are:

$$R_{11} + R_{22} - r_1 - r_2 < 0 \quad \text{and} \quad (R_{11} - r_1)(R_{22} - r_2) - R_{12}R_{21} > 0$$