

1 **An evolutionary tipping point in a changing environment**

2 **Abstract**

3 Populations can persist in directionally changing environments by evolving. Quan-
4 titative genetic theory aims to predict critical rates of environmental change be-
5 yond which populations go extinct. Here we point out that all current predictions
6 effectively assume the same specific fitness function. This function causes se-
7 lection on the standing genetic variance of quantitative traits to become increas-
8 ingly strong as mean trait values depart from their optima. Hence, there is no
9 bound on the rate of evolution and persistence is determined by the critical rate
10 of environmental change at which populations cease to grow. We then show
11 that biologically-reasonable changes to the underlying fitness function can im-
12 pose a qualitatively different extinction threshold. In particular, inflection points
13 caused by weakening selection create local extrema in the strength of selection
14 and thus in the rate of evolution. These extrema can produce evolutionary tipping
15 points, where long-run population growth rates drop from positive to negative
16 values without ever crossing zero. Generic early-warning signs of tipping points
17 are found to have little power to detect imminent extinction, and require hard-
18 to-gather data. Furthermore, we show how evolutionary tipping points produce
19 evolutionary hysteresis, creating extinction debts.

20 *Keywords:* **Evolutionary rescue, extinction, fitness function, hysteresis, math-**
21 **ematical model, quantitative genetics**

22 **Introduction**

23 Many populations currently face gradual directional changes in their environment
 24 (reviewed in Davis et al., 2005; Parmesan, 2006; Visser, 2008; Lavergne et al.,
 25 2010; Hoffmann and Sgrò, 2011). Those populations with limited dispersal and
 26 plasticity can persist only if they evolve fast enough (Lynch and Lande, 1993). The
 27 maximum rate of environmental change a population can adaptively track – and
 28 demographically tolerate – has recently received considerable theoretical attention
 29 (reviewed in Walters et al., 2012; Kopp and Matuszewski, 2013; Alexander et al.,
 30 2014).

31 Typically these studies follow a quantitative genetic approach (for alternatives
 32 see Johansson, 2008; Bertram et al., 2016; Osmond et al., 2017). They first as-
 33 sume some unimodal mapping from phenotype to absolute fitness (the ‘fitness
 34 function’). Then, for a given rate of change in the trait value that maximizes fit-
 35 ness (the ‘environmental optimum’), the fitness function is used to derive the rate
 36 of evolution in the mean trait value and the expected difference between the mean
 37 trait value and the optimum at equilibrium (the ‘steady-state lag’). The rate of
 38 environmental change that produces a steady-state lag resulting in a population
 39 mean growth rate (when rare) of zero is dubbed the ‘critical rate of environmental
 40 change’ (Lynch et al., 1991). Critical rates of environmental change are now being
 41 estimated and used to predict whether particular species will survive or go extinct
 42 in the face of global climate change (Aitken et al., 2008; Willi and Hoffmann,
 43 2009; Gienapp et al., 2013; Vedder et al., 2013).

44 To the best of our knowledge, all quantitative genetic theory developed so far
 45 implicitly assumes that the maximum rate of environmental change to which a
 46 population can adapt is determined by demography (i.e., ‘selective load’ *sensu*
 47 Lynch and Lande 1993, or ‘demographic constraint’ *sensu* Gomulkiewicz and
 48 Houle 2009). This assumption results from the shape of the specific fitness func-
 49 tions used. In particular, Gaussian fitness functions, $W(z)$, are used in models
 50 with non-overlapping generations in discrete time (Charlesworth, 1993; Bürger
 51 and Lynch, 1995, 1997; Bürger, 1999; Gomulkiewicz and Houle, 2009; Chevin
 52 et al., 2010; Matuszewski et al., 2015; Marshall et al., 2016), while quadratic
 53 fitness functions, $r(z)$, are used in models with overlapping generations in contin-
 54 uous time (Pease et al., 1989; Lynch et al., 1991; Lynch and Lande, 1993; Pole-
 55 chová et al., 2009; Aguilée et al., 2016). These are equivalent given $\log(W) = r$
 56 (Crow and Kimura, 1970, Chapter 1) and have presumably been chosen for math-
 57 ematical convenience (e.g., they maintain a normal trait distribution) as well as
 58 their ability to approximate – when near the optimum – any smooth fitness func-
 59 tion imposing stabilizing selection (Lande, 1976). This particular fitness function
 60 is therefore a relatively mild assumption under the historical paradigm of weak
 61 selection, but it becomes a strong yet biologically arbitrary assumption when en-
 62 vironments change quickly enough that populations find themselves considerably
 63 maladapted.

64 The rate of evolution in a mean trait value can be approximated by the prod-
 65 uct of additive genetic variance and the selection gradient (Lande, 1976). With
 66 overlapping generations in continuous time, the selection gradient is the deriva-

67 tive of mean fitness with respect to mean trait value (Lande, 1982, equation 11),
 68 while with non-overlapping generations in discrete time, it is the derivative of the
 69 logarithm of mean fitness (Lande, 1976, equation 7). Thus the strength of selec-
 70 tion becomes a linear function of mean phenotypic lag in all models listed above.
 71 This implies that the strength of selection has no limit and therefore that, given
 72 a large enough steady-state lag, evolution can proceed arbitrarily fast (as long as
 73 additive genetic variance remains non-zero). Population persistence is then only
 74 determined by the population mean growth rate at the steady-state lag that causes
 75 evolution to proceed as fast as the environment changes, i.e., there is a critical rate
 76 of environmental change at which populations cease to grow.

