Appendix 1 – Analysis of Population Dynamics in the Chemostat

We consider the following set of equations describing the dynamics of resources (R), bacteria (N), and bacteriophage (V), in a chemostat with washout rate ω:

$$\frac{\mathrm{d}R}{\mathrm{d}t} = -\omega(R - R_0) - \epsilon\gamma\frac{RN}{R+K}, \quad [1]$$

$$\frac{\mathrm{d}N}{\mathrm{d}t} = -\omega N + \gamma\frac{RN}{R+K} - \phi NV, \quad [2]$$

$$\frac{\mathrm{d}V}{\mathrm{d}t} = -\omega V + \beta\phi NV. \quad [3]$$

The functional form for resource uptake is generally taken to be of the Michaelis-Menten type and phage adsorption is presumed to be linear in both phage and bacteria density. Note that these equations neglect the time delay in bacterial division as well as in phage lysis (1, 2). The parameters include: R_0, resource input density; K, half-saturation constant; γ, maximal growth rate; ϵ, resource to bacteria conversion efficiency; β, burst size in terms of phage to bacteria output; and ϕ, density-dependent adsorption rate. Dimensional analysis helps in reducing the number of parameters. Rewriting all resource densities in terms of R_0, bacterial densities in terms of R_0/ϵ, phage densities in terms of $R_0\beta/\epsilon$, and times in terms of $1/\omega$, the equations become

$$\frac{\mathrm{d}R}{\mathrm{d}t} = -(R - 1) - \gamma\frac{RN}{R+K}, \quad [4]$$

$$\frac{\mathrm{d}N}{\mathrm{d}t} = -N + \gamma\frac{RN}{R+K} - \phi NV, \quad [5]$$

$$\frac{\mathrm{d}V}{\mathrm{d}t} = -V + \phi NV, \quad [6]$$

where the dimensionless parameters have the following meanings: $\gamma \to \gamma/\omega$, $K \to K/R_0$, and $\phi \to \phi\beta R_0/(\omega\epsilon)$.

The three-dimensional dynamics may be reduced to two by noting that the time derivative of $\Sigma = 1 - R - N - V$ is

$$\frac{\mathrm{d}\Sigma}{\mathrm{d}t} = -\Sigma \qquad \textbf{[7]}$$

and therefore $\Sigma(t) = \Sigma_0 e^{-t}$. The steady state is $\Sigma = 0$, and so we use the relation $R = 1 - N - V$ to generate the simplified set of equations

$$\frac{\mathrm{d}N}{\mathrm{d}t} = -N + \gamma\frac{(1-N-V)N}{1-N-V+K} - \phi NV, \qquad \textbf{[8]}$$

$$\frac{\mathrm{d}V}{\mathrm{d}t} = -V + \phi NV. \qquad \textbf{[9]}$$

The fixed points of these equations are $(0,0)$, $(1 - K/(\gamma - 1), 0)$, and $(1/\phi, V_c)$, where V_c is the solution to

$$V_c^2 + V_c(1/\phi - K - \gamma - 1) + 1/\phi[(1 - 1/\phi)(\gamma - 1) - K] = 0. \qquad \textbf{[10]}$$

We denote these three fixed points as E_1, E_2, and E_3, respectively.

The stability at E_1 is determined by a Jacobian, which has one stable eigendirection (corresponding to the death of phage when there are no bacteria) and another eigendirection that is stable whenever $\gamma < 1 + K$. When $\gamma > 1 + K$ then E_1 is an unstable saddle and E_2 is a possible equilibrium. The stability of E_2 is also determined by a Jacobian which has one zero off-diagonal element, so that its eigenvalues lie on the diagonal. One is always negative (corresponding to the stable persistence of bacteria in the absence of phage) and the second is negative whenever $1 - K/(\gamma - 1) < 1/\phi$. When $1 - K/(\gamma - 1) > 1/\phi$ then E_2 is an unstable saddle and, as it turns out, E_3 is a possible equilibrium.

