Laws of Adaptation

A course on biological evolution in eight lectures

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Lecture 8

Ways to diversity, or polymorphic LTE

Part II – continuous traits

Wednesday October 18, 16:00-17:00

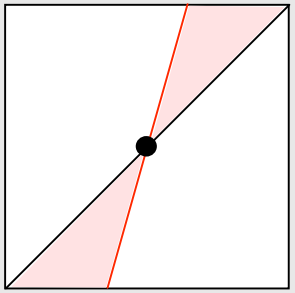
Possibility of polymorphic LTE for a continuous trait

- The previous situation is the first case where we have met a genuine polymorphic LTE and, as we have seen, it coincides exactly with the ESS predicted under the same selection regime, in the same way as the monomorphic LTE we have considered before coincide exactly with fitness maxima or ESS, independently of the genetics of the trait
- On the other hand, in the previous situation, the dimorphism was in a sense already "embedded" in the genetics (or developmental rules) of the trait, while long-term evolution essentially only contributes to "adjust" the phenotypic frequencies to their adaptively best value
- We now investigate whether similar dimorphisms can emerge from the evolution of a continuous trait, assuming the same frequency dependent selection regime we have already considered, characterized by random pair wise interactions, with payoff function $\upsilon(x',x)$. Moreover, we assume that υ has a stationary point with respect to x' at $x'=x=x^\circ$, and consider an interval $(x^\circ-d,x^\circ+d)$ sufficiently small that we can approximate $\upsilon(x',x)-\upsilon(x,x)$ by a quadratics in (x',x), by Taylor expansion about x°:

$$\upsilon(x',x)-\upsilon(x,x)=\left[A(x'-x)+2(A+B)(x-x^\circ)\right](x'-x)+o\left(d^2\right) \quad , \quad A=\frac{1}{2}\frac{\partial^2\upsilon(x',x)}{\partial x'^2}\bigg|_{x'=x=x^\circ} \quad , \quad B=\frac{1}{2}\frac{\partial^2\upsilon(x',x)}{\partial x'\partial x}\bigg|_{x'=x=x^\circ}$$

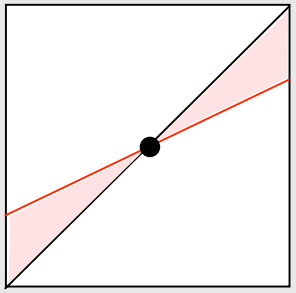
- Consider the following configurations:

I: A<0 ; A+2B> -A

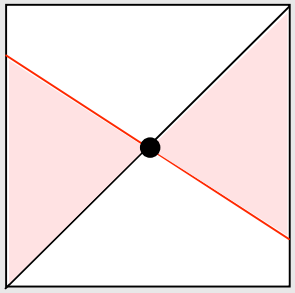


LTE
not continuously stable

II: A<0 ; 0<A+2B< -A

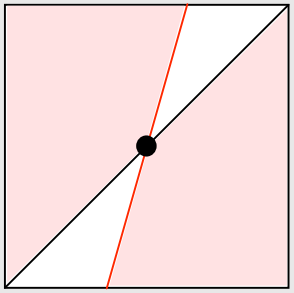


III: A<0 ; A+2B<0



LTE
continuously stable

IV: A>0 ; A+2B<B<0



not LTE
continuously stable

- In the fourth case, $x'=x=x^\circ$ is a point of minimum of $\upsilon(x',x)$ with respect to x'. It is an *evolutionarily singular point* (Geritz et al, 1998) to which long term evolution of a continuous trait tends to converge, but that can be invaded by any mutant, and in its vicinity a polymorphism is necessarily established
- An evolutionary state of this kind has been called: *polymorphic evolutionarily attractive state* (*PEAST*) by Christiansen (1991), from a population genetics perspective, and *branching point* by Geritz et al. (1998), from a non genetic, ecological point of view, because a population of clonally reproducing organism (asexual reproduction) splits in two lineages at such points
- These singularities are identified by the following conditions:

$$\left.\frac{\partial \upsilon(x',x)}{\partial x'}\right|_{x'=x=x^\circ} = 0 \quad , \quad \left.\frac{\partial^2 \upsilon(x',x)}{\partial x'^2}\right|_{x'=x=x^\circ} > 0 \quad , \quad \left.\frac{\partial^2 \upsilon(x',x)}{\partial x'^2}\right|_{x'=x=x^\circ} + \left.\frac{\partial^2 \upsilon(x',x)}{\partial x' \partial x}\right|_{x'=x=x^\circ} < 0$$

