Adaptive Dynamics Course
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The Evolution of Virulence – II

A population of hosts grows, in absence of the disease, according to the simple model

$$\frac{dN}{dt} = \left[b(N) - d\right]N \tag{1}$$

where N is population density, $b(N)$ is the density-dependent birth rate, and d is the death rate. We consider a disease that causes lifelong infection (no recovery). Infected individuals die at a rate $d + \alpha$, where α, the extra mortality caused by the disease, is called the *virulence*. All individuals are born free of the disease. The disease is transmitted between infected and susceptible individuals at rate β, such that the dynamics of susceptible (S) and infected (I) individuals are given by

$$\begin{aligned} \frac{dS}{dt} &= b(N)N - \beta SI - dS \\ \frac{dI}{dt} &= \beta SI - (d+\alpha)I \end{aligned} \tag{2}$$

with $N = S + I$.

The disease increases the rate of mortality because the pathogen is using resources to multiply in the body of the host and because it produces symptoms (such as coughing, bleeding, etc.) which enhance its transmission to other host individuals. Faster replication in the body and more symptoms ensure a higher transmission rate but cause higher mortality as well. We thus assume that β is an increasing function of virulence. Note however that β cannot exceed the contact rate between individuals, hence the function $\beta(\alpha)$ will saturate for large values of α. Different strains of the pathogen differ in their virulence, α, and in the associated transmission rate, $\beta(\alpha)$. We say that a strain is *viable* if it can spread in a disease-free population.

In this project, we study the consequences of *superinfection.* When superinfection occurs, a second strain of the pathogen infects an already infected host. Because more virulent strains replicate better in the body, it is expected that more virulent strains generally replace the less virulent strain within the host. We assume that the within-host dynamics is fast such that this replacement can be considered instantaneous. Upon superinfection, strain α_2 takes over a host infected by strain α_1 with probability $\rho(\alpha_2 - \alpha_1)$, where ρ is an increasing function.

There are very interesting results on different evolutionary scenarios depending on whether ρ is continuous or not and whether it is continuously differentiable or not. For example, a discontinuous function results if we take the within-host dynamics to be fully deterministic, such that even a slightly more virulent strain always wins. In this project however we make the mathematically most straightforward assumption that ρ is a smooth function. With this assumption, less virulent strains may win against more virulent ones with some small probability ($\rho(\alpha_2 - \alpha_1)$ is small but still positive when $\alpha_2 < \alpha_1$). This can be justified by stochastic effects within the host body.

When a mutant strain with virulence α_{mut} appears in the population infected by strain α, but the density of hosts infected with the mutant strain is still low, the dynamics of mutant-infected hosts are given by

$$\frac{dI_{mut}}{dt} = \beta(\alpha_{mut}) I_{mut} \hat{S} - \left[d + \alpha_{mut} \right] I_{mut} + \\ + \beta(\alpha_{mut}) \rho(\alpha_{mut} - \alpha) I_{mut} \hat{I} - \beta(\alpha) \rho(\alpha - \alpha_{mut}) I_{mut} \hat{I} \tag{3}$$

where $\hat{S}$ and $\hat{I}$ are the density of susceptible and of infected individuals, respectively, in the equilibrium population with the resident strain, as determined from equations (2) with virulence α and transmission rate $\beta(\alpha)$. The first term in equation (3) describes infection of susceptibles by the mutant pathogen, and the second term is death (natural plus disease-induced). The third term corresponds to superinfection by the mutant strain, when it is infecting and taking over hosts already infected with the resident strain. The last term is the loss of mutant-infected hosts due to superinfection with the resident strain.

For numerical work, assume that the disease-free population grows logistically, i.e., $b(N) = a - cN$. Use $\rho(\alpha_2 - \alpha_1) = 1 / \left[1 + v \exp\left(-k(\alpha_2 - \alpha_1) \right) \right]$ for the superinfection function, choosing parameters such that $\rho(0)$ is small (equally and less virulent strains do not take the host over too often). For the transmission rate, start with $\beta(\alpha) = \gamma / \left[1 + \eta \exp(-\kappa\alpha) \right]$ (you can explore other functions later).

Construct PIPs and show that two strains of the pathogen can coexist (remember to study only viable strains). Investigate the singular strategy and its stability properties; find examples for evolution to an ESS and for evolutionary branching. Construct the isocline plot in an example with evolutionary branching to explore the coevolution of two strains. Study the effect if *k*, the steepness of the superinfection function ρ, on the dynamics of evolution.