77 Here we show that the existence of a critical rate of environmental change
 78 depends on the choice of fitness function. Moreover, decreases in the strength of
 79 selection (the slope of the fitness function) with increasing maladaptation cause lo-
 80 cal maxima in the rate of evolution. These local maxima can create an ‘evolution-
 81 ary tipping point’, where rates of environmental change less than the tipping point
 82 result in stable steady-state lags and population persistence while rates of environ-
 83 mental change greater than the tipping point lead to an apparent existential crisis:
 84 the population ceases to adapt as the selective pressure relaxes, causing the steady-
 85 state lag to rapidly increase and the population to go extinct. This existential crisis
 86 is brought about by what is known as a saddle-node bifurcation. Many dynamical
 87 systems are thought to experience saddle-node bifurcations, from global finance
 88 to climate, and there is a substantial literature devoted to developing generic early-
 89 warning signs to detect impending bifurcations (reviewed in Scheffer et al., 2009).

Two common early-warning signs are increased variance and lag-1 autocorrelation, both of which are caused by slow recovery from perturbation, or a ‘critical slowing down’, and have been detected in climate and ecological data (Scheffer et al., 2009; Lenton, 2011). We therefore use simulations to see if generic early-warning signs have the potential to detect evolutionary tipping points, granted one has extensive time series of difficult-to-measure parameters such as mean phenotypic lag. Finally, we show how the existence of an evolutionary tipping point induces ‘evolutionary hysteresis’, which can create an extinction debt: transitory increases in mean phenotypic lags (e.g., due to sudden environmental changes) can initiate the above mentioned existential crisis, with extinction occurring many generations later even if the rate of environmental change returns to moderate levels. Overall, our results demonstrate that our current understanding of evolutionary rescue in directionally changing environments is highly sensitive to the – relatively unknown – shape of fitness functions as populations become increasingly maladapted.

Methods and Results

A general model

Following Lynch and Lande (1993), we consider a well-mixed and randomly mating population of short-lived, hermaphroditic individuals with overlapping generations in continuous time. Individuals are characterized by a quantitative trait, z , which is the sum of genetic and environmental effects, $z = g + e$. The ge-

111 netic effect is determined by a large number of equivalent, additive, and freely-
 112 recombining diploid loci. The environmental effect is an independent random
 113 normal variable with mean 0 and variance σ_e^2 . The population mean trait value is
 114 then the mean genetic effect, $\bar{z} = \bar{g}$, while the phenotypic variance is the sum of
 115 additive genetic and environmental variance, $\sigma_z^2 = \sigma_g^2 + \sigma_e^2$.

116 Ignoring frequency-dependence for simplicity, let $r(z)$ be the per capita growth
 117 rate when rare (hereafter fitness) of individuals with quantitative trait z . Let
 118 density-dependence affect all individuals equally. The expected rate of change in
 119 the current mean trait value due to natural selection on standing genetic variation
 120 is then approximately the product of standing genetic variance and the selection
 121 gradient, $E[d\bar{z}/dt] = d\bar{g}/dt \approx \sigma_g^2 \partial \bar{r} / \partial \bar{g}$, where \bar{r} is the population mean growth
 122 rate. We assume additive genetic variance remains constant at some equilibrium
 123 (which we estimate in specific examples below and compare to simulations).

124 Now assume there is some trait value, θ , that maximizes fitness, $r(\theta)$, and let
 125 this value increase linearly in time at rate k , such that its value at time t is $\theta(t) =$
 126 kt . A quasi-steady-state is then achieved when the expected rate of evolution
 127 matches the rate of change in the environment, $d\bar{g}/dt = k$. If at this steady-state
 128 the expected population mean growth rate is positive, $\bar{r} > 0$, the population will
 129 persist. If instead the growth rate is negative, $\bar{r} < 0$, the rate of environmental
 130 change is too fast and the population goes extinct. The rate of environmental
 131 change that causes an expected growth rate of zero, $\bar{r} = 0$, at steady-state is termed
 132 the critical rate of environmental change, k_c .

133 However, there is also the – yet to be discussed – possibility that such a steady-

134 state does not exist. In particular, a steady-state does not exist if the rate of evo-
 135 lution has some maximum and the rate of environmental change is beyond this.
 136 More importantly, if, over the range of phenotypic lags that allow population per-
 137 sistence, the rate of evolution is maximal at some intermediate lag, then popula-
 138 tion growth rate at steady-state will not decline continuously towards zero as the
 139 rate of environmental change increases (see supplementary online material for a
 140 more technical discussion). Instead, the long-run population growth rate will jump
 141 from a potentially large positive number to a potentially very negative number as
 142 the rate of environmental change increases through the maximum rate of evolu-
 143 tion. Technically, this is due to an inflection point in the fitness function causing
 144 a saddle-node bifurcation. When this bifurcation causes extinction we refer to the
 145 maximum rate of evolution as an ‘evolutionary tipping point’. When an evolution-
 146 ary tipping point exists it is the meaningful predictor of persistence (disregarding
 147 stochastic factors), and there is no critical rate of environmental change as defined
 148 by Lynch and Lande (1993).

