Introduction: What one must do to analyze any model

- Prove the positivity and boundedness of the solutions
- Determine the disease free equilibrium point and the model reproduction number
- Prove the stability of the disease free equilibrium
- Prove the persistence of solutions
- Prove the stability of the endemic equilibrium point
- Simulate the model

- S(t) Susceptible population
- V(t) Vaccinated population
- I(t) Infected individuals
- R(t) Recovered individuals recovery with immunity
- B(t) Cholera bacteria

• Model 1: Recovery with immunity

$$\begin{aligned} \frac{dS}{dt} &= (1-\rho)A - \beta S(t)B(t) + bV(t) - \theta S(t) - \mu_1 S(t) \\ \frac{dV}{dt} &= \rho A + \theta S(t) - bV(t) - \mu_1 V(t) \\ \frac{dI}{dt} &= \beta S(t)B(t) - (d + \alpha + \mu_1) \\ \frac{dR}{dt} &= \alpha I(t) - \mu_1 R(t) \\ \frac{dB}{dt} &= \gamma B(t) + \eta I(t) \end{aligned}$$

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• Model 2: Recovery without immunity

$$\frac{dS}{dt} = (1-\rho)A - \beta S(t)B(t) + bV(t) - \theta S(t) - \mu_1 S(t) + \alpha I(t)$$

$$\frac{dV}{dt} =
ho A + heta S(t) - bV(t) - \mu_1 V(t)$$

$$\frac{dI}{dt} = \beta S(t)B(t) - (d + \alpha + \mu_1)$$

$$\frac{dB}{dt} = \gamma B(t) + \eta I(t)$$

- Models 1 and 2 assume a mass action force of infection. The assumption is that every one who is in contact with the bacteria is infected
- in reality some people do not catch the disease and so a more appropriate force of infection is

$$\lambda = \frac{\beta S(t)B(t)}{N(t)}$$

where N(t) = S(t) + V(t) + I(t) + R(t) for Model 1 or N(t) =S(t) + V(t) + I for Model 2

Positivity and boundedness of solutions of Model 1

• Theorem: Given

 $S(0) \ge 0$, $V(0) \ge 0$, $I(0) \ge 0$, $B(0) \ge 0$, the solutions (S(t), V(t), I(t), B(t)) of Model 1 are positively invariant for all t > 0.

• Let $t_1 = \sup (t > 0 | S > 0, V > 0, I > 0, B > 0)$. From the first equation

$$\frac{dS}{dt} = (1-\rho)A - (\beta B(t) + \theta + \mu_1)S(t)$$

• The integrating factor is

$$\exp\left(\int_0^t \beta B(s)ds + (\theta + \mu_1) t\right)$$

• Multiplying the inequality above by the integrating factor, we obtain

$$\frac{\left[S(t)\exp\left\{\int_0^t\beta B(s)ds + (\theta + \mu_1)t\right\}\right]}{dt}$$

$$\geq (1 - \rho)A\exp\left(\int_0^t\beta B(s)ds + (\theta + \mu_1)t\right)$$

Solving this inequality we obtain

$$S(t) \exp\left\{\int_0^t \beta B(s) ds + (\theta + \mu_1) t\right\} - S(0)$$

$$\geq \int_0^t (1 - \rho) A \exp\{\int_0^\nu \beta B(q) dq + (\theta + \mu_1) \nu\} d\nu$$

Therefore

$$egin{aligned} S(t) &\geq S(0) \exp\left\{-\int_{0}^{t}eta B(q)dq + (\mu_{1}+ heta) t
ight\} \ &+ &\exp\left\{-\int_{0}^{t}eta B(q)dq + (\mu_{1}+ heta) t
ight\} \ & imes \int_{0}^{t}(1-
ho)A\exp\{\int_{0}^{
u}eta B(q)dq \end{aligned}$$

$$+ (\theta + \mu_1)\nu \} d\nu > 0$$

• Similarly, it can be shown that (V(t) > 0, I(t) > 0, B(t) > 0).

