

A finite-population bound on the selection limit

R. Craig Stillwell

Independent Researcher

craig.stillwell@gmail.com

Tel.: 270-491-0493

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Abstract

Fisher’s fundamental theorem is an identity. Given current gene frequencies, the partial change in mean fitness, holding genotypic fitnesses at their additive predictions, equals the additive genetic variance in fitness divided by mean fitness. Price gave that reading and Ewens proved the discrete-generation form. Lessard and Grafen have argued over what the partial change represents. Akin and Shahshahani showed that selection on a frequency simplex is the gradient flow of mean fitness under the Fisher information metric. In Ewens’s variables, allele-frequency change under genic selection is half a natural-gradient step on mean fitness, and Fisher’s rate is the squared length of that step divided by twice mean fitness.

The identity uses whatever frequencies the population has. It does not give the distance from the additive ceiling once directional selection has finished, Robertson’s selection limit. Under the infinitesimal model I bound that gap for a Wright–Fisher population. Kimura’s diffusion approximation supplies a bias. As a fraction of the ceiling the bias is exponentially small once selection dominates drift at every locus, and in fitness units it grows with the ceiling. Hoeffding’s inequality bounds the spread of the fraction that is fixed. The number of loci is the count in that inequality, where a bound on a sample mean puts the sample size. Population size enters the bias through the fixation probability. The bound assumes $N_e s \gg 1$ at each locus. Where $N_e s$ is of order one, the process is in Barton’s infinitesimal-selection regime.

Keywords: Fisher’s fundamental theorem; Price equation; natural gradient; Fisher information metric; additive genetic variance; infinitesimal model; finite populations; learning theory

1 Fisher’s fundamental theorem

Fisher stated it as a law: “the rate of increase in fitness of any organism at any time is equal to its genetic variance in fitness at that time” [Fisher, 1930]. For fifty years almost nobody could say what that sentence

29 was about [Frank and Slatkin, 1992, Edwards, 2014]. Price [Price, 1972b] saw that Fisher did not mean
30 the total change in mean fitness. He meant a partial change: replace each genotypic fitness with the value
31 predicted from the average effects of its alleles, keep those predicted values fixed, and ask how mean fitness
32 would change if only gene frequencies changed. Ewens [Ewens, 1989] proved that this partial change, in
33 discrete time, equals $V_A/\bar{W}$ exactly. Lessard [Lessard, 1997] put the argument in a form that covers more
34 genetic systems. In continuous time the division by $\bar{W}$ drops out and the partial rate is V_A .

35 That is the theorem. It is an identity for the partial change. It does not imply that mean fitness increases.
36 Dominance, epistasis, changing average effects, mutation, and a deteriorating environment all sit outside the
37 partial change [Price, 1972b, Ewens, 1989, Grafen, 2021]. The Price equation [Price, 1970, 1972a] makes
38 the same cut in other language: total change splits into a selection term, $\text{Cov}(w, z)/\bar{w}$, and a transmission
39 term. Fisher’s additive construction is the selection term written for breeding values of fitness [Frank, 2012,
40 Queller, 2017].

41 The argument since then has been about the left-hand side. Grafen [Grafen, 2015, 2018] takes the partial
42 change to be the change due to natural selection, and treats that as the point of the theorem. Ewens and
43 Lessard [Ewens and Lessard, 2015, Lessard and Ewens, 2019] do not accept either of the usual glosses—
44 “due to gene-frequency change” or “due to natural selection”—and they doubt the theorem’s long-term
45 usefulness. Lessard [Lessard, 2025] has since characterised the partial change directly: it is the part of the
46 change in a mean measurement that is invariant under any reshuffling of genes that leaves allele frequencies
47 unchanged. van Veelen [van Veelen, 2018] has a different complaint, that the theorem is not dynamically
48 sufficient. Frank [Frank, 2009, 2012] writes the same identity in information-geometric form: selection
49 maximises Fisher information, and the Price equation is the bookkeeping.

50 Akin [Akin, 1979] and Shahshahani proved the geometric form of the same fact: on a simplex, selection
51 is the gradient flow of mean fitness in the Fisher information metric. Harper [Harper, 2009, 2010] spells
52 out the consequence for Fisher’s theorem and for Kimura’s maximum principle. Baez [Baez, 2021] proves
53 the corresponding equality for Lotka–Volterra dynamics, where the squared Fisher-information speed of the
54 population distribution equals the variance in fitness. Jaćimović [Jaćimović, 2023, 2024] sorts out which
55 forms of the theorem are equalities and which are inequalities, and gives a natural-gradient theorem for
56 replicator dynamics on a Gaussian trait distribution. Those papers are not written in the discrete-generation
57 notation Ewens uses for V_A and $\bar{W}$. Section 2 puts the one-locus statement in that notation, because the
58 bound needs the one-generation recursion. Chastain, Livnat, Papadimitriou, and Vazirani [Chastain et al.,
59 2014] proved a different theorem, in a different regime: with weak recombination and no drift, selection is
60 the multiplicative-weights update. Assumption 2 below is strong selection and a finite population.

