
Constructing the Tolerance-Fecundity Trade-Off Model

Here, we show that Muller-Landau’s (2010) tolerance-fecundity trade-off model arises from equation (6) of the main text when a simpler picture of seed tolerance is assumed.

First, we must convert the sum over sites to a sum over fecundities. This can be done for the following reason: sweeping over the stress axis is equivalent to sweeping over fecundity values, as each stress level is the threshold associated with a given fecundity. Mathematically, we can always write

\[ \int (\text{integrand})\,ds = \int (\text{integrand})\,dx. \]

In our case, we will write

\[ \int_{s_m}^{s_o} \frac{r(s)T(s,f)}{\int_0^{\gamma} y\gamma T(s,y)\,dy} \,ds = -\int_{s_m}^{s_o} \frac{h(x)g(x,f)}{\int_0^{\gamma} y\gamma g(x,y)\,dy} \,dx. \]  

(A1)

where \( s_o \) and \( s_m \) are the thresholds of the least and most tolerant species, respectively. The left-hand side of equation (A1) is simply the integral term in equation (6) (main text) with the stress threshold explicitly used as the integration variable, and the functions \( h(x) \) and \( g(x,f) \) are defined to have the properties

\[ h'(x)\,dx = r(s)\,ds, \]
\[ g(x,f) = T(s(x),f), \]

where \( s(x) \) is the stress threshold of the species with fecundity \( x \). Finally, the minus sign arises because of the change in the limits of the integration given the inverse relationship between stress thresholds and fecundity: \( \int_{s_m}^{s_o} \,ds \rightarrow \int_{s_m}^{s_o} \,dx = -\int_{s_m}^{s_o} \,dx \).

To see what \( h(x) \) means, let us write \( r(s) \) as \( d\gamma/ds \), where \( \gamma(s) \) is some function of \( s \). Then, using the chain rule, we see that

\[ \frac{dh}{dx} = \frac{d\gamma}{ds}, \]

whereby we can say \( h(x) = \gamma(s(x)) \). The function \( \gamma \) is easily interpretable: \( \gamma(s) = \int r(\sigma)\,d\sigma \), that is, \( \gamma(s) \) is the total proportion of sites in the community whose stress level is equal to or less than \( s \). The function \( h(f) \), then, is the proportion of land whose stress level is equal to or less than the threshold of species \( f \). Its functional form is determined by both the environment and the biology of the organisms, as it depends on the distribution of stress in the land and on how a given fecundity translates to its stress threshold. Notice that the tolerance-fecundity trade-off, which comprises the essence of the model, requires that \( h(f) < 0 \) for all values of \( f \).

The function \( g \) is just a renaming of function \( T \) and is not hard to interpret: just as \( T(s(x),f) \) is the probability that species \( f \) can tolerate in a site with stress \( s \) (which is the threshold of species \( x \)), \( g(x,f) \) is the probability that species \( f \) can tolerate a site whose stress level is the threshold of species \( x \). Notice that, for fixed \( f \), \( g(x,f) \) is a forward sigmoid function of \( x \), while \( T(\sigma,f) \) is a backward sigmoid function of \( \sigma \) (i.e., \( g \) starts low and transitions to 1 as \( x \) increases, while \( T \) shows the opposite behavior with increasing \( \sigma \)). We change notation from \( T(\sigma,f) \) to \( g(x,f) \) to highlight this shift of focus from sites to species, which flips the function.
Appendix A from R. D’Andrea et al., Revising the Tolerance-Fecundity Trade-Off

Having justified all terms in equation (A1), we can now render our model in the form

\[
\frac{dp}{dt}(f) = m \left( -f \int_{f_0}^{f_m} \frac{h'(x)g(x,f)}{\int_y^x yp(y)g(x,y)dy} \, dx - 1 \right) p(f). \tag{A2}
\]

If we further assume that all species have a similar transition regime around their specific stress threshold, then the transition function becomes a function of a single variable, \( g(x - f) \). Although this greatly simplifies things, such an assumption unfortunately has no a priori biological foundation. It is, however, implicitly used by Muller-Landau, and we apply it here to show the compatibility between the models. With that assumption, equation (A2) reads

\[
\frac{dp}{dt}(f) = m \left( -f \int_{f_0}^{f_m} h'(x)g(x,f) \, dx - 1 \right) p(f). \tag{A3}
\]

In Muller-Landau (2010), the transition function is the unit step function \( \Theta(x - f) \) (which is 1 for positive arguments and 0 otherwise): \( g(x - f) = \Theta(x - f) \). In biological terms, this means that species with fecundity values \( x \) equal to or higher than that of the focal species with fecundity \( f \) can tolerate sites whose stress level is that of the focal species with probability 1, and species whose fecundity \( x \) is less than \( f \) cannot tolerate that stress level at all. Thus, equation (A3) finally becomes

\[
\frac{dp}{dt}(f) = m \left( -f \int_{f_0}^{f_m} \frac{h'(x)}{\int_y^x yp(y)dy} \, dx - 1 \right) p(f), \tag{A4}
\]

which is Muller-Landau’s model put in the context of a continuum of species.