The analysis of E_3 is slightly more complex. Note that $N_c = 1/\phi$ and V_c is a solution to

$$\frac{V_c}{N_c} = \frac{\gamma(1 - N_c - V_c)}{1 - N_c - V_c + K} - 1,$$

a condition that may be rewritten as

$$\frac{V_c}{N_c}(1 - N_c - V_c + K) = (\gamma - 1)(1 - N_c - V_c - \frac{K}{\gamma - 1}).$$

Because $N_c + V_c < 1$, the lhs of this equation is always greater than 0, whereas if $N_c + K/(\gamma - 1) > 1$ the rhs is less than zero. For there to be a unique solution, then $1 - K/(\gamma - 1) > 1/\phi$, in agreement with the finding that a transcritical bifurcation occurs via the instability of E_2. The only remaining question is whether or not E_3 is stable and for what set of parameters? The Jacobian is

$$J = \begin{bmatrix} J_{11} & J_{12} \\ J_{21} & J_{22} \end{bmatrix}. \qquad \textbf{[11]}$$

where the matrix elements are the usual derivatives of the fitness:

$$\begin{aligned} J_{11} &= -1 + \frac{\gamma(1 - N - V)}{1 - N - V + K} - \phi V - \frac{\gamma K N}{(1 - N - V + K)^2}, \\ J_{12} &= -\frac{\gamma K N}{(1 - N - V + K)^2} - \phi N, \\ J_{21} &= \phi V, \\ J_{22} &= -1 + \phi N. \end{aligned}$$

The determinant of the Jacobian evaluated at E_3 is positive and so the stability depends on the trace,

$$\mathrm{Tr} = \frac{-\gamma K}{\phi(1 - 1/\phi - V_c + K)^2}, \qquad [12]$$

which is always negative. Thus, whenever E_3 exists it is a stable node. E_3 is also a globally stable equilibrium, according to Dulac's criterion (3). The real part of the eigenvalues of the Jacobian for E_3 are negative, but the imaginary part may exist, leading to damped oscillations toward equilibrium. The conditions for damped oscillations are the standard result for two-dimensional systems, $4\mathrm{Tr} > \mathrm{Det}$.

Appendix 2 – Analytical Results on Diversification and Coexistence

The method of adaptive dynamics (4, 5) describes the evolution of traits under the assumptions of rare and small mutations for an ecological model with a fixed-point equilibrium. The dynamics of trait coevolution may be written as:

$$\frac{\mathrm{d}x}{\mathrm{d}t} = \frac{1}{2}\mu_n\sigma_n^2\rho_n(x,y)\left(\frac{\partial r_n'(x';x,y)}{\partial x'}\right)_{x'=x}, \qquad [13]$$

$$\frac{\mathrm{d}y}{\mathrm{d}t} = \frac{1}{2}\mu_v\sigma_v^2\rho_v(x,y)\left(\frac{\partial r_v'(y';x,y)}{\partial y'}\right)_{y'=y}. \qquad [14]$$

For the chemostat model in Eq. (6), the fitness of bacteria and phage mutants are

$$r_n' = \omega\Big(\frac{\gamma(x')}{\gamma(x)} - 1\Big) + V_c\Big(\frac{\phi(x,y)\gamma(x')}{\gamma(x)} - \phi(x',y)\Big), \qquad [15]$$

$$r_v' = \omega\Big(\frac{\phi(x,y')}{\phi(x,y)} - 1\Big), \qquad [16]$$

respectively, where V_c is the steady-state phage density derived in Eq. **10**. Denoting $k_n \equiv \mu_n \sigma_n^2 \rho_n(x,y)$ and $k_v \equiv \mu_v \sigma_v^2 \rho_v(x,y)$, two cases are relevant: (i) Limit of fast viral mutagenesis, $k_v \gg k_n > 0$; (ii) General case, $k_n, k_v > 0$.

Diversification with Fast Viral Mutation

Given $k_v \gg k_n$ and a pair of traits (x,y), then a viral mutant with trait y' invades whenever $|y'-x| < |y-x|$, i.e., mutant viruses replace one another until $y \to x$. This is a consequence of there being a single optimal viral trait for every bacterial trait. Subsequent bacterial adaptations may then be recast as a one-dimensional adaptive dynamics problem, whose evolutionary fixed point satisfies

$$\frac{\partial r_n'(x';x)}{\partial x'}|_{x'=x} = 0; \qquad \textbf{[17]}$$

the fixed point occurs at the resource uptake optimum ($x = 0$).