61 Ewens’s identity and the gradient-flow reading are taken as given. In a real population the frequencies that
62 enter both are the frequencies of a finite sample, and realized mean fitness is a random variable. Both are
63 computed after those frequencies are known. Experimental evolution needs the further number, how far
64 mean fitness sits from the additive value once selection has finished, if V_A is to be read as a prediction.

2 Allele-frequency change

Consider a single biallelic locus under viability selection with random mating, genotype fitnesses w_{11}, w_{12}, w_{22} , and frequency p of the fitness-increasing allele. Mean fitness is $\bar{W}(p) = p^2 w_{11} + 2p(1-p)w_{12} + (1-p)^2 w_{22}$, and the standard one-generation recursion (e.g. Ewens 2004) gives

$$\Delta p = \frac{p(1-p)}{2\bar{W}(p)} \frac{d\bar{W}}{dp}. \quad (1)$$

This is exact for viability selection with Hardy–Weinberg mating; it is not a diffusion approximation.

The Fisher information of a Bernoulli(p) variable is $I(p) = 1/[p(1-p)]$, so $g(p) = I(p)$ is the Fisher–Rao (Shahshahani) metric on the one-dimensional simplex $\{p, 1-p\}$, and $g^{-1}(p) = p(1-p)$. The natural gradient of a function f with respect to this metric is $g^{-1}(p)f'(p)$ [Akin, 1979, Harper, 2009]. Comparing with (1),

$$\Delta p = \frac{1}{2\bar{W}(p)} \left[g^{-1}(p) \frac{d\bar{W}}{dp} \right] = \frac{1}{2\bar{W}(p)} \nabla^{\text{nat}} \bar{W}(p). \quad (2)$$

So the change in allele frequency is half a natural-gradient step on mean fitness, with step size $1/(2\bar{W})$. This is Akin’s theorem for one biallelic locus in discrete generations [Akin, 1979, Harper, 2009, 2010, Baez, 2021, Jaćimović, 2023, 2024].

For genic selection with no dominance, $\bar{W}(p) = \bar{W}_0 + 2\alpha p$ is linear in p . Holding that line fixed, the change in mean fitness when p changes by Δp is exactly $(d\bar{W}/dp) \cdot \Delta p$, with no remainder. Substituting (1),

$$\Delta_p \bar{W} = \frac{p(1-p)}{2\bar{W}} \left(\frac{d\bar{W}}{dp} \right)^2 = \frac{g^{-1}(p)(d\bar{W}/dp)^2}{2\bar{W}} = \frac{\|\nabla^{\text{nat}} \bar{W}\|_g^2}{2\bar{W}},$$

and with $V_A = 2p(1-p)\alpha^2$ and $d\bar{W}/dp = 2\alpha$, the left side is $2p(1-p)\alpha^2/\bar{W} = V_A/\bar{W}$, which is (3) below. Fisher’s rate is the squared length of the natural gradient of mean fitness, divided by twice mean fitness. With additive fitness across unlinked loci the same calculation holds at each locus. That is the representation used below.

The gradient gives the direction of the frequency change and, through $V_A/\bar{W}$, the change in one generation. It does not say whether a finite population, with drift in every generation, finishes near the frequency that gradient was climbing. Sections 5 and 6 are about the population after selection has finished.

3 The selection limit

Write $\bar{W}$ for mean absolute fitness and A for the breeding value of fitness, so $V_A = \text{Var}(A)$. Following Ewens, let $\Delta_p \bar{W}$ be the change in mean fitness obtained by substituting additive predictions for genotypic fitnesses and holding those predictions fixed while gene frequencies change. In a population with discrete, non-overlapping generations,

$$\Delta_p \bar{W} = \frac{V_A}{\bar{W}}. \quad (3)$$

91 In continuous time the same construction gives $\partial_p \bar{W} / \partial t = V_A$. Equation (3) is not an approximation. It
 92 holds for the partial change at whatever gene frequencies the population happens to have.