- The selective process in their neighborhood is called frequency dependent *disruptive selection*
- We now investigate the long term evolution of a trait near such a point

Long term evolution of a trait near a PEAST (Matessi and Gimelfarb, 2006)

- Assume a trait that can vary in the finite interval [-1,1]
- Selection on the trait depends on random pair wise contests with payment function

$$\upsilon(x',x) = 1 + \alpha x'^2 - (\alpha+\beta)xx' + \beta x^2 \quad , \quad 0 < \alpha < \beta$$

- The limitations on α and β are necessary and sufficient for this selection regime to have a PEAST at $x°=0$
- In a population where the trait has mean $\bar{x}$ and variance s^2 the fitness of an individual of trait value x, and the population mean fitness are, respectively,

$$W(x) = W(x,\bar{x},s^2) = 1 + \alpha x^2 - (\alpha+\beta)\bar{x}x + \beta(\bar{x}^2 + s^2)$$

$$\bar{w} = \bar{W}(\bar{x},s^2) = 1 + (\alpha+\beta)s^2$$

- Notice that the mean fitness increases as the phenotypic variance in the population increases
- Notice also that in a population where the mean trait value is zero, an individual of trait value x would have greater fitness than the average population member if and only if $x^2 > s^2$; thus, if such individuals were to increase in frequency, the variance, and therefore the mean population fitness would tend to increase
- Maximum variance ($s^2=1$) and fitness would been achieved in a population containing only the two extreme trait values, (-1,1), with equal frequencies, a composition that corresponds to the unique ESS of the population game with payoff matrix

$$\begin{pmatrix} \upsilon(-1,-1) & \upsilon(-1,1) \\ \upsilon(1,-1) & \upsilon(1,1) \end{pmatrix}$$

- If the trait were controlled by one gene and only these two trait values could be expressed, this population would therefore be at the LTE of the model discussed previously (the manifold $L(h^*) = L(\frac{1}{2})$)

- Assuming that the continuous trait is controlled by one gene, its long term evolution has been investigated numerically according to the following prescriptions:

  (i) start from a monomorphic population with trait value chosen at random in [-1,1]; let AA be the corresponding genotype

