Analytic model of Nature v Nurture

Ben Phillips

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A haploid model

We imagine the simplest case, in which we have a single, biallelic locus in a haploid genome, with allele A conferring immunity from the threat, and allele a conferring susceptibility. Because individuals carrying A are immune to the threat, they cannot be trained. Individuals with a however, can receive cultural conditioning and so some portion of individuals with a survive to reproduce.

We treat time as discrete, and following mutation, birth, training, and death (in that order), we find the following recursions.

$$n_A(t+1) = b(1-d)(1-m)n_A(t) \tag{1}$$
$$n_a(t+1) = bT(1-d)(n_a(t) + mn_A(t)) \tag{2}$$

Where b is number of births, d is the probability of death, T is the probability of cultural transmission (the probability of an $a+$ individual passing on its $+$ status), and m is the mutation rate. For simplicity, we have defined mutation as being asymmetric: it is possible to lose function (by $A \to a$), but not to gain function through the oposite transformation.

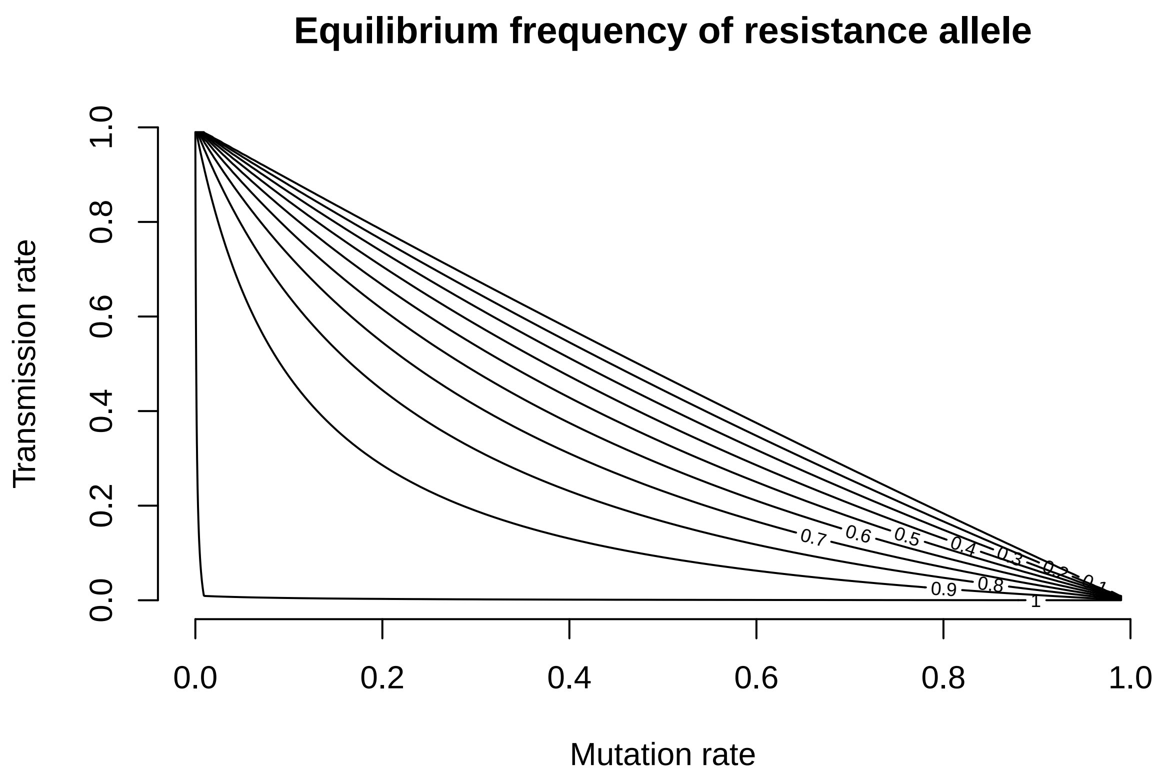
By setting $p(t) = \frac{n_A(t)}{n_A(t)+n_a(t)}$ we can define a recursion for a single variable, $p(t)$, the frequency of the resistance allele in the population.

$$p(t+1) = \frac{(1-m)p(t)}{(1-m)p(t) + T(1-p(1-m))}$$

We then look for the equilibrium values of this recursion, $\hat{p}$ which occur when $\Delta p = p(t+1) - p(t) = 0$. Working through this, and ignoring the trivial equilbrium at $\hat{p} = 0$, we find that

$$\hat{p} = \frac{1-m-T}{(1-m)(1-T)}.$$

This equilibrium is only valid when $m + T \leq 1$. We can immediately see that if mutation is not permitted ($m = 0$), the resistance allele will run to fixation. To get a sense of how this equilibrium looks when there is mutation (within the permitted parameter space), we can plot it as a surface describing $\hat{p}$ at various combinations of m and T.



Equilibrium frequency of resistance allele
Transmission rate
Mutation rate
0.0
0.2
0.4
0.6
0.8
1.0
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.9
0.8
1