93 The total change is another matter. The Price equation for a measurement z reads

$$\bar{w} \Delta \bar{z} = \text{Cov}(w, z) + E[w \Delta z]. \quad (4)$$

94 The first term is selection; the second is transmission—mutation, recombination, development, anything
 95 that makes offspring trait values differ from the parental values attached to a genotype [Frank, 2012]. If z is
 96 fitness itself and fitness is replaced by its additive prediction, the first term becomes V_A and (3) follows. The
 97 second term, and the difference between absolute fitness and breeding value, are exactly the pieces Fisher
 98 left out of the partial change.

99 In an infinite population those pieces can still wreck any claim that mean fitness increases, which is why
 100 Grafen’s completion of the theorem [Grafen, 2021] has to put mutation and stabilizing selection back into
 101 a model of the total change, and why Basener and Sanford [Basener and Sanford, 2018] get a mutational
 102 correction when they restore mutation to Fisher’s differential equation. In a finite population there is a
 103 further piece: the gene frequencies that enter (3) are those of a Wright–Fisher sample. Even if transmission
 104 were absent, realized $\bar{W}$ would jitter.

105 The bound below is on that jitter. The setting is the infinitesimal model [Fisher, 1918, Lande, 1979, Barton
 106 et al., 2017]: many loci, each of small additive effect, so that breeding values stay close to Gaussian and
 107 V_A describes the population. Write $\bar{W}^*$ for mean fitness when every one of the L loci is fixed for the allele
 108 that increases fitness. That is the additive ceiling given the alleles now segregating. Write $\bar{W}_\infty$ for mean
 109 fitness after directional selection has finished at those loci, each fixed or lost, with no new mutation. This is
 110 the selection limit Robertson [Robertson, 1960] defined for a quantitative trait, applied here to fitness. How
 111 close is $\bar{W}_\infty$ to $\bar{W}^*$?

112 Fisher asked for the partial change in one generation. The selection limit is the question that matters if the
 113 additive description is supposed to describe a population one can actually score.

114 4 Assumptions

115 **Assumption 1.** The trait (here, fitness) follows the infinitesimal model of Barton et al. [2017]: L unlinked,
 116 biallelic loci, additive effects, no dominance or epistasis in the breeding-value decomposition used to define
 117 V_A . At each locus ℓ , p_ℓ is the frequency of the allele that increases fitness, and $\alpha_\ell > 0$ is its effect, bounded
 118 and not vanishing: $p_\ell(1 - p_\ell) \geq \kappa > 0$ for every segregating locus.

119 **Assumption 2.** Reproduction is Wright–Fisher with effective size N_e . The selection coefficient s_ℓ is defined
 120 in the next section from the additive effect and the mean fitness. Require $N_e s_\ell \gg 1$ at every locus. Fixation
 121 outcomes at unlinked loci are assumed independent; linkage, and dependence induced by a shared finite
 122 population, are outside the bound. The fixation probability is Kimura’s diffusion approximation with s_ℓ held
 123 fixed, not the fixation probability of the Wright–Fisher chain. For Moran reproduction the same diffusion

124 formula applies after the usual rescaling of N_e and s_ℓ [Alexandre et al., 2025].

125 The second assumption is what makes a locus-by-locus tail possible. When $N_e s_\ell$ is of order one, drift
 126 and selection are comparable at that locus, and Kimura's probability is no longer close to 0 or 1. That is
 127 Barton's [Barton, 2017] infinitesimal-selection regime, taken up in the discussion. It is also where Ewens
 128 and Lessard's doubts about the long-term use of the theorem are hardest to dismiss. Computing the partial
 129 change more carefully will not make realized mean fitness follow V_A .

130 5 A bound

131 At each locus, whether the fitness-increasing allele ultimately fixes or is lost is random. Write $W_{b,\ell}$ for
 132 the absolute fitness contributed by the rest of the genome. The three genotypes then have absolute fitness
 133 $W_{b,\ell}$, $W_{b,\ell} + \alpha_\ell$, and $W_{b,\ell} + 2\alpha_\ell$, and the population mean is $\bar{W} = W_{b,\ell} + 2\alpha_\ell p_\ell$. Section 2 gives $\Delta p_\ell =$
 134 $p_\ell(1 - p_\ell)\alpha_\ell/\bar{W}$. Kimura's diffusion for relative fitnesses 1, $1 + s$, $1 + 2s$ has drift $p(1 - p)s/(1 + 2sp)$
 135 [Kimura, 1962]. The two drifts agree at leading order in s when $s_\ell = \alpha_\ell/\bar{W}$ and $\alpha_\ell \ll \bar{W}$, the infinitesimal
 136 regime. Dividing the three absolute fitnesses by $\bar{W}$ does not put them in the form 1, $1 + s_\ell$, $1 + 2s_\ell$. The
 137 diffusion freezes s_ℓ at its initial value. Under that approximation, the probability that locus ℓ fixes for the
 138 favored allele is

$$u(p_\ell) = \frac{1 - e^{-4N_e s_\ell p_\ell}}{1 - e^{-4N_e s_\ell}}. \quad (5)$$