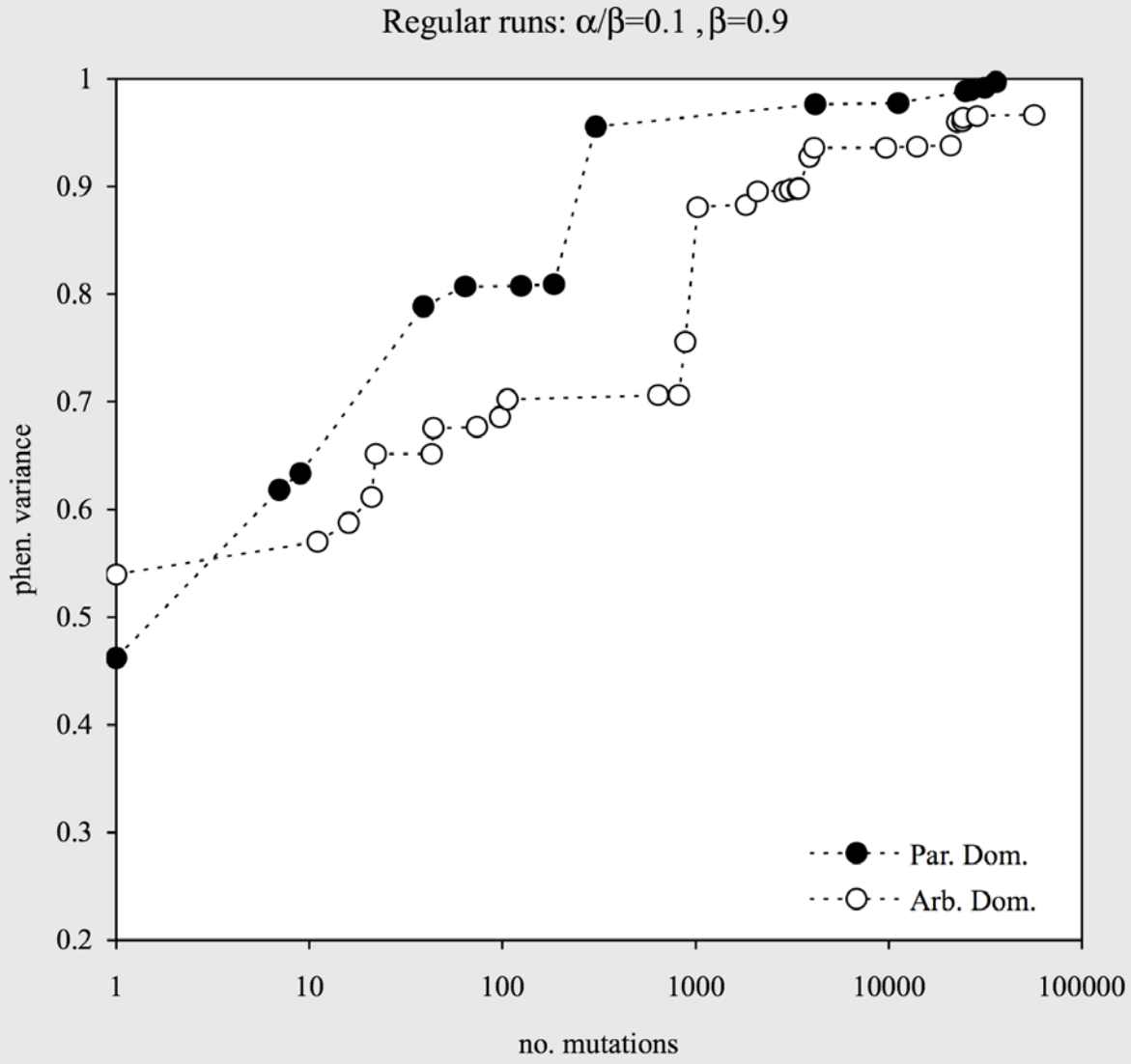
  (ii) introduce a mutant allele A′ at a small frequency (2×10^{-7}) and assign to all new genotypes, carrying the mutant allele, trait values chosen at random in [-1,1], either without restrictions (*arbitrary dominance*, AD), or with the condition that the trait value of an heterozygote is bounded by the trait values of the corresponding homozygotes (*partial dominance*, PD)

  (iii) iterate the recursion equations of the short term dynamics till apparent equilibrium (change of gene frequencies $\leq10^{-12}$ in one generation) is attained; to avoid spurious accumulation of alleles discard any allele that has a frequency $\leq10^{-7}$; if any change has occurred in the population, it is considered that a successful invasion has taken place

  (iv) repeat the procedure from point (ii) above for a large number of cycles (at least 10^5 but most of the time 10^6 or more)