149 To demonstrate the effect of changes in the shape of the commonly assumed
 150 fitness function more concretely, we will next compare results arising from the
 151 ‘traditional’ fitness function to those arising from an alternative fitness function
 152 that imposes a limit on the rate of evolution (see the supplementary material for
 153 detailed derivations). In doing so we do not mean to imply that our alternative fit-
 154 ness function is necessarily always more biologically relevant than the traditional.
 155 Our alternative fitness function is used only to demonstrate that subtle changes in
 156 the shape of the fitness function may have dramatic effects on our predictions for

157 adaptation and persistence in a rapidly changing world.

158 **The traditional fitness function**

159 We begin with the traditional fitness function in continuous time, $r(z) = r_m - (\theta -$
 160 $z)^2/(2\sigma_w^2)$ (Lynch and Lande, 1993, equation 1), where r_m is the maximum per
 161 capita growth rate and σ_w^2 determines the strength of stabilizing selection (stronger
 162 if smaller) around θ . Averaging over the phenotypic distribution, we find that pop-
 163 ulation mean growth rate, \bar{r} , is reduced by the magnitude of the mean phenotypic
 164 lag, $\bar{l} = \theta - \bar{z}$, and by standing genetic variance (Lande and Shannon, 1996), e.g.,
 165 when the mean trait value matches the optimum, $\bar{l} = 0$, the mean growth rate is
 166 $\bar{r}_m = r_m - \sigma_z^2/(2\sigma_w^2)$. Furthermore, this function implies that as mean trait value
 167 departs from the optimum population growth rate declines ever more rapidly, and
 168 there is no bound on how negative it can become (gray curve in Figure 1A).

169 The expected rate of evolution given the current mean genotypic value is
 170 $d\bar{g}/dt = \sigma_g^2(\theta - \bar{g})/\sigma_w^2$ (Lynch and Lande, 1993, equation 5). This is a linear
 171 function of the expected mean phenotypic lag, $E[\bar{l}] = \theta - \bar{g}$, and therefore as lag
 172 increases so too does the rate of evolution, without bound (gray curve in Figure
 173 1B). Thus, there is always a solution to the quasi-steady-state equation $d\bar{g}/dt = k$,
 174 i.e., there is always some expected mean lag, $E[\bar{l}] = \hat{l}$, that produces the required
 175 rate of evolution.

176 In this particular case the steady-state lag is $\hat{l} = k\sigma_w^2/\sigma_g^2$ (gray curve in Figure
 177 1C). Evaluating the population mean growth rate at this lag gives the expected
 178 long-run population growth rate for an infinitely large population in a determinis-

179 tic environment. Increasing rates of environmental change cause a smooth decline
 180 in this long-run growth rate (gray curve in Figure 1D). We can therefore solve for
 181 the rate of environmental change, k , that makes the long-run growth rate 0, giving
 182 the critical rate of environmental change, $k_c = \sigma_g^2 \sqrt{2\bar{r}_m/\sigma_w^2}$ (Lynch and Lande,
 183 1993, equation 11).

184 **An alternative fitness function**

185 Here we alter the assumption that fitness declines increasingly fast as trait val-
 186 ues depart from the optimum. Instead, we depict a scenario where, far from the
 187 optimum, small departures from the optimum have smaller and smaller fitness
 188 consequences. This could result from selection becoming weaker with increasing
 189 maladaptation (for which there is some evidence; Agrawal and Whitlock, 2010),
 190 which in turn could be caused by a lower bound on fitness (i.e., there is some
 191 maximum rate at which a population can decline). For example, when selection
 192 acts only through birth rate, which cannot be negative, while death rate ($m > 0$)
 193 is fixed, Malthusian fitness is bounded below by $-m$. However, we would like
 194 to emphasize that growth rates do not have to be bounded below for evolutionary
 195 tipping points to exist – all that is required is an inflection point.

196 Consider an alternative fitness function $r(z) = r_m - d [1 - \exp(-(\theta - z)^2 / (2\sigma_w^2))]$.

197 This is a Gaussian fitness function (in *continuous* time) with maximum growth rate
 198 r_m at $z = \theta$ and minimum growth rate $r_m - d$, achieved as lags tend to plus or mi-
 199 nus infinity. For comparison, the alternative fitness function has been constructed
 200 such that when $d = 1$ it is equivalent to the traditional fitness function, to second

order, when trait values are near the optimum. Averaging over the phenotypic distribution, we find that the population mean growth rate (black curve in Figure 1A) has an inflection point at mean lag $E[\bar{l}] = V^{1/2}$, where $V = \sigma_w^2 + \sigma_z^2 + \sigma_\theta^2$.

The expected rate of evolution is $d\bar{g}/dt = d\sigma_g^2\sigma_w E[\bar{l}] \exp[-E[\bar{l}]^2/(2V)]/V^{3/2}$ (black curve in Figure 1B). The rate of evolution is no longer a linear function of expected mean lag, $E[\bar{l}]$. Instead, there is a maximum rate of evolution, $k_{tip} = d\sigma_g^2\sigma_w \exp(2)/V$, at the inflection point, $E[\bar{l}] = V^{1/2}$.

