Relationship of Environment and Growth Rate Equations to Determining Average Growth Rate

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When the time to fixation >>> than the time to change environments, the growth rate of an organism in the varying environments is simply the average growth rate across all environments (Desai 2015). I will introduce the notation used, its general meaning, and how it relates to our specific project. We define a function, x(t), that defines the environment as a function of time t. In our case, our function x(t), is the concentration of Pyrimethamine as a function of time t. From there, we define another function m(t), which defines the growth rate as a function of time t. We can redefine the function m(t) to be a function of the environment x(t) such that m(t) = m(x(t)). In our case, the function m(t) is the function that determines the logistic curve and allows us to calculate growth rate of an allele at any concentration, x. This function m(x(t)) in our case is dependent on three parameters, $R00,IC_{50}$, and c. These functions are displayed below.

$$x(t) = (11.193e^{-0.40051(t \bmod{168})} + 0.1723e^{-0.006777(t \bmod{168})} -11.364e^{-0.4146(t \bmod{168})}) * \frac{1}{248710}$$
(1)

$$m(x(t)) = \frac{R_{00}}{1 + \exp\left(\frac{IC_{50} - x(t)}{c}\right)}$$
(2)

We calculate time-averaged fitness with the following formula:

$$\overline{m} = \frac{1}{\tau} \int_0^\tau m(x(t))dt \tag{3}$$

In the above equation, we integrate over all possible growth rate values as a function of time and then divide that by the total time τ to obtain the average growth rate value.

Thinking further on this, we don't even need to know the specific formula for x(t). Rather, we just need to know the probability density function of the environment (i.e. the probability that the environment is of value y).

However, in our particular case, our environment solely consisted of one parameter: Pyrimethamine concentration. We can imagine that environments might consist of multiple parameters (e.g. temperature and pressure). Thus, we would like to generalize our approach. In the case of two parameters x_1 and x_2

$$m(x(t)) = m(x_1(t), x_2(t))$$

Thus, to calculate the average fitness, we calculate the growth rate over all possible combinations of environments. In order to do this, we would need to know the joint probability density of $x_1(t), x_2(t)$. We can imagine a 3-D plot of growth rate as a function of t_1 and t_2 . To find the average value, we would integrate over one of the axes, t_1 and then the other, t_2 , and calculate the average (similar to finding the volume of a surface).

$$\overline{m} = \frac{1}{\tau_1 * \tau_2} \int_{t_1=0}^{\tau_1} \left[\int_{t_2=0}^{\tau_2} m(x_1(t), x_2(t)) dt_1 \right] dt_2$$

This can be generalized up to n parameters.

$$\overline{m} = \frac{1}{\tau_1 * \tau_2 * \dots * \tau_n} \int_{t_1=0}^{\tau_1} \int_{t_2=0}^{\tau_2} \dots \int_{t_n=0}^{\tau_n} m(x_1(t), x_2(t), \dots, x_n(t)) dt_1 dt_2 \dots dt_n$$