Boundedness of the solution

- Theorem: All solutions (S(t), V(t), I(t), B(t)) of Model 1 are bounded.
- Proof: Model 1 is split into two, the human population and the pathogen population
- From the first three populations (human populations0, we obtain

$$\begin{pmatrix} \frac{d(S+V+I)}{dt} \end{pmatrix} = A - \mu_1 (S+V+I) - (d+\alpha) I \\ \leq A - \mu_1 (S+V+I)$$

Then

$$\lim_{t\to\infty}\sup\left(S+V+I\right)\leq\frac{A}{\mu_1}$$

• From the first three equations, we obtain

$$\frac{dS(t)}{dt} \leq (1-\rho)A - (S+V+I) + b\left(\frac{A}{\mu_1} - S\right)$$

Hence

$$\mathcal{S}(t) \leq rac{\mathcal{A}\left(b+\left(1-
ho
ight)\mu_{1}
ight)}{\mu_{1}\left(\mu_{1}+b+ heta
ight)}$$

• It is easy to show that

$$V(t) \leq \left(rac{A(heta+
ho\mu_1)}{\mu_1(\mu_1+b+ heta)}
ight)$$

• For the bacteria we have

$$rac{dB(t)}{dt} \leq rac{\eta A}{\mu_1} - \mu_2 B(t)$$

Hence

$$B(t) \leq \left(\frac{\eta A}{\mu 1 \mu_2}\right)$$

• All solutions of Model 1 are bounded. The feasible region for the human population is

$$egin{aligned} \Omega_{\mathcal{H}} &= \left(S, \ V, \ I
ight) \left|S + V + I \leq \left(rac{A}{\mu_1}
ight), \ 0 \leq S \leq S(t) \ &\leq \left(rac{A\left(b + \left(1 -
ho
ight)\mu_1
ight)}{\mu_1\left(\mu_1 + b + heta
ight)}
ight), \ 0 \ &\leq V \leq \left(rac{A\left(heta +
ho\mu_1
ight)}{\mu_1\left(\mu_1 + b + heta
ight)}
ight), \ I \geq 0, \end{aligned}$$

• The feasible region for the pathogen population for Model 1 is

$$\Omega_B = \left(B|0 \le B \le \left(rac{\eta A}{\mu 1 \mu_2}
ight)
ight)$$

 Define Ω = Ω_H × Ω_B. Let IntΩ denote the interior of Ω. The region Ω is a positively invariant region with respect to the Model 1. Hence the Model 1 is mathematically and epidemiologically well possed in Ω.

• Model 1 has a disease free equilibrium given by

$$(S_0, V_0, 0, 0) = \left(rac{A(b + (1 -
ho) \mu_1)}{\mu_1(\mu_1 + b + heta)}, rac{A(heta +
ho \mu_1)}{\mu_1(\mu_1 + b + heta)}, 0, 0
ight)$$

• The Model 1 can be written as

$$\frac{dX}{dt} = F - \nu,$$



• and

$$\nu = \begin{pmatrix} (d + \alpha + \mu_1)I \\ -\eta I + \mu_2 B(t) \\ -(1 - \rho)A + \beta SB + \mu_1 S + \theta S - bV \\ -\theta S + \mu_1 V + bV - \rho A \end{pmatrix}$$

 ${\ensuremath{\bullet}}$ The Jacobian of ${\ensuremath{\mathcal{F}}}$ is

$$\mathbf{F} = \left(\begin{array}{cc} 0 & \beta S_0 \\ \\ 0 & 0 \end{array}\right)$$

• The Jacobian of ν is

$$\mathbf{V} = \begin{pmatrix} \mu_1 + d + \alpha & 0 \\ \\ -\eta & \mu_2 \end{pmatrix}$$

 ${\scriptstyle \bullet}$ The inverse of ${\bf V}$ is

$$\mathbf{V}^{-1} = \left(egin{array}{ccc} rac{1}{d+lpha+\mu_1} & 0 \ rac{\eta}{\mu_2(d+lpha+\mu_1)} & rac{1}{\mu_2} \end{array}
ight)$$

