

A lottery model of density-dependent selection

Keywords: r/K selection, absolute fitness, eco-evo, Grime's triangle, competition-colonization trade-off, fluctuating selection, storage effect.

Abstract

Fitness is typically represented in heavily simplified terms in evolutionary genetics, often using constant selection coefficients

This excludes fundamental ecological factors such as dynamic population size or density-dependence from the most genetically-realistic treatments of evolution, a problem that inspired MacArthur's influential but problematic r/K theory.

Following the spirit of r/K -selection as a general-purpose theory of density-dependent selection

new model of density-dependent selection by generalizing the fixed-density classic lottery model of territorial acquisition to accommodate arbitrary population densities.

We show that, with density dependence, co-existence is possible in the lottery model in a stable environment.

Inspired by natural *Drosophila* populations, we consider co-existence under strong, seasonally-fluctuating selection coupled to large cycles in population density, and show that co-existence (stable polymorphism) is promoted via a combination of the classic storage effect and density-regulated population growth.

17 Introduction

18 The density-dependent selection literature contains some of the earliest explicit analyses of the
19 interplay between ecology and evolution [Travis et al., 2013]. Much of this work grew out of
20 MacArthur’s r/K -selection scheme [MacArthur, 1962, MacArthur and Wilson, 1967] in which
21 r -selection favors faster growth at low density, whereas K -selection favors the ability to keep
22 growing at high density.

23 Although r and K are named after the common “carrying capacity” parameterization of the
24 logistic model, the concepts of r - and K -selection are not restricted to that model [MacArthur and
25 Wilson, 1967].

26 Yet selection does not only change relative genotypic proportions. Ultimately, it involves the
27 births and deaths of individuals, and is therefore intimately connected to changes in absolute
28 abundance ?. This immediately poses a challenge: any description of evolution grounded in
29 abundances needs to specify how population density is regulated, as well as how fitness depends
30 on density, which may differ between genotypes (density-dependent selection). As a result,

31 One of the simplest and most widely used models of selection is to assign genotypes constant
32 selection coefficients describing how their relative proportions change over time. This model is
33 common in population genetics, where its simplicity is useful for analyzing the detailed time
34 course of genotypic frequencies.

35 Nevertheless, much of the density-dependent selection literature has adopted variants of the
36 logistic model, often in the setting of Mendelian inheritance ?.

37 with genotype-specific K values parameterizing growth ability at high density. A closely
38 related approach is to add Lotka-Volterra-type inter-genotypic competition terms with α com-
39 petition coefficients, which adds “ α -selection” to the mix Case and Gilpin 1974, Gill 1974, Joshi
40 et al. 2001.

41 variant that allows for inter-genotypic versus intra-genotypic
42 or explicit resource consumption [Tilman, 1982], are much more complicated.

r/K scheme [MacArthur, 1962, MacArthur and Wilson, 1967] is now almost exclusively known as a framework for understanding life-history traits, and judged on its failure in that role [Boyce, 1984, Pianka, 1970, Reznick et al., 2002, Stearns, 1977].

in a simplified, territorial model of growth, dispersal and competition.

We revisit the classic lottery model of Chesson and Warner [1981], which has two features that make it well suited for this role, but one critical flaw that we rectify here.

The first feature is that the lottery representation of competition is particularly concise. Mature individuals (“adults”) each require their own territory, whereas newborn individuals (“propagules”) disperse to, and subsequently compete for, territories made available by the death of adults. Territorial contest among propagules leaves a single victorious adult per territory, the victor chosen at random from the propagules present, with probabilities weighted by a coefficient for each type representing competitive ability, akin to a lottery [Sale, 1977].

The second feature is the close connection between the lottery model and one of the foundational models of population genetics, the Wright-Fisher model of genetic drift, which we discuss further below.

The critical flaw of the classic lottery model is that it breaks down at low densities (few propagules dispersing to each territory), precluding density-dependent behaviour. Our first task is to analytically extend the classic lottery model to correctly account for low density behavior (sections “Model” and “Mean field approximation”).

Taking an example inspired by recent studies of rapid, seasonal evolution in *Drosophila* [Bergland et al., 2014], we discuss how environmental fluctuations might stabilize polymorphisms when population density is cyclical.