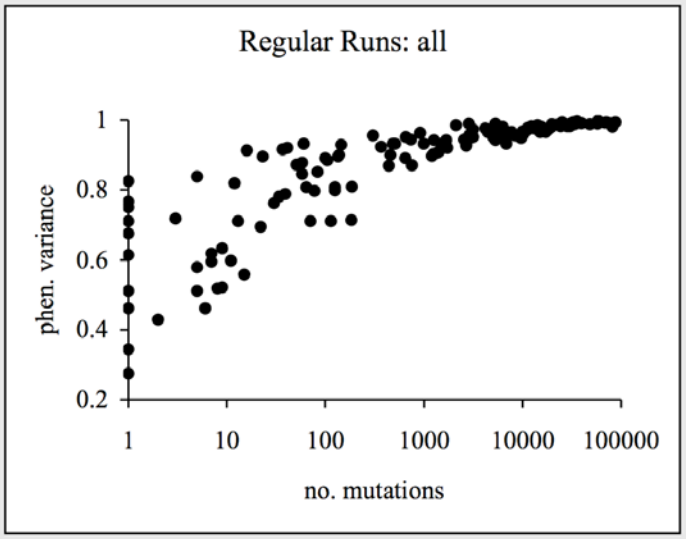
  (v) computation runs have been executed for a number of values of the selection parameters (α,β) and runs with any given combination of parameter values have been replicated

An example:

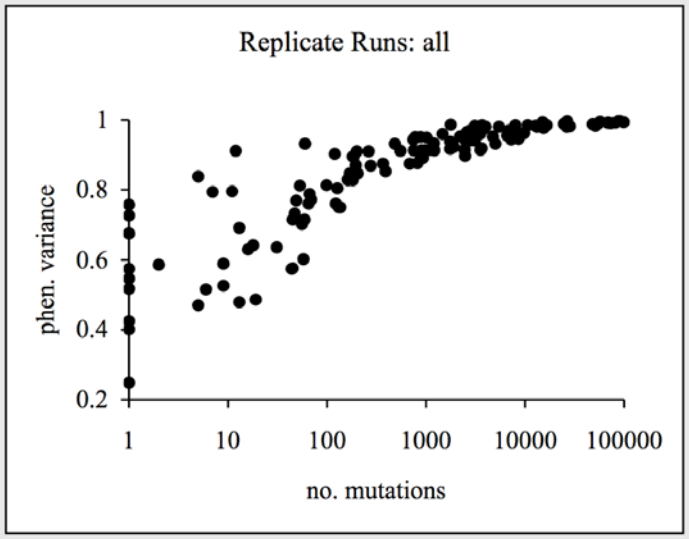

Regular runs: α/β=0.1 , β=0.9
phen. variance
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
1
10
100
1000
10000
100000
no. mutations
Par. Dom.
Arb. Dom.

Results

- In all runs (except one with AD) at termination the mean was in absolute value less than 10^{-3} and the variance exceeded 0.95, indicating that the $L\left(\frac{1}{2}\right)$ manifold had been almost attained
- In this respect there was no essential difference between AD and PD, except that with PD evolution was faster
- The terminal genetic configuration – number of alleles and dominance relations between alleles – was very variable among runs; the number of alleles varied between 2 and 3 with PD, between 4 and 7 with AD. This indicates that once the $L\left(\frac{1}{2}\right)$ manifold has been achieved, any genetic configuration supporting it is adaptively equivalent
- The specific values of the selection parameters, corresponding to different selection strength, had no perceptible influence on the course of long term evolution



collective scatter plot of ten runs with PD each with different values of the selection parameters



collective scatter plot of ten replicates of runs with PD with the same values of the selection parameters

$$W(x) = W(x, \bar{x}, s^2) = 1 + \alpha x^2 - (\alpha + \beta)\bar{x}x + \beta(\bar{x}^2 + s^2)$$
$$\bar{w} = \bar{W}(\bar{x}, s^2) = 1 + (\alpha + \beta)s^2$$

The $L\left(\frac{1}{2}\right)$ manifold is the unique LTE

- To prove this assertion we need to complement Lessard (1984), to account for the fact that in the present system mutations can generate all sorts of trait values different from the pair {-1,1}
- But from Lessard (1984) we already know that, when the population only contains trait values from {-1,1}: (i) $L\left(\frac{1}{2}\right)$ is a short term equilibrium if it can be reached; (ii) no mutation introducing trait values only from {-1,1} can perturb the population away from this manifold; (iii) no other short term equilibrium exists with this property
- Thus we only have to prove that mutations with trait values taken from the interval (-1,1) cannot invade L, and that no uninvadable equilibrium with such trait values exists
- Consider a population at a short term, one-gene polymorphic equilibrium with n alleles, $\{A_1,\ldots,A_n\}$, of frequencies $\hat{\mathbf{p}} = (\hat{p}_1,\ldots,\hat{p}_n)$, and suppose that a mutant allele A_0, of frequency $\varepsilon(t)\approx 0$ at generation t=0,1,…, is introduced
- The frequency of A_0 is subject to the recursion