When the rate of environmental change is less than this maximum rate of evolution, $k < k_{tip}$, the steady-state lag is $\hat{l} = (Vw_k)^{1/2}$ (solid black curve in Figure 1C), where w_k is the solution to $w_k e^{w_k} = (kV)^2/(d\sigma_g^2\sigma_w)^2$ (i.e., $w_k(x)$ is the Lambert W function, and here $x = (kV)^2/(d\sigma_g^2\sigma_w)^2$; Lehtonen, 2016). If this lag remains biologically valid (real) at the point where the expected long-run population growth rate becomes zero, there is a critical rate of environmental change, k_c , that determines persistence. If, on the other hand, there is no valid steady-state lag that gives a population growth rate of zero then there is no ‘critical rate of environmental change’, as typically defined (Lynch and Lande, 1993). Instead, it is the maximum rate of evolution that determines persistence (with weak selection this occurs when $d[1 - \exp(-1/2)] < r_m < d$; the upper bound is required to ensure the population goes extinct as lag tends to infinity), and the maximum rate of evolution is an ‘evolutionary tipping point’ (black curves in Figure 1D).

When the rate of environmental change is less than the maximum rate of evolution the population mean growth rate is $\bar{r} = r_m - [1 - \sigma_w \exp(-\hat{l}/(2(\sigma_w^2 + \sigma_z^2)))] > 0$. This can be substantially positive right up to the tipping point (where $\hat{l} = V^{1/2}$)

when the maximum growth rate is large, $r_m \approx d$. However, as soon as the rate of environmental change increases above the maximum rate of evolution, the mean lag increases quickly without bound, leading to a population growth rate of $\bar{r} \approx r_m - d$, and therefore rapid extinction when the maximum population growth rate is small, $r_m \ll d$. In any case, at the evolutionary tipping point, long-run population growth rates go from positive values to negative values without ever crossing zero, causing what may appear to be highly sustainable populations to rapidly begin to go extinct.

Simulations

We next use stochastic, individual-based simulations to (i) compare the dynamics arising from the traditional and alternative fitness functions, (ii) examine generic early-warning signs of approaching tipping points, and (iii) demonstrate the consequences of evolutionary hysteresis.

Simulation methods

We use discrete time simulations with non-overlapping generations (as described in Bürger and Lynch, 1995), which allows us to compare our results to previous studies and provides us with analytical predictions for the additive genetic variance (equations 14 and 15 in Bürger and Lynch, 1995) as well as empirically justified parameters (Bürger and Lynch, 1995). To convert our continuous time models into discrete time, we set the expected number of offspring per parent to $B = \exp(r_m)$ and the probability of survival to adulthood $W(z) =$

245 $\exp[r(z) - r_m]$, such that growth rates in the absence of density-dependence are
 246 equivalent, $BW(z) = \exp[r(z)]$ (Crow and Kimura, 1970, Chapter 1). Example
 247 scripts (Python Software Foundation, version 3.5; <http://www.python.org>) are pro-
 248 vided in the supplementary material.

249 Briefly, each individual's trait is determined by n additive, freely-recombining
 250 diploid loci plus a random normal environmental effect with mean 0 and variance
 251 1. All simulations are initiated as in Bürger and Lynch (1995); we create 5 ances-
 252 tral alleles at each locus, their effects being random normal variables with mean
 253 0 and variance $(0.1\alpha)^2$. The first generation of individuals are then created by
 254 randomly choosing two ancestral alleles for each locus, with replacement. Sim-
 255 ple density dependence then acts by randomly choosing K individuals if there are
 256 more than K . These pair at random (potentially leaving one individual out) and
 257 each pair produces $2B$ offspring by fair Mendelian transmission. Each gamete
 258 mutates with probability $n\mu$. If it does mutate one locus is chosen at random and
 259 a random normal effect, with mean 0 and variance α^2 , is added. Viability selec-
 260 tion then acts, with survival probability $W(z)$. A maximum K surviving offspring
 261 become the parents of the next generation. The first 1,000 generations are used as
 262 a burn-in with $k = 0$. Simulations continue until the population goes extinct or the
 263 maximum number of generations is reached (11,000 in Figures 2 and 4; 201,000
 264 in Figure 3).

265 **Comparing the dynamics arising from traditional and alternative fitness func-**
 266 **tions**

267 Figure 2 shows the effect of the rate of environmental change on evolution and
 268 persistence with the traditional (A-E) and alternative fitness functions (F-J). Panels
 269 A-C and F-H show that our analytical predictions (broken lines; discrete time
 270 analysis in the supplementary online material) for steady-state lag, equilibrium
 271 additive genetic variance, and population mean growth rate perform fairly well for
 272 those populations that persist (black circles). In particular, the simulation results
 273 are intermediate between our predictions using the neutral (dotted) and stochastic-
 274 house-of-cards (dashed) approximations for the genetic variance (equations 14
 275 and 15 in Bürger and Lynch, 1995), which therefore provide reasonable bounds.
 276 Comparing Figure 2B to the circles in figure 6 in Bürger and Lynch (1995) further
 277 suggests that our simulation method is accurate.