Model

We assume that reproductively mature individuals (“adults”) each require their own territory to survive and reproduce (Fig. 1). All territories are identical, and the total number of territories is

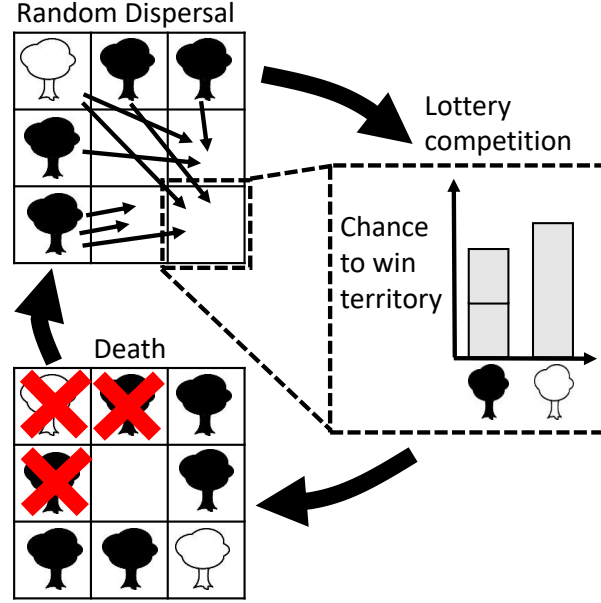


Figure 1: Each iteration of our model has three elements. First, propagules are produced by adults and dispersed at random (only propagules landing on unoccupied territories are shown). Lottery competition then occurs in each unoccupied territory (only illustrated in one territory). Each genotype has a probability proportional to $c_i x_i$ of securing a given territory, where c_i measures competitive ability and x_i is the number of propagules that disperse there. In the illustrated territory, the black genotype disperses more propagules but is a poorer competitor. Territories are then made available by adult mortality (red crosses).

68 T . Time t advances in discrete iterations, each representing the time from birth to reproductive
69 maturity. In iteration t , the number of adults of the i 'th genotype is $n_i(t)$, the total number of
70 adults is $N(t) = \sum_i n_i(t)$, and the number of unoccupied territories is $U(t) = T - N(t)$.

71 We assume that the n_i and T are large enough that stochastic fluctuations in the n_i ("drift")
72 can be ignored. We derive deterministic equations for the expected change in the n_i over time,
73 leaving the evaluation of drift for future work. This is an excellent approximation when the n_i
74 are all large. However, we also do not evaluate the initial stochastic behaviour of adaptive mutant
75 lineages while they are at low abundance. When considering new mutations, we therefore restrict
76 our attention to begin with the earliest (lowest n_i) deterministic behavior of mutant lineages (the
77 transition to deterministic growth occurs at an abundance n_i of order equal to their inverse
78 expected absolute growth rate; Uecker and Hermisson 2011).

Each iteration, adults produce new offspring (“propagules”), m_i of which disperse to unoccupied territories. We assume that adults cannot be ousted from their territories, so that m_i only includes propagules landing on unoccupied territories. Propagules disperse at random over the unoccupied territories, regardless of distance from their parents, and independently of each other. There is no interaction between propagules (e.g. avoidance of territories crowded with propagules). Loss of propagules during dispersal is subsumed into m_i .

In general, m_i will increase with n_i , and will depend on population density N . For example, if b_i is the number of successfully dispersing propagules produced per genotype i adult, then the loss of propagules due to dispersal to occupied territories implies $m_i = b_i(1 - N/T)n_i$, akin to Levins’ competition-colonization model [Levins and Culver, 1971, Tilman, 1994]. In section “Cyclical birth and death rates” we evaluate Eq. (4) numerically using this functional form for m_i , with b_i assumed to be constant.

In “Invasion of rare genotypes and coexistence”, we assume the simpler form $m_i = b_i n_i$, with constant b_i , meaning that all propagules land on unoccupied territories (a form of directed dispersal). This simplifies the mathematics without affecting the results of those sections, which only depend on the low-frequency invasion behavior of Eq. (4). Note that due to our assumption of uniform dispersal, the parameter b_i can be thought of as a measure of “colonization ability”, which combines fecundity and dispersal ability [Bolker and Pacala, 1999, Levins and Culver, 1971, Tilman, 1994].

The number of individuals of the i ’th genotype landing in any particular territory is denoted x_i . We assume that x_i follows a Poisson distribution $p_i(x_i) = l_i^{x_i} e^{-l_i} / x_i!$, where $l_i = m_i / U$ is the mean territorial propagule density. This approximation becomes exact when the n_i are large enough that drift in n_i can be ignored (Appendix A).

When multiple propagules land on the same territory, the victor is determined by lottery competition: genotype i wins a territory with probability $c_i x_i / \sum_j c_j x_j$, where c_i is a constant representing relative competitive ability (Fig. 1).