139 Write $X_\ell \in \{0, 1\}$ for that eventual outcome, so $P(X_\ell = 1) = u(p_\ell)$, and $\bar{W}_\infty = \bar{W}_0 + 2 \sum_\ell \alpha_\ell X_\ell$ for
 140 whatever baseline $\bar{W}_0$ the other loci contribute. The bound uses two properties of (5): an upper bound on
 141 $1 - u(p_\ell)$, and Hoeffding's inequality under the independence assumed above.

142 **Theorem 1.** *Under Assumptions 1 and 2, let $\theta = \min_\ell N_e s_\ell p_\ell$ and $\kappa_0 = (1 - e^{-4N_e \min_\ell s_\ell})^{-1} \geq 1$. Set*
 143 *$B = \kappa_0(\bar{W}^* - \bar{W}_0) e^{-4\theta}$. For every $\varepsilon > B$,*

$$P(\bar{W}^* - \bar{W}_\infty > \varepsilon) \leq \exp\left(-\frac{\kappa(\varepsilon - B)^2}{V_A}\right). \quad (6)$$

144 The proof is Appendix A. B is a bias. Fixation at each locus is probable, so the expected shortfall $\bar{W}^* -$
 145 $E[\bar{W}_\infty]$ is at most B . The fraction of the ceiling in that bias is

$$\frac{B}{\bar{W}^* - \bar{W}_0} = \kappa_0 e^{-4\theta}.$$

146 Once θ at the weakest locus is a few units, this fraction is exponentially small. Hoeffding's inequality [Ho-
 147 effding, 1963] then bounds the upper tail of the shortfall, a sum of L independent terms, one per locus, each
 148 in $[0, 2\alpha_\ell]$. Given independent indicators with success probabilities $u(p_\ell)$, Hoeffding's inequality is exact.
 149 Those probabilities are one-locus diffusion approximations with s_ℓ held fixed. Theorem 1 is a statement
 150 about that approximation.

151 N_e sets the fraction, not the width of the tail. Once every locus has $N_e s_\ell p_\ell \gtrsim 1$, Kimura's formula puts

the favored allele near certain fixation, and the missing fraction is small however many loci there are. The absolute shortfall B still scales with the ceiling $\bar{W}^* - \bar{W}_0$. A larger population makes loss of the favored allele rarer at every locus. That is the same place N_e enters Robertson’s [Robertson, 1960] limit: in the fixation probability.

L sets how tightly the fraction of the ceiling clusters around its expectation. For loci of equal effect (Appendix B), with $F = (\bar{W}_\infty - \bar{W}_0)/(\bar{W}^* - \bar{W}_0)$,

$$P(|F - E[F]| > \eta) \leq 2 \exp(-2L\eta^2). \quad (7)$$

At fixed V_A , spreading the same variance over more loci narrows the spread of this fraction around its mean. The gap in fitness units grows. For equal effects and a common $p_\ell(1 - p_\ell) = \kappa$, the ceiling equals $\sqrt{2V_AL/\kappa}$, and B grows with the ceiling. Adding loci at fixed V_A does not close the gap in fitness units. One locus of large effect is a coin flip for nearly the whole ceiling. A hundred loci of small effect, carrying the same V_A , share that risk, and the fraction averages.

Corollary 2. *If $V_A = 0$, there is no additive change, and (3) already gives $\Delta_p \bar{W} = 0$. If $N_e s_\ell = O(1)$ at some locus, Assumption 2 fails there. The fixation probability is not close to 0 or 1, B is not a small fraction, and (6) says little. That locus is in Barton’s [Barton, 2017] infinitesimal-selection regime. Equation (3) still gives the partial change. It says little about the selection limit.*

If $s_\ell = 0$, the diffusion formula reduces to $u(p_\ell) = p_\ell$ (Appendix C). The expected contribution of that locus at the limit is its current contribution. Raising N_e does not close a gap that selection is not there to close. Lemma 1 does not cover this case: its bias bound divides by $1 - e^{-4N_e s_\ell}$.