278 With the traditional fitness function, population growth rates decline as the
 279 rate of environmental change increases (Figure 2C), as expected from the ana-
 280 lytical theory. However, in contrast to analytical expectations, the growth rates
 281 of surviving populations do not reach values close to zero. Thus, even with a
 282 traditional fitness function we see a dynamic similar to that expected from an
 283 evolutionary tipping point: a small increase in the rate of environmental change
 284 causes populations with a relatively large growth rate to suddenly begin to go
 285 extinct. This dynamic is likely caused by a negative feedback between genetic
 286 variance, which is constant in the analytical theory, and mean lag (as described in
 287 Bürger and Lynch, 1995). When genetic variance declines, the population evolves

288 slower and the mean lag increases. Vice versa, when the mean lag increases, se-
 289 lection becomes stronger and genetic variance declines. Since large lags cause
 290 low growth rates, this feedback can spiral to extinction. The extinction spiral can
 291 be initiated by either a bout of reduced genetic variance caused by random ge-
 292 netic drift or a period of increased mean lag because beneficial genotypes fail to
 293 arise by chance (given segregation and mutation are random events). This spi-
 294 ral is therefore reminiscent of “mutational meltdown” (Lynch and Gabriel, 1990),
 295 where genetic drift increases the probability of fixing deleterious alleles. The ex-
 296 tinction spiral observed here, in a changing environment, additionally involves
 297 the loss of genetic variance due to genetic drift (including a reduced probability of
 298 maintaining beneficial alleles) and a deterministic decrease in the rate of beneficial
 299 mutations ($\sim n\mu NB$ per generation when the lag is sufficiently large).

300 With the alternative fitness function, population growth rates of surviving pop-
 301 ulations also fail to reach values near zero as the rate of environmental change in-
 302 creases (Figure 2H), this time as expected from the analytical theory. In addition,
 303 the rate of environmental change that causes extinction is roughly what we ex-
 304 pect the evolutionary tipping point to be given the genetic variance is intermediate
 305 between the two analytical predictions.

306 Panels D-E and I-J further show how the transition from persistence to extinc-
 307 tion is fairly abrupt for both fitness functions. Although, with these parameters,
 308 the transition might be slightly more abrupt in the presence of an evolutionary
 309 tipping point, the traditional fitness function exhibits similarly sharp transitions as
 310 carrying capacity, and thus effective population size, is increased (see supplemen-

311 tary material for results with a traditional fitness function and $K = 1024$). An in-
 312 crease in the sharpness of the transition from persistence to extinction with larger
 313 population size is also demonstrated in figure 2B in Bürger and Lynch (1995).

314 **Early-warning signs of evolutionary tipping points**

315 Two common, generic early-warning signs of saddle-node bifurcations are in-
 316 creases in lag-1 autocorrelation and in temporal variation (Scheffer et al., 2009;
 317 Lenton, 2011). If these metrics can reliably predict a nearby evolutionary tip-
 318 ping point they may be useful in pinpointing at-risk populations whose population
 319 growth rates do not advertise the possibility of imminent extinction (Figure 2H).

320 Generic early-warning signs are only predicted to work when a gradual change
 321 in a parameter brings the system closer to a saddle-node bifurcation (Boettiger
 322 and Hastings, 2012). We therefore ran simulations where the rate of environmen-
 323 tal change, k , increased from 0 by a small amount each generation. Panels A
 324 and B of Figure 3 show how mean phenotypic lags (black) increase and popula-
 325 tion growth rates (gray) decrease as the rate of environmental change speeds up
 326 over time, for both the traditional fitness function and the alternative fitness func-
 327 tion (10 replicates for each). Panels B-F show the changes in the early-warning
 328 signs: temporal variation and lag-1 autocorrelation (calculated within each repli-
 329 cate using non-overlapping windows of 3000 generations, each data point 100
 330 generations apart). As measured by Kendall rank correlation coefficients (Dakos
 331 et al., 2008), temporal variance increases in all cases (all $\tau > 0$; panel G) and
 332 the increase in variance is not more consistent when approaching the evolution-

333 ary tipping point than it is when approaching the critical rate of environmental
 334 change [two-sided t -test comparing Kendall's τ in variance between traditional
 335 and alternative fitness functions: $T = -0.48$, $p = 0.64$, $df = 12.41$ (mean lag) and
 336 $T = 1.75$, $p = 0.11$, $df = 10.84$ (population growth)]. An increase in temporal
 337 variance therefore does not provide a reliable signal of nearby evolutionary tip-
 338 ping points. On the other hand, the Kendall rank correlation coefficients in lag-1
 339 autocorrelation are generally greater when approaching the evolutionary tipping
 340 point than when approach the critical rate of environmental change [panel H; two-
 341 sided t -test comparing Kendall's τ in lag-1 autocorrelation between traditional
 342 and alternative fitness functions: $T = -3.18$, $p = 0.01$, $df = 18$ (mean lag) and
 343 $T = -2.89$, $p = 0.01$, $df = 13.05$ (population growth)]. However, the majority of
 344 the τ 's for lag-1 autocorrelation are negative except those for population growth
 345 rate with the alternative fitness function, but the mean of this distribution is not
 346 significantly different from zero (two-sided t -test: $T = 1.31$, $p = 0.22$, $df = 9$).
 347 Thus, a consistent increase in the lag-1 autocorrelation of growth rate may pro-
 348 vide a hint that a population is approaching an evolutionary tipping point, but the
 349 absence of this pattern says little.

