

S4 - mathematical supporting information for Smart & Phillips (2020). Optimizing targeted gene flow to maximize local genetic diversity: when and how to act under various scenarios of environmental change.

Frequency of favourable alleles required to optimally adapt an individual to management time M .

We model the environmental trait optimum at a given management time unit (v_M), by the sigmoidal relationship:

$$v_M = \frac{2c}{1 + \exp(-m(M - (\frac{M}{2})))} \quad (1)$$

Where c represents a number of standard deviations of the trait mean, M our management time unit, and m a constant that controls the gradient of state change in the system. Thus by changing either c or m we can explore varying demographic pressures (see main text). Our aim here is to define the frequency of favourable alleles required to adapt an introduced population to management time. Individuals have maximum fitness when their trait value at management time, z_M , closely matches to the environmental optimum of that management time step, v_M , i.e. when $z_M = v_M$.

Individuals are adapted to a management time point, dictated by the number of favourable alleles (f_M) present across all biallelic, phenotypic influencing loci ($2n_p$):

$$z_M = 2f_M n_p \cdot d \quad (2)$$

Each of these alleles contributes a certain amount to their trait value dictated by an effect size, d :

$$d = \sqrt{\frac{h^2 V_E}{2n_p f_M (1 - h^2)(1 - f_M)}}$$

Each locus with phenotypic effects (within n_p) has an equal and additive effect on the individuals expected trait value, $E(z)$. Two alleles are possible at each locus, with alleles having a value of either 0 or d , where $d > 0$. This additive effect size d is calculated as a function of the environmental variance (V_E), the trait heritability (h^2), and is chosen such that the stated heritability is achieved at initialization (given V_E , n_p , and the initial frequency of alleles with effect size d , f):

$$V_G = \frac{h^2 V_E}{1 - h^2}$$

As we have defined v_M above (1), and noting (2), we then equate and solve to find the frequency of alleles required to adapt an individual to a future management time unit, $\hat{f}_M$:

$$2f_t n_p \cdot \sqrt{\frac{h^2 V_E}{2n_p f_t (1 - h^2)(1 - f_t)}} = \frac{2c}{1 + \exp(-m(t - (\frac{t}{2})))}$$

Given an input value for m and c , we simplify the above resulting in an equation which describes the proportion of loci required to house a beneficial allele in order to adapt an introduced cohort to a future management time unit, $\hat{f}$:

$$\hat{f}_M = \frac{v_M^2}{2n_p V_G + v_M^2}$$