6 The same inequality for a sample mean

Bottou and Bousquet [Bottou and Bousquet, 2008] split the excess risk of a learning algorithm into approximation error, estimation error, and optimization error. The first comes from the hypothesis class, the second from using a finite sample, and the third from stopping before the minimum. Extra samples do not repair a class that cannot represent the target, and a longer run does not repair a sample that was too small.

$\bar{W}^*$ is fixed by which loci are segregating and by their effects. Asking whether mutation or a different set of loci would raise that ceiling is a question about the standing variation, and Theorem 1 does not address it.

Equation (7) is Hoeffding’s inequality. For the mean of n independent observations bounded in $[0, 1]$, the same inequality is $P(|\hat{\mu} - \mu| > \eta) \leq 2 \exp(-2n\eta^2)$. In (7) the number of terms is L , one fixation indicator per locus. N_e is not that number. It does not appear in the exponent. Drift is weaker in a larger population, and a sample mean is tighter in a larger sample, so it is easy to treat N_e as the sample size. In this bound the count being averaged is the number of loci.

N_e enters through $\theta = N_e s_\ell p_\ell$, which sets B . The bias is the shortfall left because fixation has not been pushed to certainty. It shrinks when $N_e s_\ell$ grows. It does not shrink when L grows. Optimization error in the Bottou–Bousquet split behaves in that one respect: it shrinks when the algorithm is run longer or harder,

185 and a larger training set does not remove it. Kimura’s formula and a convergence bound for an optimizer
 186 are different equations. The match is limited to where the parameters sit: L is the number of terms in the
 187 average, and N_e sets the fixation probability.

188 Chastain and colleagues [Chastain et al., 2014] proved that weak selection with free recombination, and no
 189 drift, is the multiplicative-weights update. Those assumptions do not overlap Assumption 2. Their result
 190 matches two dynamical systems. Equation (7) matches one inequality.

191 **7 Numerical values**

192 The factor $e^{-4\theta}$ at a locus depends only on $N_e sp$. Take one locus with $N_e = 200$ and $p = 0.5$. At $s = 0.05$,
 193 $N_e s = 10$ and $\theta = 5$; $e^{-4\theta} = e^{-20} \approx 2 \times 10^{-9}$, and $\kappa_0 \approx 1$. At $s = 0.015$, $N_e s = 3$, $\theta = 1.5$,
 194 $e^{-4\theta} = e^{-6} \approx 0.0025$, a quarter of one percent of that locus’s contribution to the ceiling. At $s = 0.006$,
 195 $N_e s = 1.2$, $\theta = 0.6$, $e^{-4\theta} \approx 0.09$. This is the approach to Barton’s infinitesimal regime, where $N_e s$ at a
 196 locus stops being comfortably above one. These are values at a single locus. A genome cannot assign every
 197 locus the same large s : $s_\ell = \alpha_\ell / \bar{W}$ and $\sum_\ell 2\alpha_\ell p_\ell = \bar{W} - \bar{W}_0$, so the selection coefficients share one mean.

198 Separately, for equal-effect loci, (7) says how many loci pin the realized fraction within η of its expectation
 199 with probability 0.95: $2 \exp(-2L\eta^2) = 0.05$ gives $L \gtrsim 1.8/\eta^2$. For $\eta = 0.1$, $L \approx 185$; for $\eta = 0.05$,
 200 $L \approx 740$. Those are ordinary counts for a polygenic fitness component, in the range already discussed when
 201 one asks whether V_A in fitness predicts a response [Walsh and Lynch, 2018]. Raising L at fixed V_A does not
 202 change the N_e required for a given fractional bias. It tightens the fraction around that bias. The shortfall in
 203 fitness units still scales with the ceiling.

204 **8 Other readings of the theorem**

205 Grafen [Grafen, 2018] reads the partial change as the effect of natural selection. Ewens and Lessard [Lessard
 206 and Ewens, 2019] reject that reading, and Lessard’s later characterisation by reshuffling invariance does not
 207 use it [Lessard, 2025]. They agree on the arithmetic. Theorem 1 uses that arithmetic and then asks when the
 208 selection limit lies close to the additive ceiling.

209 Grafen’s completion of the theorem [Grafen, 2021] puts mutation and stabilizing selection into the total
 210 change, and it argues that Fisher was talking about directional selection on the underlying traits. That
 211 changes what $\bar{W}^*$ ought to be. The tail in Theorem 1 is the randomness of fixation around the ceiling one
 212 has settled on. Mutation changes the ceiling.