350 **Evolutionary hysteresis**

351 In the presence of an evolutionary tipping point, a population experiencing a
 352 slowly changing environment, $k < k_{tip}$, is expected to attain a sustainable steady-
 353 state lag. Deterministically, it will maintain increasing yet sustainable steady-state
 354 lags as the rate of environmental change increases, until the rate of environmental

355 change increases beyond the tipping point, $k_{tip} < k$. Weakening selection then
 356 causes the steady-state lag to make a discontinuous jump (or be lost entirely), and
 357 the population begins to go extinct. However, even if we ignore demographics and
 358 extinction, the dynamics as we decrease the rate of environmental change through
 359 the tipping point are not the same. For example, with the alternative fitness func-
 360 tion used here, when the rate of environmental change is beyond the tipping point,
 361 $k_{tip} < k$, the mean lag quickly increases towards infinity as selection becomes
 362 vanishingly weak. Decreasing the rate of environmental change below the tipping
 363 point, $k < k_{tip}$, then only results in a stable steady-state lag if the current mean lag
 364 has remained small enough to produce a rate of evolution greater than the current
 365 rate of environmental change. Otherwise the mean lag falls outside the basin of
 366 attraction of the stable steady-state lag, where selection is too weak to allow it to
 367 catch-up. Since the dynamics of the system passing through the tipping point in
 368 one direction are not the same when passing through in the opposite direction, we
 369 can say that the state of the system depends on its history, which is called hys-
 370 teresis. Because in this case hysteresis involves an evolving trait, we call the phe-
 371 nomenon of the attainment of a steady-state lag depending on the past history of
 372 environmental change ‘evolutionary hysteresis’. Hysteresis has been described in
 373 other evolutionary contexts, which differ from ours by involving feedbacks with
 374 demography; temporary reductions in the size of habitat patches can cause per-
 375 manent losses of genetic polymorphism (Kisdi and Geritz, 1999) and temporary
 376 increases in the rate of migration between habitat patches can cause permanent
 377 reductions in population size (Ronce and Kirkpatrick, 2001).

378 Now considering demographics in our case, note that a short period of fast en-
 379 vironmental change, $k_{tip} < k$, can cause eventual extinction, even after the rate of
 380 environmental change has been reduced below the tipping point, $k < k_{tip}$. In other
 381 words, evolutionary hysteresis produces an extinction debt. Extinction debts have
 382 also been predicted in non-evolving communities of competitors exposed to habi-
 383 tat destruction (Tilman et al., 1994) and in evolving communities of competitors
 384 exposed to gradually changing environments (Norberg et al., 2012), but neither of
 385 these debts are caused by evolutionary hysteresis and both are only predicted to
 386 occur when the environment remains in its changed state.

387 Evolutionary hysteresis can also be induced by a sufficiently large jump in the
 388 optimum or mean trait value, as either of these can displace the mean lag from
 389 the basin of attraction of a sustainable steady-state lag. Figure 4 shows how a
 390 large jump in the optimum trait value can result in evolutionary rescue in the ab-
 391 sence of evolutionary tipping points (panels A-D) but evolutionary hysteresis and
 392 an extinction debt in their presence (panels E-F). In this example, the optimum
 393 trait value increases by a small amount each generation ($k = k_1 < k_{tip}$) for the first
 394 5000 generations. The optimum then makes a much larger jump at generation
 395 5000, and from there continues to increase at the original rate ($k = k_1$). Regard-
 396 less of whether there is a tipping point, the large jump in the optimum trait value
 397 at generation 5000 causes mean lags to increase so much that populations begin
 398 to decline. However, in the absence of a tipping point, the increase in mean lag
 399 also causes the strength of selection, and hence the rate of evolution, to increase,
 400 which rescues half of the replicates from extinction. In sharp contrast, the evo-

401 lutionary tipping point causes selection to become weaker when the mean lag is
 402 increased at generation 5000. The rate of evolution thus slows and the mean lag
 403 increases dramatically, causing 9/10 replicates go extinct (the mean lag of one
 404 lucky replicate does not escape the basin of attraction; dotted line in panel E). For
 405 these parameter values, extinction tends to occur ≈ 300 generations after the jump
 406 in the optimum, meaning that short term environmental perturbations can lead to
 407 extinctions far into the future (i.e., an extinction debt).

408 **Discussion**

409 Adaptive evolution requires population persistence, heritable variation, and se-
 410 lection. Previous authors have shown how persistence (e.g., Lynch and Lande,
 411 1993; Bürger and Lynch, 1995) and variation (Gomulkiewicz and Houle, 2009)
 412 can constrain evolution. However, because of the specific fitness functions com-
 413 monly assumed in theoretical quantitative genetics for the sake of mathematical
 414 convenience, the idea that selection can also constrain evolution has, up till now,
 415 largely been overlooked. In particular, we have shown that when the strength of
 416 selection does not uniformly increase with maladaptation, selection itself can be
 417 the limiting factor determining the ability of a population to evolve and persist in
 418 the face of directional environmental change. With limiting selection, a qualita-
 419 tively different persistence threshold arises, a difficult to detect evolutionary tip-
 420 ping point that gives rise to an extinction debt. This is particularly worrying given
 421 that all current quantitative genetic predictions effectively use the same specific

422 fitness function, which assumes selection is never limiting.