• The spectral radius of \mathbf{FV}^{-1} is

$$\rho(\mathbf{FV^{-1}}) = \frac{\eta \beta A \left[b + (1 - \rho)\mu_1\right]}{\mu_1 \mu_2 (\mu_1 + \theta + b)(\mu_1 + \alpha + d)}$$

• The reproduction number is

$$R_0 = \frac{\eta \beta A [b + (1 - \rho)\mu_1]}{\mu_1 \mu_2 (\mu_1 + \theta + b)(\mu_1 + \alpha + d)}$$

- We want to discuss the local and global stability of the DFE of Model 1
- Theorem: The DFE is locally asymptotically stable for $R_0 < 1$ and unstable for $R_0 > 1$.
- to prove this, we define new variables

$$x_1 = S - S_0, \ x_2 = V - V_0, \ x_3 = I, \ x_4 = B$$

• The associated linear system is:

$$\dot{X} = MX$$

Where

$$M = \begin{pmatrix} -(\theta + \mu_1) & 0 & 0 & -\beta S_0 \\ \theta & -(b + \mu_1) & 0 & 0 \\ 0 & 0 & 0 & \beta S_0 - (d + \alpha \mu_1) \\ 0 & 0 & \eta & -\mu_2 \end{pmatrix}$$

X = (x₁, x₂, x₃, x₄)^T) and T denotes transpose of a matrix.

Eigenvalues

• Two of the Eigenvalues of *M* are

$$\lambda_1=-\left(b+\mu_1
ight)<\mathsf{0},\quad\lambda_2=-\left(heta+\mu_1
ight)<\mathsf{0}$$

The other two are given by

$$\lambda_{3,4} = \frac{1}{2} \left(-\mu_2 \pm \sqrt{\mu^2 + 4\eta(d + \alpha + \mu_1)Z} \right)$$

= $\frac{1}{2} \left(-\mu_2 \pm \sqrt{\mu^2 + 4\eta(d + \alpha + \mu_1)(R_0 - 1)} \right)$
 $Z = \left(\frac{\beta A(b + (1 - \rho)\mu_1)}{\mu_1(\mu_1 + b + \theta)(d + \alpha + \alpha)} - 1 \right)$

 Both λ₃ and λ₄ are negative hence the DFE is locally stable for R₀ < 1.

- The DFE is globally stable for $R_0 < 1$ and unstable for $R_0 > 1$.
- The Model can be subdivided into two sets X₁ = (S, V) and X₂ = (I, B) so that X = (X₁, X₂)^T
- The sub-system X_1 is given by

$$\frac{dS}{dt} = (1-\rho)A - \beta S(t)B(t) + bV(t) - \theta S(t) - \mu_1 S(t)$$
$$\frac{dV}{dt} = \rho A + \theta S(t) - bV(t) - \mu_1 V(t)$$

• The sub-system X_2 is given by $\frac{dI}{dt} = \beta S(t)B(t) - (d + \alpha + \mu_1)$ $\frac{dB}{dt} = \gamma B(t) + \eta I(t)$

• It is easy to show that the sub-system $X_1 = (S, V)$ is globally asymptotically stable at

$$X_1^* = \left(\frac{A\left(b + (1 - \rho)\mu_1\right)}{\mu_1\left(\mu_1 + b + \theta\right)}, \ \frac{A\left(\theta + \rho\mu_1\right)}{\mu_1\left(\mu_1 + b + \theta\right)}\right)$$

• The matrix $A_2(X)$ from subsystem X_2 is given by

$$A_2(X) = \begin{pmatrix} -(\mu_1 + d + \alpha) & \beta S \\ \eta & -\mu_2 \end{pmatrix}$$

• The maximum of $A_2(X)$ occurs at the DFE given by

$$A_2(X) = \begin{pmatrix} -(\mu_1 + d + \alpha) & \beta S_0 \\ \eta & -\mu_2 \end{pmatrix}$$

• The spectral bound of $\alpha(A_2(\bar{X})A_2(X))$ is $R_0 \leq 1$.