213 Frank’s geometric form of the identity [Frank, 2009, 2012, 2025], and the natural-gradient reading in Sec-
 214 tion 2 [Akin, 1979, Harper, 2009, 2010, Baez, 2021, Jaćimović, 2023, 2024], describe the instantaneous
 215 rate. The Fisher information metric on the simplex does not contain N_e or L . Frank’s force–metric–bias
 216 decomposition of the Price equation likewise does not produce them. Sections 5 and 6 are about where the
 217 finite population finishes.

van Veelen’s [van Veelen, 2018] point still stands. Higher moments of the fitness distribution still determine how V_A changes, and Theorem 1 describes $\bar{W}_\infty$, not a closed recursion for the distribution on the way there. Robertson [Robertson, 1960] calculated the expected limit and its half-life. Paixão and Barton [Paixão and Barton, 2016] extended the expectation to epistasis. Theorem 1 is a tail around Kimura’s approximation to Robertson’s expectation. His expected fractional shortfall depends on N_e and s , not on L . So does $B/(\bar{W}^* - \bar{W}_0) = \kappa_0 e^{-4\theta}$. The number of loci sets how tightly the fraction clusters around that expectation. The shortfall in fitness units grows with the ceiling.

9 Discussion

Ewens and Lessard [Ewens and Lessard, 2015] concluded that the fundamental theorem is of little long-term use. The partial change is not the total change, so the identity does not imply that mean fitness increases, and average effects move as frequencies move. A finite population adds a more ordinary reason for the same conclusion. The missing fraction of the ceiling depends on $N_e s_\ell p_\ell$ at each locus. A more polygenic basis does not, by itself, force one to a larger N_e in order to keep that fraction small. If $N_e s_\ell$ is of order one at a locus, that locus is far from certain fixation, and the other loci do not make up the missing fraction. The identity can hold in every generation while the selection limit sits well short of the ceiling.

Price’s split is the one this uses: selection in one term, transmission in the other. Ewens’s identity is the selection term written for breeding values of fitness. Robertson [Robertson, 1960] gave the expected limit of response from standing variance. Theorem 1 puts a tail on Kimura’s approximation to that expectation. The fractional bias depends on N_e , s , and the allele frequencies. The spread of the fraction depends on L . At fixed V_A , more loci make the fraction more predictable, because each locus is a smaller share of the ceiling and the shares are independent under Assumptions 1 and 2. The gap in fitness units grows with the ceiling.

Barton’s [Barton, 2017] infinitesimal-selection regime, $N_e s_\ell = O(1)$ at most loci, lies outside the theorem. Fixation is not nearly certain, B is not a small fraction, and, as Barton shows for stabilizing selection on many traits, a drift-load calculation takes over. Neutral and nearly neutral contributions to fitness are in that regime. One can still compute $\Delta_p \bar{W}$ from the current frequencies. Realized mean fitness at the limit will not track it.

The additivity assumed here is Ewens’s. V_A is the standing variance, not the variance after selection has eroded it [Bulmer, 1971] or mutation has restored it. Dominance and epistasis sit in the transmission term and in the difference between genotypic fitness and A . If they are large, $\bar{W}^*$ is the wrong ceiling, and the bound is about the wrong object. Equation (3) was always a statement about the additive piece.

Equation (7) is Hoeffding’s inequality on the fixation indicators, with L in the place that inequality gives to the sample size. N_e enters the bias through Kimura’s $u(p)$. Chastain and colleagues’ [Chastain et al., 2014] equivalence remains a separate result, proved for weak selection without drift.

The empirical question is open. In an experimental population where N_e , s , and the allele frequencies can be estimated at the loci that carry V_A , does the selection limit fall inside the distance (6) allows? If it usually

falls outside, the identity is not the part that failed. Transmission, linkage strong enough to correlate the loci, or an $N_e s_\ell$ that was never large at a locus that mattered, would. Those are ordinary failures in quantitative genetics, and they are what one would look for. Most of the commentary since Price has been about what the partial change means. The partial change is an identity. The selection limit is the quantity an experiment can miss.

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Competing interests

Declarations of interest: none.

Data availability

No data were used. The derivations are in Appendices A–C.

Declaration of generative AI

During preparation the author used GitHub Copilot and Claude (Anthropic) for language editing. The author takes full responsibility for the text.

A The bias, from Kimura’s fixation probability

Let there be L unlinked, biallelic loci. At locus ℓ , let $p_\ell \in (0, 1)$ be the frequency of the allele that increases fitness, with additive effect $\alpha_\ell > 0$ per copy and no dominance, so that mean fitness at frequency vector $p = (p_1, \dots, p_L)$ is

$$\bar{W}(p) = \bar{W}_0 + 2 \sum_{\ell=1}^L \alpha_\ell p_\ell, \quad (8)$$

where $\bar{W}_0$ collects everything besides these L loci and is held fixed. This is the same additive decomposition used to define $V_A = \sum_\ell 2p_\ell(1 - p_\ell)\alpha_\ell^2$ above. The additive ceiling is $\bar{W}^* = \bar{W}(\mathbf{1}) = \bar{W}_0 + 2 \sum_\ell \alpha_\ell$.