$$\varepsilon(t+1) = \varepsilon(t)\frac{\bar{w}_0(\hat{\mathbf{p}})}{\bar{w}(\hat{\mathbf{p}})} + o(\varepsilon)$$

where $\bar{w}(\hat{\mathbf{p}})$ is the mean fitness of the resident population before introduction of A_0, and

$$\bar{w}_0(\hat{\mathbf{p}}) = \sum_{i=1}^{n} W(X(A_0A_i))\hat{p}_i$$

- Hence A_0 invades if $\bar{w}_0(\hat{\mathbf{p}}) - \bar{w}(\hat{\mathbf{p}}) > 0$ and is eliminated if $\bar{w}_0(\hat{\mathbf{p}}) - \bar{w}(\hat{\mathbf{p}}) < 0$
- Let $\bar{x}(\hat{\mathbf{p}})$ and $s^2(\hat{\mathbf{p}})$ be the mean and the variance of the trait in the resident population before introduction of A_0, and

$$\bar{x}_0(\hat{\mathbf{p}}) = \sum_{i=1}^{n} X(A_0A_i)\hat{p}_i \quad , \quad s_0^2(\hat{\mathbf{p}}) = \sum_{i=1}^{n} X^2(A_0A_i)\hat{p}_i$$

- Then: $$\bar{w}_0(\hat{\mathbf{p}}) - \bar{w}(\hat{\mathbf{p}}) = \alpha\left[s_0^2(\hat{\mathbf{p}}) - s^2(\hat{\mathbf{p}})\right] - (\alpha+\beta)\bar{x}(\hat{\mathbf{p}})\bar{x}_0(\hat{\mathbf{p}}) + \beta\bar{x}^2(\hat{\mathbf{p}})$$

- Suppose now that the resident population is at equilibrium on $L\left(\frac{1}{2}\right)$, so that the mean of the trait is zero and its variance is one, and consider any mutant allele A_0 such that $|X(A_0A_i)|\leq 1$, with *strict inequality* at least for some i=1,…,n.
- Clearly, $s_0^2(\hat{\mathbf{p}}) < 1$. Hence

$$\bar{w}_0(\hat{\mathbf{p}}) - \bar{w}(\hat{\mathbf{p}}) = \alpha\left[s_0^2(\hat{\mathbf{p}}) - 1\right] < 0 \quad \text{since} \quad \alpha > 0$$

  so that A_0 is eliminated, as we had to prove
- To complete the proof that $L\left(\frac{1}{2}\right)$ is a LTE we now should show that also mutant alleles A_0 such that $|X(A_0A_i)|=1$ for all i=1,…,n, but $|X(A_0A_0)|<1$, are eliminated; this case however is more cumbersome because first order approximation of the recursion for $\varepsilon(t)$ is no longer sufficient and one has to look at the second order approximation. For this reason the proof is avoided here, but can be found in the original article
- Now we show instead that there is no other LTE beside $L\left(\frac{1}{2}\right)$. Suppose, in fact, that the resident population is at an equilibrium which *is not* on $L\left(\frac{1}{2}\right)$, so that necessarily

$$\bar{x}(\hat{\mathbf{p}}) \neq 0 \text{ or } s^2(\hat{\mathbf{p}}) < 1 \text{ or both}$$

  and introduce a mutant allele A_0 with the properties that

$$\left|X(A_0A_i)\right| = 1 \quad \forall\, i = 1,\ldots,n \quad \Leftrightarrow \quad s_0^2(\hat{\mathbf{p}}) = 1 \quad \text{and} \quad \text{if} \quad \bar{x}(\hat{\mathbf{p}}) \neq 0 \quad \text{then} \quad \operatorname{sign}\left(\bar{x}_0(\hat{\mathbf{p}})\right) = -\operatorname{sign}\left(\bar{x}(\hat{\mathbf{p}})\right)$$

