

On-Line Appendix 1: Stability of Model

Equations (5a-g) can be used to find the equilibrium values of the model. From equation (5a), we obtain

$$N^* = \frac{1}{\rho} \left(\frac{a_{RR}}{b} - 1 \right). \quad (\text{A1a})$$

From equation (5d) we obtain:

$$X_{rr}^* = \frac{b + \alpha}{\beta}. \quad (\text{A1b})$$

From equation (5b) we obtain

$$Y_{rr}^* = \frac{b(a_{rr} - a_{RR})(b + \alpha)}{(a_{RR}(b + \alpha) - a_{rr,dis}b)\beta} \quad (\text{A1c})$$

We next use equation (5c) to obtain *Allele_R*. After some manipulations, we obtain

$$Allele_R^* = \frac{-B - \sqrt{B^2 - 4AC}}{2A} \quad (\text{A1d})$$

where

$$A = 0.25(F - 1)a_{rr}^2$$

$$B = -a_{RR}(1 - 0.5F)V$$

$$C = V \left[V - (b + \beta Y_{rr}^*) X_{rr}^* \frac{a_{RR}}{b} \right]$$

where

$$V = a_{RR}(N^* - X_{rr}^* - Y_{rr}^*) + a_{rr}X_{rr}^* + a_{rr,dis}^*Y_{rr}^*.$$

It is also clear that the following relation holds;

$$X_{RR}^* + X_{Rr}^* = N^* - X_{rr}^* - Y_{rr}^* = \frac{a_{RR} - b}{\rho b} - X_{rr}^* - Y_{rr}^*. \quad (\text{A1e})$$

From equations (A1d) and (A1e) X_{RR}^* and X_{Rr}^* can be calculated individually. Below, the particular equilibrium values for $F = 1$ and $F = 0$ are used.

The stability of equations (A1a-d) can be examined using Routh-Hurwitz criteria. We consider two cases.

A. $F = 1$, selfing. Consider only the case when infected individuals are not able to reproduce.

In this case, X_{Rr} does not exist in the model. The only equilibrium value of those above that becomes more specific at $F = 1$ is $Allele_R$, which becomes:

$$Allele_R = 2(N^* - X_{rr}^* - Y_{rr}^*).$$

Then, since there are no Rr-heterozygotes, we have

$$X_{RR}^* = (N^* - X_{rr}^* - Y_{rr}^*).$$

It is easiest to use the original set of equations (1a-d) to evaluate stability, which reduce to

$$\begin{aligned} \frac{dX_{RR}}{dt} &= \frac{a_{RR} X_{RR}}{1 + \rho(X_{RR} + X_{rr} + Y_{rr})} - bX_{RR} \\ \frac{dX_{rr}}{dt} &= \frac{a_{rr} X_{rr}}{1 + \rho(X_{RR} + X_{rr} + Y_{rr})} - bX_{rr} - \beta Y_{rr} X_{rr} \\ \frac{dY_{rr}}{dt} &= \beta Y_{rr} X_{rr} - (b + \alpha)Y_{rr} \end{aligned} \quad (A2)$$

The equilibrium now takes the form $E^* = (X_{RR}^*, X_{rr}^*, Y_{rr}^*)$. The Jacobian matrix for this system has the form:

$$J = \begin{vmatrix} j_{11} & j_{12} & j_{13} \\ j_{21} & j_{22} & j_{23} \\ 0 & j_{32} & 0 \end{vmatrix}$$

where

$$j_{11} = \frac{-a_{RR}\rho X_{RR}^*}{[1 + \rho(X_{RR} + X_{rr} + Y_{rr})]^2}$$

$$j_{12} = \frac{-a_{RR}\rho X_{RR}^*}{[1 + \rho(X_{RR} + X_{rr} + Y_{rr})]^2}$$

$$j_{13} = \frac{-a_{RR}\rho X_{RR}^*}{[1 + \rho(X_{RR} + X_{rr} + Y_{rr})]^2}$$

$$j_{21} = \frac{-a_{rr}\rho X_{rr}^*}{[1 + \rho(X_{RR}^* + X_{rr}^* + Y_{rr}^*)]^2}$$

$$j_{22} = \frac{-a_{rr}\rho X_{rr}^*}{[1 + \rho(X_{RR}^* + X_{rr}^* + Y_{rr}^*)]^2}$$

$$j_{23} = \frac{-a_{rr}\rho X_{rr}^*}{[1 + \rho(X_{RR}^* + X_{rr}^* + Y_{rr}^*)]^2} - \beta X_{rr}^*$$

If we define

$$A_1 = j_{11} + j_{22} + j_{33}$$

$$A_2 = j_{21}j_{12} + j_{23}j_{32} - j_{11}j_{22}$$

$$A_3 = -j_{11}j_{23}j_{32} + j_{13}j_{21}j_{32}$$

It can be shown that the Routh-Hurwitz criteria

$$A_1 < 0, \quad A_1A_2 - A_3 > 0$$

are satisfied for any set of parameters and the equilibrium is stable.

