

Salmon straying description

Model Description

Some expectations and intents of the model: Here we consider two populations: a local population N_i and a remote population N_j . The populations each have a trait value x_i and x_j that evolve over time, and directly ‘sets’ the maximum recruitment rate (the rate of recruitment at low population densities). Each population in its respective site has an optimum trait value θ_i where the rate of recruitment is maximized if $x_i = \theta_i$. If there is no straying between these populations (such that they are independent), then the trait value should evolve towards the optimum ($x_i \rightarrow \theta_i$) and the recruitment rate will become maximized. If there is straying between populations at rate m , then the traits in each respective location will be pulled away from the optimum, and recruitment rates will be lower, i.e. have lower fitness. As m becomes large, the populations should act as a single population.

Using the discrete population framework from Shelton and Mangel (2011), we have the following population dynamic equation for a local population i and the population that is straying into it j .

$$N_i(t+1) = (N_i(t) - mN_i(t) + mN_j(t)) e^{-Z} + \left((R_i[\mu_i(t)|\theta_i] + \tilde{P})(N_i(t) - mN_i(t)) + (R_i[\mu_j(t)|\theta_i] + \tilde{P})mN_j(t) \right) e^{-\beta(N_i(t) - mN_i(t) + mN_j(t))} \quad (1)$$

where the first line determines the number of individuals that survive from time t to time $t+1$, and the second and third line accounts for the recruitment of individuals from the surviving population from time t to time $t+1$. Moreover, there is a demographic process error term included in the above dynamic equation, where $\tilde{P} \sim \mathcal{N}(0, s)$ where in the below example $s = 0.001$

Survival: the probability of survival is e^{-Z} ... if $Z = 0.5$ (Shelton and Mangel 2011), the probability of survival is 60%. This survival probability is enacted on 1) The number of local individuals that return minus the number local individuals that stray ($N_i(t) - mN_i(t)$), in addition to the number of remote individuals that immigrate into the local patch $mN_j(t)$, and it is assumed that they all have equal probability of surviving.

Recruitment: The second line of the equation determines the recruitment from local individuals $N_i(t) - mN_i(t)$ and incoming strays $mN_j(t)$, as a function of their mean trait value at time t and given the local trait optimum θ_i , where the recruitment rate at low population densities is

$$R_i[\mu_i(t)|\theta_i] = \int_{-\infty}^{\infty} r_{\max} \exp \left\{ -\frac{(x_i(t) - \theta_i)^2}{2\tau^2} \right\} \text{pr}(x_i(t)|\mu_i, \sigma^2) dx_i(t) \\ = \frac{r_{\max}\tau}{\sqrt{\sigma^2 + \tau^2}} \exp \left\{ -\frac{(\theta_i - \mu_i(t))^2}{2(\sigma^2 + \tau^2)} \right\}. \quad (2)$$

This means that it is the mismatch between the trait mean $\mu_i(t)$ and the local optimum θ_i that determines the growth rate at low population densities.

The third line of the equation determines recruitment from straying individuals (with density $mN_j(t)$), such that the recruitment rate is determined by the mismatch between the optimum trait value θ_i and the mean trait value of the incoming individuals μ_j .

As shown above, the mean traits of both populations (the local mean trait value μ_i as well as the remote mean trait value μ_j) also change through time. Because individuals from the local population are being mixed with individuals from the remote population, the resulting trait distribution is a mixed normal. We assume that the distribution that results after the remote and local populations are mixed together *and reproduce* is normal with a mean value determined from a mixed-normal distribution and constant variance over time. This assumption may be tested a few different ways if we deem it necessary down the road - as a first order approximation, it's probably fine. The mean trait value thus changes through time according to the difference equation

$$\mu_i(t+1) = w_i\mu_i(t) + (1 - w_i)\mu_j(t) + \frac{\partial}{\partial \mu_i} \ln (w_i R_i[\mu_i(t)|\theta_i] + (1 - w_i) R_i[\mu_j(t)|\theta_i]) \quad (3)$$

where

$$w_i = \frac{N_i(t) - mN_i(t)}{N_i(t) - mN_i(t) + mN_j(t)}. \quad (4)$$

The first two factors in equation ?? determine the mixed normal average of the now-mixed local and remote populations. This mixed normal is weighted by the proportion of the population that is local and remote, respectively, which depends on the stray rate m . The third part of the above equation determines how the mean trait changes through time due to natural selection (from Lande), which is proportional to the change in mean fitness with respect to the mean trait (phenotype).

