Reproduction number derivations

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Basic Reproduction Number (R_0)

Expanding on the model presented in Halstead et al 2018, we incorporate additional model parameters and agrochemical sensitivities to arrive at the following model of schistosomiasis transmission in the presence of agrochemical pollution:

$$\frac{dS}{dt} = f_N(q)\left(1 - \frac{N}{K_N(q)}\right)(S+E) - \mu_N(q)S - P\psi S^n - \beta MS \tag{1}$$

$$\frac{dE}{dt} = \beta MS - \mu_N(q)E - P\psi E^n - \sigma E \tag{2}$$

$$\frac{dI}{dt} = \sigma E - (\mu_N(q) + \mu_I)I - P\psi I^n \tag{3}$$

$$\frac{dW}{dt} = \lambda C - (\mu_H + \mu_W)W \tag{4}$$

$$\frac{dP}{dt} = f_P\left(1 - \frac{P}{K_P}\right)P - \mu_P(q)P \tag{5}$$

where:

$$M(t) = W_F m v(q) \pi_M(q) \tag{6}$$

$$W_F = 0.5 W H \phi(W, \kappa) \tag{7}$$

$$C(t) = I\theta(q)\pi_C(q) \tag{8}$$

$$\psi = \frac{\alpha(q)}{1 + \alpha T_h N^n} \tag{9}$$

$$N = S + E + I \tag{10}$$

We employ the next generation matrix methodology to develop an analytic expression for $R_0(q)$, the agrochemical-sensitive basic reproduction number. We define $R_0(q)$ as the expected number of mated adult female worms, W_F, produced by a single mated adult female worm in an entirely susceptible human host population within an ecosystem where agrochemical concentration is equal to q. We begin by linearizing the disease system about the disease free steady state, implying $S = N$ and $E = I = W = 0$, by solving for the equilibrium number of snails, N^*, and predators, P^*, respectively. Assuming $n = 1$, implying a Holling's type II functional response, we have:

$$0 = f_P\left(1 - \frac{P^*}{K_P}\right) - \mu_P(q) \tag{11}$$

$$0 = f_N(q)\left(1 - \frac{N^*}{K_N(q)}\right) - \mu_N(q) - P^*\psi^* \tag{12}$$

$$\psi^* = \frac{\alpha(q)}{1 + \alpha T_h N^*} \tag{13}$$

We subsequently restrict our attention to the linearized subsystem of equations governing infectious state dynamics:

$$\frac{dE}{dt} = \beta M N^* - (\mu_N(q) + P\psi + \sigma)E \tag{14}$$
$$\frac{dI}{dt} = \sigma E - (\mu_N(q) + \mu_I + P\psi)I \tag{15}$$
$$\frac{dW}{dt} = \lambda C - (\mu_H + \mu_W)W \tag{16}$$
$$\tag{17}$$

We next build matrices $\mathbf{T}$ and $\mathbf{\Sigma}$ corresponding to the generation of new infections and transitions between infected states, respectively, and we take the product $\mathbf{T}(-\mathbf{\Sigma}^-)$ to produce the system's next generation matrix with large domain, K_L.

$$\mathbf{T} = \begin{bmatrix} 0 & 0 & 0.5\beta H m v(q)\pi_M(q)N^* \\ 0 & 0 & 0 \\ 0 & \lambda\theta(q)\pi_C(q) & 0 \end{bmatrix} \tag{18}$$

$$\mathbf{\Sigma} = \begin{bmatrix} -(\mu_N(q) + P^*\psi^* + \sigma) & 0 & 0 \\ \sigma & -(\mu_N(q) + P^*\psi^* + \mu_I) & 0 \\ 0 & 0 & -(\mu_H + \mu_W) \end{bmatrix} \tag{19}$$

$$\mathbf{K_L} = \begin{bmatrix} 0 & 0 & \frac{0.5\beta H m v(q)\pi_M(q)N^*}{(\mu_W+\mu_H)} \\ 0 & 0 & 0 \\ \frac{\sigma\lambda\theta(q)\pi_C(q)}{(\mu_N(q)+P^*\psi^*+\sigma)(\mu_N(q)+P^*\psi^*+\mu_I)} & \frac{\lambda\theta(q)\pi_C(q)}{\mu_N(q)+P^*\psi^*+\mu_I} & 0 \end{bmatrix} \tag{20}$$

Next,$\mathbf{K_L}$ reduces to $\mathbf{K}$ (shown below) the next generation matrix for only those states which are states at infections, E and W.

$$\mathbf{K} = \begin{bmatrix} 0 & \frac{0.5\beta H m v(q)\pi_M(q)N^*}{(\mu_W+\mu_H)} \\ \frac{\sigma\lambda\theta(q)\pi_C(q)}{(\mu_N(q)+P^*\psi^*+\sigma)(\mu_N(q)+P^*\psi^*+\mu_I)} & 0 \end{bmatrix} \tag{21}$$

Given $\mathbf{K}$, we can then compute the spectral radius which is interpreted as $R_0(q)$:

$$R_0(q) = \left(\frac{0.5\sigma\lambda\theta(q)\pi_C(q)\beta H m v(q)\pi_M(q)N^*}{(\mu_N(q) + P^*\psi^* + \sigma)(\mu_N(q) + P^*\psi^* + \mu_I)(\mu_W + \mu_H)} \right)^{\frac{1}{2}} \tag{22}$$

In addition, we don't consider any density dependence, setting $\phi(W) = 1$, as these functions are not relevant at a disease free state. R_0 is a measure of disease spread within a completely susceptible population and is therefore inadequate when the interest lies in studying an established pathogen in a setting where density dependence within the pathogen population regulates transmission.

Effective Reproduction Number (R_{eff})