

Two neat “genetic architecture hacks”:

Effective migration rates with complete divergence

For L divergently selected loci with selection and dominance coefficients s_i and h_i , $i = 1, \dots, L$, where the two populations are near complete fixation for their respective locally beneficial allele, we get, at position x in the genome, the following expression for m_e :

$$m_e(x) = m \times \exp \left(- \sum_{i=1}^L \frac{s_i h_i}{m + r(x, x_i) + s_i h_i} \right)$$

This will be a reasonable approximation as long as $N_e sh \gg m$ and $N_e sh \gg 1$, so that selection is much stronger than both drift and migration.

This can be obtained by considering the reproductive value of a migrant individual in the resident background, or by an *ad hoc* extrapolation of two-locus theory to the multi-locus setting, see Barton and Bengtsson (1986), Aeschbacher et al. (2017), Sachdeva (2022), Zwaenepoel, Sachdeva, and Fraïssé (2024).

Effective population size under BGS

In the “background selection regime” (see Good et al. (2014)), we can use the following expression (Hudson and Kaplan 1994):

$$N_e(x) = N \times \exp \left(- \sum_{i=1}^G \frac{u_i}{s_i \left(1 + r(x, x_i) \frac{(1-s_i)}{s_i} \right)^2} \right)$$

Where there are G sites with recurrent deleterious mutations at rate u_i and (haploid) selection coefficient s_i , $i = 1, \dots, G$. This should hold more or less whenever it provides reasonable N_e ’s – see Good et al. (2014), Buffalo and Kern (2024).

This can be derived, more or less, from the structured coalescent, where the different subpopulations are deleterious backgrounds, see Hudson and Kaplan (1994), Charlesworth, Nordborg, and Charlesworth (1997), Nordborg (1997), Charlesworth and Charlesworth (2010), Good et al. (2014), Santiago and Caballero (1995), Santiago and Caballero (1998), Santiago and Caballero (2016), Buffalo and Kern (2024).

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