Reproduction is Wright–Fisher with effective size N_e . On a background fitness $W_{b,\ell}$ from the rest of the genome, the three genotypes have absolute fitness $W_{b,\ell}$, $W_{b,\ell} + \alpha_\ell$, and $W_{b,\ell} + 2\alpha_\ell$, so $\bar{W} = W_{b,\ell} + 2\alpha_\ell p_\ell$ and $\Delta p_\ell = p_\ell(1 - p_\ell)\alpha_\ell / \bar{W}$. Kimura’s diffusion for relative fitnesses $1, 1 + s, 1 + 2s$ has drift $p(1 - p)s / (1 + 2sp)$. The drifts agree through first order in s when $s_\ell = \alpha_\ell / \bar{W}$ and $\alpha_\ell \ll \bar{W}$. The formula below freezes that s_ℓ . It is not obtained by dividing the three absolute fitnesses by $\bar{W}$. Kimura’s [Kimura, 1962] diffusion

approximation then gives the probability that locus ℓ , started at p_ℓ , eventually fixes for the favored allele:

$$u(p_\ell) = \frac{1 - e^{-4N_e s_\ell p_\ell}}{1 - e^{-4N_e s_\ell}}. \quad (9)$$

The eventual outcomes $X_1, \dots, X_L \in \{0, 1\}$ ($X_\ell = 1$ if locus ℓ fixes for the favored allele) are assumed independent, as in Assumption 2, with $P(X_\ell = 1) = u(p_\ell)$. Linkage, and dependence through a shared finite population, lie outside the argument. The mean fitness once every locus has resolved is

$$\bar{W}_\infty = \bar{W}_0 + 2 \sum_{\ell=1}^L \alpha_\ell X_\ell, \quad (10)$$

a random variable because the X_ℓ are random. This is Robertson's [Robertson, 1960] selection limit, computed one locus at a time.

Lemma 1 (Bias). Let $\theta = \min_\ell N_e s_\ell p_\ell$ and $\kappa_0 = (1 - e^{-4N_e \min_\ell s_\ell})^{-1} \geq 1$. Then

$$0 \leq \bar{W}^* - E[\bar{W}_\infty] \leq \kappa_0 (\bar{W}^* - \bar{W}_0) e^{-4\theta} =: B. \quad (11)$$

Proof. From (9),

$$1 - u(p_\ell) = \frac{e^{-4N_e s_\ell p_\ell} - e^{-4N_e s_\ell}}{1 - e^{-4N_e s_\ell}} \leq \frac{e^{-4N_e s_\ell p_\ell}}{1 - e^{-4N_e s_\ell}},$$

dropping the subtracted term in the numerator, which only increases the bound and preserves it as an inequality. The function $x \mapsto (1 - e^{-4N_e x})^{-1}$ is decreasing in $x > 0$, so replacing s_ℓ by $\min_\ell s_\ell$ in the denominator can only increase the right-hand side. The exponent is $-4N_e s_\ell p_\ell$. Replacing $N_e s_\ell p_\ell$ by $\theta = \min_\ell N_e s_\ell p_\ell$ replaces that exponent by the larger number -4θ , which increases the bound. Hence $1 - u(p_\ell) \leq \kappa_0 e^{-4\theta}$ for every ℓ . Summing,

$$\bar{W}^* - E[\bar{W}_\infty] = \sum_{\ell} 2\alpha_\ell (1 - u(p_\ell)) \leq \kappa_0 e^{-4\theta} \sum_{\ell} 2\alpha_\ell = \kappa_0 (\bar{W}^* - \bar{W}_0) e^{-4\theta}.$$

□

Under Assumption 2, $N_e s_\ell \gg 1$ for every locus, so $N_e \min_\ell s_\ell \gg 1$, κ_0 is close to 1, and θ is large enough that B is a small fraction of $\bar{W}^* - \bar{W}_0$ once $\theta \gtrsim 1$ –2. Given Kimura's u , (11) is an algebraic bound and holds for every finite N_e , s_ℓ , and p_ℓ . The diffusion step that produced u is the approximation.