- Hence,

$$\bar{w}_0(\hat{\mathbf{p}}) - \bar{w}(\hat{\mathbf{p}}) = \alpha\left[1 - s^2(\hat{\mathbf{p}})\right] + (\alpha+\beta)\left|\bar{x}(\hat{\mathbf{p}})\bar{x}_0(\hat{\mathbf{p}})\right| + \beta\bar{x}^2(\hat{\mathbf{p}}) > 0 \quad \text{since} \quad \alpha,\beta > 0$$

  so that A_0 invades, as we had to prove

Buildup of "genetic-free" dimorphism (Matessi and Gimelfarb, 2006)

- It seems that adaptive dimorphism of the type considered in ESS theory and by Lessard (1984) can, in principle, also emerge from the long term evolution of a continuous trait when selection is disruptive

- But this result is once again too much dependent on the specific genetic structure assumed for the trait: one gene with arbitrary or partial dominance

- Even within the one-gene case, had we assumed *additive* alleles – a special case of partial dominance occurring when $X(A_iA_j)=e(A_i)+e(A_j)$ – dimorphism would have been impossible, because already with two alleles there would be necessarily three morphs: $X(A_1A_1) \neq X(A_1A_2) \neq X(A_2A_2)$
- In fact, in the case of one-gene and additivity, for a trait limited to the interval [-1,1], it can be shown (Matessi, Gimelfarb and Gavrilets, 2001) that with disruptive selection identical to that considered sofar there is a unique LTE, with two alleles of equal frequency, A_1 and A_2 say, of effects $e_- = -0.5$ and $e_+ = 0.5$ respectively. The mean of the trait is zero but the variance is only 0.5, because the majority phenotype is $X(A_1A_2) = 0$, with a frequency of 0.5
- With two genes, assuming, as is generally the case in reality, that variation of each gene alone can only cover part of the total range of variability of a trait, [-1,1] in our model, even if the limitation of additivity is removed there cannot be less that three morphs (-1,0,1) and variance at a LTE remains well below the maximum level of 1.0, unless recombination between the genes is rather small. Of course, with several genes the variation of the trait at equilibrium would rapidly become almost continuous, presumably without any significant difference between additivity and free dominance

- There is however a particular model of genetic expression and develoment, of a continuous trait with *variation limited to a finite range*, which can quite easily lead to sharp dimorphism in long term evolution under disruptive selection, with any kind of genetics or even without any genetic variation of the primary trait, and that could be feasible for some biological characters

Variable expression of a trait

- The genetic expression of traits is never exact: there always is a certain amount of variation at constant genotype, due to a variety of internal and external factors and disturbances
- Moreover, as documented by abundant experimental evidence, such *non-genetic* variation can in its turn be *modulated by genetic factors* that may be subject to natural or artificial selection
- For example there is a well known and important phenomenon, known as *genetic canalization*, consisting in the fact that in adaptive traits that are kept by natural selection near an optimal value, non-genetic variation (and minor a-specific genetic noise) is more or less repressed by genetic and developmental factors that can be experimentally disrupted, thus revealing large amounts of hidden variation
- We may thus assume that in the same way as variability of expression can be genetically reduced, it can also be magnified by appropriate genetic factors

- Consider therefore a genetically determined continuous trait that, in the absence of expression variability, would have some value $x \in [-1,1]$ but, due to external disturbances, actually assumes a different value $y \in [-1,1]$, a random variable with *Beta distribution* over [-1,1], of mean x