423 One obvious question that follows from our work is what fitness functions
 424 look like in nature. Much of our knowledge about the shape of empirical fitness
 425 functions comes from four main sources: selection gradient analysis (Lande and
 426 Arnold, 1983), cubic spline analysis (Schluter, 1988), aster analysis (Shaw et al.,
 427 2008; Shaw and Geyer, 2010), and mutation accumulation/reverse genetics (re-
 428 viewed in de Visser and Krug, 2014). Selection gradient analysis is a linear or
 429 quadratic regression of fitness on trait value. Thus, even if fitness was measured
 430 as growth rate or lifetime fitness (r or $W \approx \exp(r)$, respectively) it would not be
 431 possible to detect potential tipping points (inflection points in r or in $\log(W)$),
 432 and hence is of little value here. Cubic spline analysis removes the parametric
 433 constraint, and thus could suggest the presence of inflection points if one mea-
 434 sured lifetime fitness (e.g., Réale et al., 2003; Wilson et al., 2005). However, most
 435 cubic spline analyses relate only one aspect of absolute fitness (e.g., survival) to
 436 trait value (e.g., Figure 4 in Reimchen and Nosil, 2002). Conflicting selection at
 437 other life-stages (e.g., Robinson et al., 2006) could therefore drastically change
 438 the shape of this function. Meanwhile, aster analysis is designed to calculate life-
 439 time fitness and can simultaneously estimate fitness functions (e.g., Figure A2 in
 440 Shaw et al., 2008). However, aster analysis fits a quadratic as the fitness function
 441 (parametric bootstrap on a scaled measure of fitness; Shaw et al., 2008) and there-
 442 fore may also miss inflection points. Thus, combining lifetime fitness estimates
 443 from aster with nonparametric cubic spline analysis – along with experimentally-
 444 induced environmental change (e.g., Weis et al., 2014) or phenotypic manipula-

445 tion (e.g., Sinervo et al., 1992; Simons, 2009) to probe the tails of fitness functions
 446 – is one promising way to identify potential evolutionary tipping points. Finally,
 447 mutation accumulation and reverse genetics can be used to construct mutant geno-
 448 types and evaluate their fitness, producing incredibly detailed fitness landscapes
 449 of microbial populations in the lab (e.g., Figure 2 in Bank et al., 2016). Beginning
 450 from near the optimal genotype and with fitness measured as population growth
 451 rate, a pattern of antagonistic (positive) epistasis between deleterious mutations
 452 (i.e., each additional mutation adds a smaller detrimental effect to $r = \log(W)$)
 453 would indicate that selection gets weaker with maladaptation and therefore that
 454 an evolutionary tipping point might exist. It has been suggested that antagonistic
 455 epistasis is more likely in organisms with simpler genomes, where there is less
 456 genetic robustness (Sanjuán and Elena, 2006) – suggesting such organisms might
 457 be more likely to experience evolutionary tipping points – but it is unclear if this
 458 result will hold up to more data (Agrawal and Whitlock, 2010). It is worth not-
 459 ing that sterilizing or lethal mutations (in particular those that cause $W(z) = 0$ or
 460 $r(z) \rightarrow -\infty$), which are difficult to detect in studies that do not construct mutants
 461 (e.g., mutation accumulation), create strong synergistic (negative) epistasis (e.g.,
 462 Lalić and Elena, 2012) and hence reduce the possibility of tipping points induced
 463 by limiting selection. At the same time, these mutations impose their own kind of
 464 tipping point by putting an irreversible end to all lineages that acquire them.

465 In the process of illustrating how limiting selection can cause evolutionary tip-
 466 ping points, we unexpectedly discovered a sudden transition from relatively large
 467 positive growth rates to extinction with small changes in the rate of environmental

468 change in simulations of the ‘traditional’ quantitative genetics model (Figure 2C).
 469 This transition is caused by a negative feedback between genetic variance and
 470 maladaptation (Bürger and Lynch, 1995), a process akin to mutational meltdown
 471 (Lynch and Gabriel, 1990) but with a stronger dependence on the maintenance
 472 of genetic variance and the acquisition of beneficial mutations, both of which are
 473 necessary for populations to persist in changing environments. The extinction
 474 spiral observed here therefore differs from evolutionary tipping points, which are
 475 caused by negative feedbacks between maladaptation and the strength of selec-
 476 tion (opposite to above), and which are expected to occur even in infinitely large
 477 populations and when genetic variance is constant. The expected effects also dif-
 478 fer, as is exemplified in Figure 4, where it is shown that only the evolutionary
 479 tipping point strongly diminishes the probability of evolutionary rescue for these
 480 parameter values. While it has been noticed that simulated populations tend to go
 481 extinct at rates of change less than the critical in the traditional model, and the
 482 reasons for it have been discussed (Bürger and Lynch, 1995), the implications for
 483 detecting populations near extinction thresholds has not been appreciated. Just as
 484 predicted near an evolutionary tipping point, small changes in the rate of environ-
 485 mental change in the traditional model can cause populations with relatively large
 486 positive growth rates to suddenly go extinct, giving little information on how to,
 487 for example, triage populations of conservation concern. Thus, while critical rates
 488 of environmental change estimated from simple analytical models may give us
 489 rough estimates of the conditions under which extinction or persistence will oc-
 490 cur, the added complexities of a dynamic genetic variance and limiting selection

⁴⁹¹ add caution to their interpretation and use.