B The tail, from Hoeffding's inequality

Write $D_\ell = 2\alpha_\ell(1 - X_\ell)$, so $D_\ell \in [0, 2\alpha_\ell]$ almost surely, the D_ℓ are independent, and

$$\bar{W}^* - \bar{W}_\infty = \sum_{\ell=1}^L D_\ell =: S.$$

298 By Lemma 1, $E[S] \leq B$. Hoeffding's [Hoeffding, 1963] inequality for a sum of independent bounded
 299 random variables gives, for every $t > 0$,

$$P(S - E[S] > t) \leq \exp\left(-\frac{2t^2}{\sum_{\ell}(2\alpha_{\ell})^2}\right) = \exp\left(-\frac{t^2}{2\sum_{\ell}\alpha_{\ell}^2}\right). \quad (12)$$

300 Under Assumption 1, every segregating locus has $p_{\ell}(1 - p_{\ell}) \geq \kappa > 0$, so $V_A = \sum_{\ell} 2p_{\ell}(1 - p_{\ell})\alpha_{\ell}^2 \geq$
 301 $2\kappa \sum_{\ell} \alpha_{\ell}^2$, i.e. $\sum_{\ell} \alpha_{\ell}^2 \leq V_A/(2\kappa)$. The denominator of the exponent in (12) is $2\sum_{\ell} \alpha_{\ell}^2$. Replacing $\sum_{\ell} \alpha_{\ell}^2$
 302 by the larger quantity $V_A/(2\kappa)$ increases that denominator, up to V_A/κ , and so makes the exponential bound
 303 larger (weaker, and still valid):

$$P(S - E[S] > t) \leq \exp\left(-\frac{\kappa t^2}{V_A}\right). \quad (13)$$

304 *Proof of Theorem 1.* Fix $\varepsilon > B \geq E[S]$ and set $t = \varepsilon - E[S] \geq \varepsilon - B > 0$. Then

$$P(S > \varepsilon) = P(S - E[S] > \varepsilon - E[S]) \leq \exp\left(-\frac{\kappa(\varepsilon - E[S])^2}{V_A}\right) \leq \exp\left(-\frac{\kappa(\varepsilon - B)^2}{V_A}\right),$$

305 using (13) and then $\varepsilon - E[S] \geq \varepsilon - B > 0$ together with the fact that $x \mapsto \exp(-\kappa x^2/V_A)$ is decreasing
 306 for $x > 0$. □

307 Theorem 1 is written in absolute fitness units, and neither B nor the exponent's dependence on V_A and
 308 κ involves L explicitly. To see how L governs the spread of outcomes, specialize to loci of equal effect,
 309 $\alpha_{\ell} \equiv \alpha$ and $p_{\ell} \equiv \bar{p}$ (so $\kappa = \bar{p}(1 - \bar{p})$). Then $V_A = 2\kappa L\alpha^2$, so $\alpha^2 = V_A/(2\kappa L)$, and $\bar{W}^* - \bar{W}_0 = 2L\alpha$.
 310 Let $F = (\bar{W}_{\infty} - \bar{W}_0)/(\bar{W}^* - \bar{W}_0) = (1/L) \sum_{\ell} X_{\ell}$ be the fraction of the ceiling captured. Applying the
 311 two-sided form of Hoeffding's inequality to the average of L independent $[0, 1]$ -valued terms X_{ℓ} ,

$$P(|F - E[F]| > \eta) \leq 2\exp(-2L\eta^2), \quad (14)$$

312 which is (7). The growth of the ceiling is algebra, not a concentration inequality: with equal effects and
 313 $p_{\ell}(1 - p_{\ell}) = \kappa$, $\bar{W}^* - \bar{W}_0 = \sqrt{2V_AL/\kappa}$. The absolute spread of S around its mean, from (13), does
 314 not shrink as L grows at fixed V_A . The fraction of that growing ceiling concentrates at rate L . Given
 315 independence, both concentration statements are Hoeffding's inequality applied to the same X_{ℓ} , once in
 316 fitness units and once as a fraction.

317 C The neutral limit

318 Lemma 1 divides by $1 - e^{-4N_e s_{\ell}}$, so it does not apply at $s_{\ell} = 0$. The diffusion formula does. As $s_{\ell} \rightarrow 0$,
 319 L'Hôpital's rule on (9) gives $u(p_{\ell}) \rightarrow p_{\ell}$, which is also the fixation probability of a neutral allele. The
 320 expected contribution of the locus at the limit is then its current contribution, $2\alpha_{\ell}p_{\ell}$, and $E[\bar{W}_{\infty}]$ receives
 321 no drift-driven push toward the ceiling. Raising N_e does not close a gap that selection is not there to close.
 322 This is the case stated after Corollary 2.

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