B. $F=0$, outcrossing. In this case, it is easiest to use the set of equations (5a-g), and the model reduces to

$$\frac{d(Allele_R)}{dt} = \left(\frac{a_{RR}}{1 + \rho N} - b \right) Allele_R \quad (A3a)$$

$$\frac{dN}{dt} = \frac{a_{RR}(N - X_{rr} - Y_{rr}) + a_{rr}(X_{rr} + Y_{rr})}{1 + \rho N} - bN - \alpha Y_{rr} \quad (A3b)$$

$$\frac{dX_{rr}}{dt} = \frac{(gamX_r)^2}{gamX_r + gamX_R} - (b + \beta Y_{rr})X_{rr} \quad (A3c)$$

$$\frac{dY_{rr}}{dt} = \beta Y_{rr} X_{rr} - (b + \alpha)Y_{rr} \quad (A3d)$$

where $N = X_{RR} + X_{Rr} + X_{rr} + Y_{rr}$ and $Allele_R = 2X_{RR} + X_{Rr}$. The positive equilibrium is given by

$$N^* = \frac{a_{RR} - b}{b\rho}, \quad X_{rr}^* = \frac{b + \alpha}{\beta}, \quad Y_{rr}^* = \frac{(a_{rr} - a_{RR})(b + \alpha)b}{(a_{RR}(b + \alpha) - a_{rr,dis}b)\beta}$$

$$Allele_R^* = \frac{2}{a_{RR}} \left[V - \sqrt{V^2 - a_{RR}V(N^* - X_{rr}^* - Y_{rr}^*)} \right] \quad V = a_{RR}(N^* - X_{rr}^* - Y_{rr}^*) + a_{rr}X_{rr}^* + a_{rr,dis}Y_{rr}^*$$

The local stability of the positive equilibrium $E^* = (Allele_R^*, N^*, X_{rr}^*, Y_{rr}^*)$ can be carried out by linearizing the system (A3a-d) at the equilibrium. The Jacobian matrix takes the form

$$\begin{bmatrix} 0 & j_{12} & 0 & 0 \\ 0 & j_{22} & j_{23} & j_{24} \\ j_{31} & j_{32} & j_{33} & j_{34} \\ 0 & 0 & j_{43} & 0 \end{bmatrix}$$

where the j_{ij} ($i, j=1, 2, 3, 4$) are the partial derivatives of the functions in (A.2a,b,c,d) evaluated

$$\text{at: } E^* = (Allele_R^*, N^*, X_{rr}^*, Y_{rr}^*)$$

$$\begin{aligned}
j_{12} &= -\frac{b^2 \rho \text{Allele}_R^*}{a_{RR}} \\
j_{22} &= \frac{-\rho \Delta b^2}{a_{RR}^2} \\
j_{23} &= b \left(\frac{a_{rr}}{a_{RR}} - 1 \right) \\
j_{24} &= b \left(\frac{a_{rr}}{a_{RR}} - 1 \right) - \alpha \\
j_{31} &= -\frac{b}{\Delta} G \quad G = [(b + \beta Y_{rr}^*) X_{rr}^* \Delta (1 + \rho N)]^{1/2} \\
j_{32} &= \frac{b^2 G}{\Delta^2 a_{RR}^2} \left[\frac{2a_{RR}^2 \Delta}{b} - \frac{a_{RR}^2 G}{b} - \rho G \Delta \right] \\
j_{33} &= \frac{b(a_{rr} - a_{RR}) G (\Delta + 0.5 * a_{RR} \text{Allele}_R)}{\Delta^2 a_{RR}} - (b + \beta Y_{rr}^*) \\
j_{34} &= \frac{b(a_{rr} - a_{RR}) G (\Delta + 0.5 a_{RR} \text{Allele}_R)}{\Delta^2 a_{RR}} - \beta X_{rr} \\
j_{43} &= \beta Y_{rr}^*
\end{aligned}$$

where

$$\Delta = a_{RR} N^* + a_{rr} X_{rr}^* + a_{rr,dis} Y_{rr}^* - a_{RR} (X_{rr}^* + Y_{rr}^*)$$