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643 Figure legends

Figure 1: Visual overview of the modelling approach. Population mean growth rates, \bar{r} , shown in **A**, are derived by integrating the traditional (*gray*) and alternative (*black*) fitness functions, $r(z)$, over the phenotypic distribution, $p(z)$. Taking the derivative of mean population growth rate with respect to the mean trait value, $d\bar{r}/d\bar{z}$, gives the selection gradients shown in **B**. Setting the rate of evolution equal to the rate of change in the environmental optimum ($\sigma_g^2 d\bar{r}/d\bar{z} = k$; where the dashed line intersects the solid curves in **B**) gives the steady-state lags, \hat{l} , shown in **C**. With the traditional fitness function all steady-state lags are stable (filled circles in **B** and solid lines in **C**), while those that are on the decreasing portion of the selection gradient with the alternative fitness function are unstable (open circle in **B** and dashed lines in **C**). Evaluating population mean growth rate at a stable steady-state lag gives the long-run population growth rates shown in **D**. The rate of change that causes a long-run growth rate of zero is the critical rate of environmental change. Because the long-run population growth rate with an alternative fitness function switches sign without crossing zero at the bifurcation point in **C**, we call this rate of environmental change an evolutionary tipping point. Parameters: $r_m = \log(2)$, $\sigma_w^2 = 9$, $\sigma_e^2 = 1$, $\sigma_g^2 \approx 0.18$, and $d = 1$.

Figure 2: Discrete-time, individual-based simulation results with traditional (**A-E**) and alternative (**F-J**) fitness functions. In discrete time the traditional fitness function is $W(z) = \exp[-(\theta - z)^2/(2\sigma_w^2)]$ (Bürger and Lynch, 1995, equation 1) and the alternative fitness function is $W^*(z) = \exp[d(W(z) - 1)]$. “Population growth rate” is the number of offspring surviving viability selection (before density-dependence) divided by the number of parents, minus one. “Fraction extinct” is the number of replicates that go extinct before the end of the simulation (generation 11,000). In **A-C** and **F-H**, circles give mean values over the last 10 recorded time points (every 100 generations) for each replicate simulation (10 for each rate of environmental change), or over all recorded time points since the burn-in if less than 10 time points since the burn-in. Gray circles are replicates that went extinct before the end of the simulation. Broken curves in **A-C**, and **F-H** give analytic results using the stochastic-house-of-cards (dashed) and neutral (dotted) approximations for genetic variance (equations 14 and 15 in Bürger and Lynch, 1995). Parameters as in Bürger and Lynch (1995): $B = 2$, $\sigma_w^2 = 9$, $\sigma_e^2 = 1$, $K = 512$, $\mu = 2 \times 10^{-4}$, $\alpha^2 = 0.05$, $n = 50$, and $d = 1$.

Figure 3: Generic early-warning signs of tipping points. Here the rate of environmental change, k , gradually increases from 0 by 10^{-6} phenotypic units every generation, eventually causing extinction. With the traditional fitness function (**A-C**) there is no saddle-node bifurcation and extinction occurs as the rate of environmental change approaches $k = 0.175$, as in Figure 2. On the other hand, with the alternative fitness function (**D-F**) there is a saddle-node bifurcation and extinction is caused by an evolutionary tipping point near $k = 0.125$, as in Figure 2. Nevertheless, in both cases the temporal variance in mean phenotypic lag (*black*) and population growth rate (*gray*) tend to increase (**B,E**) and Kendall rank correlation coefficients, τ , do not differ significantly between the two fitness functions (**G**; details in text). **C** and **F** show the dynamics of lag-1 autocorrelation in mean phenotypic lag and population growth rate for both fitness functions, and the Kendall rank correlation coefficients (**H**) indicate that a consistent increase in the lag-1 autocorrelation of population growth rate may be the best predictor of an approaching evolutionary tipping point for this set of parameters (details in text). Shown are ten replicate simulations for each fitness function, with parameters as in Figure 2. Variance and lag-1 autocorrelation are measured for each replicate separately, using non-intersecting windows of 30 consecutively recorded time points, each 100 generations apart.

Figure 4: Evolutionary hysteresis prevents evolutionary rescue and creates an extinction debt. Here the optimum trait value increases gradually ($k = 0.1$), experiences a sudden jump (5 phenotypic units) at generation 5000, and from there continues to increase at the gradual rate ($k = 0.1$). With the traditional fitness function (**A-D**), the sudden increase in mean lag at generation 5000 causes an increase in the strength of selection and hence in the rate of evolution, rescuing populations from extinction. With the alternative fitness function (**E-F**), the mean lag increases to values that are often just beyond the basin of attraction of the steady-state lag at $k = 0.1$ (dotted line in **E**, using the neutral approximation for genetic variance; $k = 0.1$ is beyond the tipping point with the stochastic-house-of-cards approximation for genetic variance). (**F**) The rate of evolution then declines (except in one lucky replicate that does not escape the basin of attraction), causing further increases in the mean lag, which further decreases the rate of evolution, and so on, leading to an apparent existential crisis. Broken lines show the maximum rate of evolution using the neutral (dotted) and stochastic-house-of-cards (dashed) approximations for genetic variance. (**G**) The ever increasing mean lag lowers the population mean growth rate, eventually reaching values below replacement (horizontal line). (**H**) This drop in population growth rates ultimately, some ~ 300 generations later, results in extinction. The horizontal line is the maximum number of parents, K . Here the fitness functions (see Figure 2) are multiplied by $(1 - d')$, the probability that an optimally adapted individual survives viability selection. This generalization gives more flexibility in minimum growth rate without affecting the strength of selection. Parameters as in Figure 2, except $B = 3$ and $d' = 0.1$.