The fixed point, $(x = 0, y = 0)$, is a locally evolutionarily stable strategy (ESS) (5) when

$$\frac{\partial^2 r_n'(x';x)}{\partial x'^2}|_{x'=x=0} < 0, \qquad \textbf{[18]}$$

or written in terms of the fixed points and parameters:

$$-\frac{\omega}{\xi_n^2} + \phi_0 V_c \Big(\frac{\xi_n^2 - \xi_v^2}{\xi_n^2 \xi_v^2} \Big) < 0. \qquad \textbf{[19]}$$

Because the system is convergence stable, evolutionary branching occurs whenever there is not an ESS, i.e.,the branching criterion is

$$\frac{\xi_n}{\xi_v} > \sqrt{1 + \frac{\omega}{\phi_0 V_c}}. \qquad \textbf{[20]}$$

Diversification in the General Case

The general case of arbitrarily scaled trait evolution rates, k_n and k_v, is significantly more difficult than when $k_v \gg k_n$. For two-dimensional flows, the use of graphical pairwise invasibility plots (5) for determining evolutionary branching is no longer practical. Under certain circumstances, the solution of an evolutionary fixed point may undergo a Hopf bifurcation depending on the relative trait evolution rates. In higher dimensions (such as in coevolutionary dynamics) the asymptotic stability of an evolutionary fixed point (x_c, y_c) is determined by the Jacobian (6)

$$J = \begin{bmatrix} k_n \frac{\partial F_n}{\partial x} & k_n \frac{\partial F_n}{\partial y} \\ \\ k_v \frac{\partial F_v}{\partial x} & k_v \frac{\partial F_v}{\partial y} \end{bmatrix} |_{(x=x_c, y=y_c)}, \qquad \textbf{[21]}$$

where

$$F_n = \frac{\partial r_n'(x'; x, y)}{\partial x'}|_{x'=x}; \qquad F_v = \frac{\partial r_v'(y'; x, y)}{\partial y'}|_{y'=y}.$$

Evaluation of second partial derivatives leads to the following form for the Jacobian of the adaptive dynamics model whose mutant fitness values are presented in Eqs. **15** and **16**,

$$J = \begin{bmatrix} [-\frac{\omega}{\xi_n^2} + \phi_0 V_c(\frac{1}{\xi_v^2} - \frac{1}{\xi_n^2})]k_n & -\frac{\phi_0 V_c}{\xi_v^2} k_n \\ \\ \frac{\omega}{\xi_v^2} k_v & -\frac{\omega}{\xi_v^2} k_v \end{bmatrix}. \qquad \textbf{[22]}$$

The condition for asymptotic stability is that $\mathrm{Tr}J < 0$ and $\mathrm{Det}J > 0$. When the one-dimensional system is a local ESS satisfying Eq. **19**, algebraic manipulation reveals that both diagonal terms of the two-dimensional Jacobian are negative, and hence the two-dimensional evolutionary fixed point

is a stable node independent of the mutation rates (k_n, k_v). The co-ESS condition is the same as in the case of fast viral mutagenesis: $\xi_n/\xi_v < \sqrt{1+\frac{\omega}{\phi V_c}}$. However when the evolutionary fixed point of the one-dimensional system is not locally evolutionarily stable, then algebraic manipulation of the two-dimensional Jacobian reveals that the diagonal terms are of opposite signs. We must then replace the prior condition for branching, Eq. **20**, with the following:

$$\left(\frac{\xi_v}{\xi_n}\right)^2 > \frac{\omega/(\phi_0 V_c) - k_v/k_n}{\omega/(\phi_0 V_c) + 1}. \qquad \textbf{[23]}$$

References

[1] Chao, L., Levin, B. R. & Stewart, F. M. (1977) *Ecology* **58**, 369–378.

[2] Beretta, E., Solimano, F. & Tang, Y. (2002) *Discrete Continuous Dyn. Syst.* **2**, 495–520.

[3] Brauer, F. & Castillo-Chavez, C. (2001) *Mathematical Models in Population Biology and Epidemiology* (Springer, New York).

[4] Dieckmann, U. & Law, R. (1996) *J. Math. Biol.* **34**, 579–612.

[5] Geritz, S. A. H., Metz, J. A. J., Kisdi, E. & Meszéna, G. (1997) *Phys. Rev. Lett.* **78**, 2024–2027.

[6] Dieckman, U., Marrow, P. & Law, R. (1995) *J. Theor. Biol.* **176**, 91–102.