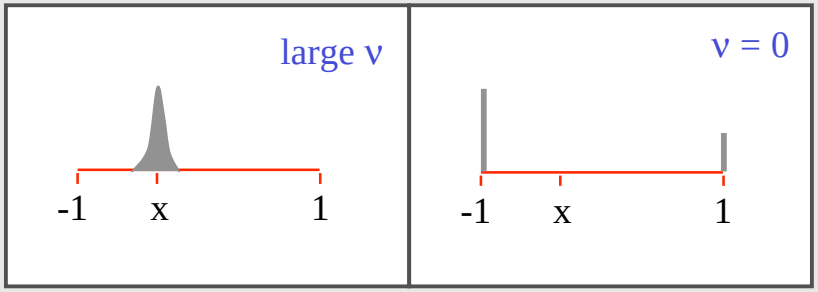
  $y = Y(G) \sim$ Beta distribution over [-1,1] : expressed trait value of individual of genotype G

  $E\{y|G\} = x = X(G) \in [-1,1]$: *genotypic value*, exclusively determined by genotype

$$\mathrm{Var}\{y \mid G\} = \frac{1 - X^2(G)}{\nu + 1} \quad , \quad \nu \geq 0$$

$$X(G) = \pm 1 \Rightarrow Y(G) = X(G) \, , \forall \, \nu > 0$$

$$\nu = 0 \Rightarrow \begin{cases} \Pr\{y = -1 \mid G\} = \dfrac{1 - X(G)}{2} \\ \Pr\{-1 < y < 1 \mid G\} = 0 \\ \Pr\{y = 1 \mid G\} = \dfrac{1 + X(G)}{2} \end{cases}$$



Distribution of trait value given genotypic value x

- According to this model, the case of strict genetic determination considered so far obtains for $\nu \to \infty$, while the purely dimorphic case considered by Lessard (1984) obtains for $\nu = 0$. Observe that this model is independent of any specific assumption about the genetic determination of the genotypic value X(G), that could be controlled by any number of genes, with any type of dominance pattern among their alleles

Selection on the primary trait

- Assume exactly the same disruptive selection regime considered so far. Hence an individual of trait value y' confronting an opponent of trait value y experiences a fitness payoff

$$\upsilon(y',y) = 1 + \alpha y'^2 - (\alpha+\beta)yy' + \beta y^2 \quad , \quad 0 < \alpha < \beta$$

so that in a population where the overall mean and variance of the trait are $\bar{y}$ and s^2, the fitness of an individual of phenotype y, and the mean population fitness are respectively

$$W(y) = W(y,\bar{y},s^2) = 1 + \alpha y^2 - (\alpha+\beta)\bar{y}y + \beta(\bar{y}^2 + s^2) \quad , \quad -1 \le y \le 1$$

$$\bar{w} = \bar{W}(\bar{y},s^2) = 1 + (\alpha+\beta)s^2$$

- However, only selection among genotypes is evolutionarily effective. Hence we need to evaluate the selection experienced by individuals that have the same genotype G, that is the same genotypic value x=X(G). This is given by the expectation of W(y) with respect to y, conditional on G
- Moreover observe that, if the mean and variance of the genotypic values in the population are $\bar{x}$ and s_G^2, then

$$\bar{y} = E\{y\} = E\{X(G)\} = \bar{x} \quad , \quad -1 \le \bar{x} \le 1$$

$$s^2 = \mathrm{Var}\{y\} = \frac{1 - \bar{x}^2 + \nu s_G^2}{1+\nu}$$

- Hence, the fitness of individuals of genotypic value x, and the mean population fitness can be written in terms of genetic parameters as

$$W_G(x) = W_G(x,\bar{x},s_G^2) = 1 + \alpha\frac{1+\nu x^2}{1+\nu} - (\alpha+\beta)\bar{x}x + \beta\frac{1+\nu(\bar{x}^2+s_G^2)}{1+\nu} \quad , \quad -1 \le x \le 1$$

$$\bar{w} = \bar{W}_G(\bar{x},s_G^2) = 1 + (\alpha+\beta)\frac{1-\bar{x}^2+\nu s_G^2}{1+\nu}$$