You can see from the elements of the difference equations that demographics directly impact the evolution of trait means due to how the local and remote trait averages at time t contribute to the trait mean at time $t + 1$.

I. RESULTS

Initial results – subject to to change: As the proportion of strays increases, the average traits of both populations veer farther from their optimal values, and this results in the decline of the population steady state (because the recruitment rate is now sub-optimal for both populations). This is the nice, expected result.

The unexpected result are the alternative stable states that arise for lower values of m . Just where these alternative stable states arise depends on the variance as well as the difference in optimal trait values between sites ($\theta_1 - \theta_2$), but you can see that this has big impacts on the portfolio effect. Which trajectory goes to the higher or lower alternative stable state is random - an effect of the process noise injected into the system. The change in the PE appears to be caused by large spikes in the variance of individual population trajectories where the alternative stable states begin (at the fold bifurcation). This is a well-known phenomenon that forms the basis for early warning signals of phase transitions.

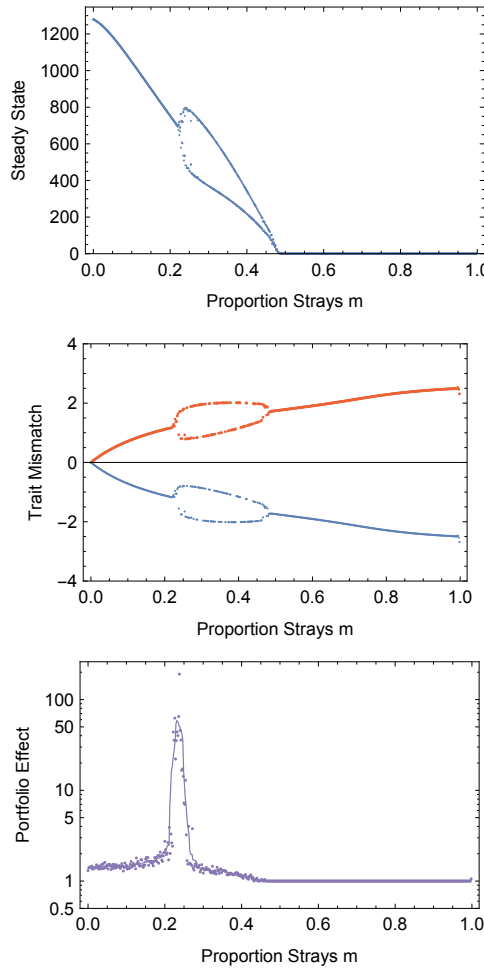


Figure 1:

The differences in optimal trait values between sites ($\theta_1 - \theta_2$) influence at what straying rate the alternative stable states appear. Large differences in θ_1 and θ_2 can be interpreted as high environmental heterogeneity. A cursory analysis shows that increasing environmental heterogeneity tends to lower the stray rate value m^* at which the maximum PE is expected to occur. Moreover, if the trait variance is much larger than the difference in optimal trait values between sites (such that selection is weaker), the alternative stable state phenomenon disappears, as does the spike in the portfolio effect.

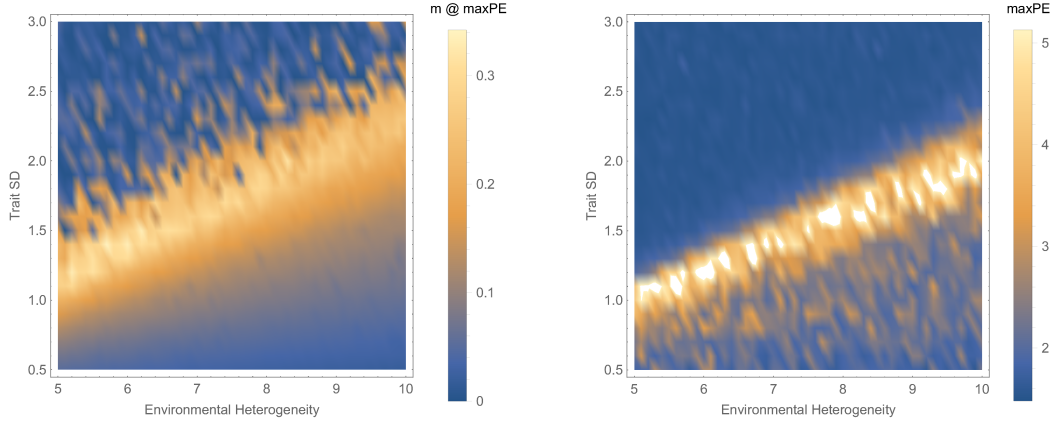


Figure 2:

II. DISCUSSION