The characteristic equation takes the form $\lambda^4 + a_1 \lambda^3 + a_2 \lambda^2 + a_3 \lambda + a_4 = 0$, where

$$\begin{aligned}
a_1 &= -(j_{22} + j_{33}) \\
a_2 &= j_{22} j_{33} - j_{23} j_{32} - j_{34} j_{43} \\
a_3 &= j_{22} j_{34} j_{43} - j_{12} j_{23} j_{31} - j_{24} j_{32} j_{43} \\
a_4 &= -j_{12} j_{24} j_{43} j_{31}
\end{aligned}$$

The Routh-Hurwitz criteria implies that the positive equilibrium $E^* = (A_R^*, N^*, X_{rr}^*, Y_{rr}^*)$ is

asymptotically stable if

$$a_1 > 0, a_1 a_2 - a_3 > 0, a_1 a_2 a_3 - a_1^2 a_4 - a_3^2 > 0 \quad (\text{A4})$$

Using the parameter values in Table 1, we can verify that all inequalities in (A4) are satisfied for

that specific case. Thus, the positive equilibrium is asymptotically stable (see Figure 1a).

However, we have not yet been able to demonstrate that positive equilibria for all possible parameter values are stable. Extensive numerical evaluations lead us to conjecture that the $F = 0$ case, like the $F = 1$ case, is always stable, and also that the model is stable for $0 \leq F \leq 1$. Note that the two cases $F = 1$ and $F = 0$ differ only in the first term on the right hand side of equation (5c),

$$\frac{(gamX_r)^2 + F(gamX_R)(gamX_r)}{gamX_r + gamX_R}$$

For $F = 1$, this becomes $gamX_r$, while for $F = 0$, this becomes $(gamX_r)^2/(gamX_r + gamX_R)$.

Numerical examination of the effects of different values of F and different equilibrium values of $gamX_r$ and $gamX_R$ have failed to show any tendency towards instability for the model. However, other contact functions than βX_{rr} have not been examined for stability, and may lead to instability.

On-Line Appendix 2: Individual-Based Model

The individual-based model is an exact analog of the population described by equations (1a,b,c,d). A starting population of 10,000 individuals is used. Each is assigned randomly to one of the three genotypes types, RR , Rr , or rr , and the individual carries a ‘genotype ID’, 1, 2, or 3, that tells whether it is an RR , Rr , rr . This gives an initial population X_{RR} , X_{Rr} , and X_{rr} .

At each time step, Δt , the probability of a non-infected individual dying natural mortality is $b\Delta t$. If the individual is infected, then the probability is $(b + \alpha) \Delta t$. The probability of reproduction producing an individual of a given genotype on time step Δt is calculated as follows:

$$Pr ob(reproduction) = (gamX_R + gamX_r) \times fseedX_{ij} \times \Delta t$$

Where $fseedX_{ij}$ can take on different values, depending on whether ij is RR , Rr , or rr , and depending on the value of F :

$$fseedX_{RR} = (fgamX_R)^2 + F \times fgamX_R \times fgamX_r$$

$$fseedX_{Rr} = 2 \times (1 - F) \times fgamX_R \times fgamX_r$$

$$fseedX_{rr} = (fgamX_r)^2 + F \times fgamX_R \times fgamX_r$$

and

$$fgamX_i = \frac{gamX_i}{gamX_R + gamX_r}$$

where

$$gamX_R = \frac{a_{RR}X_{RR} + 0.5a_{Rr}X_{Rr}}{1 + \rho N}$$

$$gamX_r = \frac{a_{rr}X_{rr} + a_{rr}Y_{rr} + 0.5a_{Rr}X_{Rr}}{1 + \rho N},$$

and where Y_{rr} is the number of infected individuals (see main text for other definitions). A disease is allowed to enter at some predetermined point in time, when the number of RR alleles is very small. This is done by inserting 10 infected individuals for 10 time steps. On each time step, the probability of an rr individual being infected is

$$\text{Prob}(\text{infection}) = \beta \times 10 \times X_{rr} \times \Delta t$$

Each new infected individual carries the ‘genotype ID’ 4, and adds to the population size of infected individuals, Y_{rr} .