- This fitness representation has basically the same structure as that considered in the previous model without variability of expression. In fact, assuming as before, that the trait is controlled by a single gene, all the results obtained in that case concerning the long term evolution of the primary trait, can be shown to carry over to this case
- In particular, the manifold $L\left(\frac{1}{2}\right)$, where only two genotypic values, -1 and 1, coexist at equal frequencies, is the unique LTE also in this case. It follows from the assumptions of the model that, whenever such manifold is achieved, since $x = \pm 1$, expression variability is no longer observable because the non-genetic variance is reduced to zero. This means that only two trait values, identical to the genotypic values, are found in the population

Selection on genes controlling the extent of expression variability

- The genetic configuration just described might not be achieved if we suppose that genes that modulate the parameter ν, defining the amount of non-genetic variation of the trait, do exist
- Let then $\nu=N(H)$ be a function of a segment H of the genotype, consisting of one or more genes, and suppose that in a population monomorphic for $\nu=N(H)$ a mutation arises at one of these genes leading to the new genotype H' and to the mutant varibility parameter $\nu'=N(H')$
- The fitness of these mutants that have genotypic value $x=X(G)$, $W_H(\nu',x)$, is computed by taking the expectation of W(y) with respect to y, conditional on both G and H':

$$W_H(x,\nu') = W_H\left(x,\nu',\bar{x},s_G^2,\nu\right) = 1+\alpha\frac{1+\nu' x^2}{1+\nu'} - (\alpha+\beta)\bar{x}x + \beta\frac{1+\nu\left(\bar{x}^2+s_G^2\right)}{1+\nu} \quad , \quad -1 \le x \le 1$$

which, if the resident population is monomorphic also for $x=X(G)$, reduces to

$$W_H(x,\nu') = W_H\left(x,\nu',x,0,\nu\right) = 1+\alpha\left(\frac{1+\nu' x^2}{1+\nu'} - x^2\right) + \beta\left(\frac{1+\nu x^2}{1+\nu} - x^2\right) \quad , \quad -1 \le x \le 1$$

while the mean population fitness is

$$\bar{W}_G\left(x,0\right) = 1+(\alpha+\beta)\frac{1-x^2}{1+\nu}$$

- From this we verify immediately that, provided $x \neq \pm 1$, a mutant of expression variability invades this resident population if and only if it induces a greater variability; in fact

$$W_H(x,\nu',x,0,\nu) - \bar{W}_G(x,0) = \alpha \frac{1-x^2}{(1+\nu')(1+\nu)}(\nu-\nu') > 0 \quad \text{for} \quad \nu' < \nu \quad , \quad \forall\, x \in (-1,1)$$

- Moreover, it can be proved that this is true not only for a totally monomorphic population as shown here, but also in a population that is genetically polymorphic for the primary trait, a condition that is to be expected to prevail under disruptive selection. Hence long term evolution of genes that control the variability of expression of the primary trait tend to enhance such variability to its maximum. In other words: $\nu^\circ = 0$ is a LTE for ν
- Considering the simultaneous evolution of the primary trait (controlled by a single locus) and of its expression variability we conclude that the LTE configuration is the union of the following states

  (1) a strictly genetic dimorphism with $x = y = \pm 1$ (at equal frequencies), and $\nu \geq 0$

  (2) a phenotypic dimorphism, with $y = \pm 1$ (at equal frequencies), and $\nu = \nu^\circ = 0$, supported by a number of genotypic values indifferently distributed in [-1,1], determining various probability of expressing one or the other morph

  (3) a phenotypic dimorphism, with $y = \pm 1$, and $\nu = \nu^\circ = 0$, supported by a genetic monomorphism with genotypic value fixed at $x = 0$ in order to ensure equal probabilities of expressing the two morphs

- It is clear, therefore, that in all cases, from a phenotypic point of view, these configurations are just different ways in which the $L\left(\frac{1}{2}\right)$ manifold is realized and maintained in the population. If we take into account that this result would remain broadly valid even if the primary trait were controllod by several loci (as supported by numerical explorations) it seems that a complex genetic structure (primary genes and modifiers of expression) is required in order to produce what ESS theory can predict with amazing lightness