Non-Linear Models Cont’d: Symbiosis

Symbiosis

3rd interaction regime will consider is symbiosis where interaction of benefit to all species. Model has form:

\[
\frac{dx}{dt} = \mu_1 x \left(1 - \frac{x}{K_1} + c_{12} \frac{y}{K_1} \right) \\
\frac{dy}{dt} = \mu_2 y \left(1 - \frac{y}{K_2} + c_{21} \frac{x}{K_2} \right)
\]  \hspace{1cm} (4.26)

where pop’n sizes \(x, y\) grow logistically in absence of other with different carrying capacities \(K_1, K_2\) respectively.

The +ive parameters \(c_{12}, c_{21}\) indicate +ive effect that each species has on the other.

\(\mu_1, \mu_2\) are rate constants.

Setting \(u_1 = \frac{x}{K_1}, u_2 = \frac{y}{K_2}\), 
& \(\tau = \mu_1 t\), Eqn.(4.26) reduces to:

\[
\frac{du_1}{d\tau} = u_1 (1 - u_1 + \alpha_{12} u_2) \\
\frac{du_2}{d\tau} = \xi u_2 (1 - u_2 + \alpha_{21} u_1)
\]  \hspace{1cm} (4.27)

where (non-dim’l) parameters given by \(\xi = \mu_2/\mu_1, \alpha_{12} = c_{12} K_2/K_1, \alpha_{21} = c_{21} K_1/K_2\).

The steady-states of Eqn.(4.27) are given by

\((\dot{u}_1, \dot{u}_2) = (0, 0) \equiv (u, v) = (0, 0) \) or \((1 + \alpha_{12} u_2, 1 + \alpha_{21} u_1)\)

Leads to 4 cases:

\[(0, 0) \) or \((0, 1) \) or \((1, 0) \) or \(( \frac{1 + \alpha_{12}}{1 - \alpha_{12} \alpha_{21}}, \frac{1 + \alpha_{21}}{1 - \alpha_{12} \alpha_{21}})\)

where final case is only relevant if \(\alpha_{12} \alpha_{21} < 1\).
Next, can find Jacobian matrix, at a steady-state \((\bar{u}_1, \bar{u}_2)\):

\[
A(\bar{u}_1, \bar{u}_2) = \begin{pmatrix}
1 - 2\bar{u}_1 + \alpha_{12}\bar{u}_2 & \alpha_{12}\bar{u}_1 \\
\xi\alpha_{21}\bar{u}_2 & \xi(1 - 2\bar{u}_2 + \alpha_{21}\bar{u}_1)
\end{pmatrix}
\]

(4.28)

So at the steady states, get:

for 1st Steady State \((0, 0)\) \(A = \begin{pmatrix} 1 & 0 \\ 0 & \xi \end{pmatrix}\)

for 2nd Steady State \((1, 0)\) \(A = \begin{pmatrix} -1 & \alpha_{12} \\ 0 & \xi(1 + \alpha_{21}) \end{pmatrix}\)

for 3rd Steady State \((0, 1)\) \(A = \begin{pmatrix} 1 + \alpha_{12} & 0 \\ \xi\alpha_{21} & -\xi \end{pmatrix}\)

\(\alpha\)'s +ive, \(\Rightarrow\) \((0, 0)\) is unstable node, \((1, 0)\) & \((0, 1)\) saddles.

4th steady-state has e-values given by zeros of

\[
\lambda^2 - \text{trace}(A)\lambda + \det(A) = 0
\]

(4.29)

For stability need \(\Re(\lambda_1, \lambda_2) < 0\), only true for +ive coeffs of eqn(4.29). So \(\text{trace}(A) < 0\) - always true for \(\alpha_{12}\alpha_{21} < 1\) and \(\det(A) > 0 \equiv \frac{\xi(1 + \alpha_{12})(1 + \alpha_{21})(1 + \alpha_{12}\alpha_{21})}{1 - \alpha_{12}\alpha_{21}} > 0\)

which is again satisfied with \(\alpha_{12}\alpha_{21} < 1\).
Non-Linear Models Cont’d: Symbiosis

- See this on phase-plane plots in Fig 4.5 (a),(b).
- These were calculated for $\alpha_{12} = 0.5$, $\alpha_{21} = 0.25$ & $\xi = 2$ in Fig 4.5(a) (i.e. $\alpha_{12}\alpha_{21} < 1$) giving a stable steady-state (i.e. stable node) for the fourth case at $\left(\frac{12}{2}, \frac{10}{2}\right)$.
- Fig 4.5(b) shows a similar plot with $\alpha_{12} = 1.5$, $\alpha_{21} = 1.25$ & $\xi = 2$ (i.e. $\alpha_{12}\alpha_{21} > 1$) giving instabilities everywhere.

Figure 4.5: Symbiosis Phase-Plane Plots
Infectious Diseases
- Can be classified into 2 broad categories:
  - those caused by viruses and bacteria (*microparasitic* diseases such as smallpox, measles),
  - those due to worms (*macroparasitic* diseases such as malaria).
- Main distinction btw them:
  - former reproduce within the host & are transmitted directly from one host to another,
  - latter require some vector (i.e. must be insect-borne, entertainment-borne etc.) for transmission.
- We will focus purely on microparasitic diseases.

Cannot view virus & host organism as a predator-prey system, for a number of reasons:
- virus pop’n in the individual host can vary greatly, thus model would not provide a definite answer to question of how many succumb to disease.
- predator-prey models also presume random interaction between predator and prey whereas parasitic disease is typically spread by close proximity or contact btw infected and healthy individuals.
- key question is how the disease spreads in the population, something difficult to model using the Predator-prey model.
To model diseases, pop’n divided into 3 groups:
- susceptible (i.e. those not immune to disease),
- infectives (those who can infect non-immunes),
- removed (dead or in quarantine or immune).

Symbols $S, I, R$ denote these resp groups at time $t$.

Following assumptions are made:
- rate of change of infectives $\propto$ number of contacts btw $I$ & $S$
  (or each $I$ infects a constant fraction $\beta$ of $S$ per unit time)
- the number of $I$ who become $R$ is proportional to $I$

Equations are thus:

$$
\dot{S} = -\beta IS \\
\dot{I} = \beta IS - \nu I \\
\dot{R} = \nu I
$$

(4.30)

$\beta, \nu$ are infection & removal rates, $\dot{S} = \frac{dS}{dt}$ etc.

$\beta$ governs speed of disease spread
$\nu$ governs rate infected hosts die/otherwise removed.

By adding 3 equations, it will be obvious that

$$
\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0,
$$

i.e. $S + I + R = N$ for constant (initial) population $N$.

Rest of the initial conditions are

$S(0) = S_0 > 0, \ I(0) = I_0 > 0, \ R(0) = 0$.

Given these initial conditions from Eqn.(4.30b) get:

$$
\left. \frac{dl}{dt} \right|_{t=0} = l_0 (\beta S_0 - \nu) \left\{ \begin{array}{ll}
< 0, & \text{if } S_0 < \nu/\beta = \rho \\
> 0, & \text{if } S_0 > \nu/\beta = \rho
\end{array} \right. (4.31)
$$
A plot of $S$, $I$ and $R$ is shown in Fig 4.6.

**Figure 4.6**: SIR Model for $\rho = 100$: Susceptible, Infected, Removed
To further analyse the model, consider the \((S, I)\) phase plane in Fig. 4.7. Can express Eqn.\(\text{s}(4.30a,b)\) as
\[
\frac{dl}{ds} = \frac{l(\beta S - \nu)}{-\beta IS} = -1 + \frac{\rho}{S},
\]
provided \(l \neq 0\). Can derive:
\[
l(t) = l_0 - S(t) + \rho \ln S(t) + S_0 - \rho \ln S_0
\]
provided \(I \neq 0\). Can derive:
\[
l(t) = l_0 - S(t) + \rho \ln S(t) + S_0 - \rho \ln S_0
\]
From Eqn.\(4.33\) & Fig. 4.7 that \(l_{\text{max}}\) reached when \(S = \rho\).
Trajectories are shown for various values of \((S_0, I_0)\) &., as above with predator-prey, all move anti-clockwise.
A trajectory starts on line \(I + S = N\) (as \(R(0) = 0\)) & susceptible pop'n decreases with time.
If \((S_0, I_0)\) is in epidemic region (right of \(\rho = 4\) in Fig. 4.7), \(I\) \(\uparrow\) initially until \(S = \rho\).
How does disease eventually die out with SIR model?

From Eqns (4.30a,c):

\[
\frac{dS}{dR} = \frac{-\beta IS}{\nu T} = -\frac{S}{\rho},
\]

Thus \( S = S_0 e^{-R/\rho} \). But, \( \forall t \geq 0, R \leq N \) this means \( S(t) \geq S_0 e^{-N/\rho} \), i.e. as \( t \to \infty \), \( S > 0 \).

But, from Eqn. (4.30c) \( \frac{dR}{dt} > 0 \) \( \forall t \geq 0 \), so, if need to keep \( R \leq N \), then need \( \frac{dR}{dt} \to 0 \), as \( t \to \infty \).

From Eqn. (4.30c), this can only happen if \( I(\infty) = 0 \).

Upshot of this is that lack of infectives wipes out disease & not lack of susceptibles.