In the classic lottery model [Chesson and Warner, 1981], unoccupied territories are assumed

106 to be saturated with propagules from every genotype $l_i \gg 1$. From the law of large numbers,
 107 the composition of propagules in each territory will then not deviate appreciably from the mean
 108 composition l_1, l_2, \dots, l_G (G is the number of genotypes present), and so the probability that geno-
 109 type i wins any particular unoccupied territory is approximately $c_i l_i / \sum_j c_j l_j$. Let $\Delta_+ n_i$ denote the
 110 number of territories won by genotype i . Then $\Delta_+ n_1, \Delta_+ n_2, \dots, \Delta_+ n_G$ follow a multinomial dis-
 111 tribution with U trials and success probabilities $\frac{c_1 l_1}{\sum_j c_j l_j}, \frac{c_2 l_2}{\sum_j c_j l_j}, \dots, \frac{c_G l_G}{\sum_j c_j l_j}$, respectively. Genotype i
 112 is expected to win $c_i l_i / \sum_j c_j l_j$ of the U available territories, and deviations from this expected
 113 outcome are small (since T is large by assumption), giving

$$\Delta_+ n_i(t) = \frac{c_i l_i}{\sum_j c_j l_j} U(t) = b_i n_i \frac{1}{L} \frac{c_i}{\bar{c}}, \quad (1)$$

114 where $\bar{c} = \sum_j c_j m_j / M$ is the mean propagule competitive ability for a randomly selected propag-
 115 ule, $L = M/U$ is the total propagule density and $M = \sum_j m_j$ is the total number of propagules.

116 There is a close connection between the classic lottery model and the Wright-Fisher model of
 117 genetic drift [Svardal et al., 2015]. In the Wright-Fisher model, genotype abundances are sampled
 118 each generation from a multinomial distribution with success probabilities $w_i n_i / \sum_j w_j n_j$, where
 119 w is relative fitness and the n_i are genotype abundances in the preceding generation. Population
 120 size N remains constant. This is mathematically equivalent to the classic lottery model with non-
 121 overlapping generations ($d_i = 1$ for all i) and $w_i = b_i c_i$. Thus, the classic lottery model allows
 122 us to replace the abstract Wright-Fisher relative fitnesses w_i with more ecologically-grounded
 123 fecundity, competitive ability and mortality parameters b_i , c_i and d_i , respectively. Since birth and
 124 death rates affect absolute abundances, this allows us to evaluate selection at different densities
 125 (after appropriate extensions are made), in an otherwise very similar model to the canonical
 126 Wright-Fisher. We therefore expect that drift in realized values of n_i in our extended lottery
 127 model should be similar to that in the Wright-Fisher model, but we leave this for future work.

128 In our extension of the classic lottery model, we do not restrict ourselves to high propagule
 129 densities. Eq. (1) is nonsensical if even a single type has low propagule density ($l_i \ll 1$): genotype

130 i can win at most m_i territories, yet Eq. (1) demands $c_i l_i / \sum_j c_j l_j$ of the U unoccupied territories,
 131 for any value of U . Intuitively, the cause of this discrepancy is that individuals are discrete.
 132 Genotypes with few propagules depend on the outcome of contests in territories where they
 133 have at least one propagule present, not some small fraction of a propagule as would be implied
 134 by small l_i in the classic lottery model. In other words, deviations from the mean propagule
 135 composition l_1, l_2, \dots, l_G are important at low density.

136 We expect that a fraction $p_1(x_1) \dots p_G(x_G)$ of the U unoccupied territories will have the
 137 propagule composition x_1, \dots, x_G . Genotype i is expected to win $c_i x_i / \sum_j c_j x_j$ of these. Ignoring
 138 fluctuations about these two expectations (due to our no-drift, large T , large n_i approximation),
 139 genotype i 's territorial acquisition is given by

$$\Delta_+ n_i(t) = U(t) \sum_{x_1, \dots, x_G} \frac{c_i x_i}{\sum_j c_j x_j} p_1(x_1) \dots p_G(x_G), \quad (2)$$

140 in our extended lottery model, where the sum only includes territories with at least one propag-
 141 ule present. Note that unlike the classic lottery model, not all unoccupied territories are claimed
 142 each iteration, since under Poisson dispersal a fraction e^{-L} remain unoccupied.

143 We assume that mortality only occurs in adults (Fig. 1; setting aside the juvenile deaths
 144 implicit in territorial contest), and at a constant, genotype-specific per-capita rate $0 \leq d_i \leq 1$, so
 145 that the overall change in genotype abundances is

$$\Delta n_i(t) = \Delta_+ n_i(t) - d_i n_i(t). \quad (3)$$

146 Results

147 Mean Field Approximation

148 Eq. (2) involves an expectation over the time-dependent dispersal distributions p_i , and is thus
 149 too complicated to give intuition about the dynamics of density-dependent lottery competition.

We now evaluate this expectation using a “mean field” approximation.

Similarly to the high- l_i approximation of classic lottery model, we replace the x_i with appropriate mean values, although we cannot simply replace x_i with l_i . For a genotype with low propagule density $l_i \ll 1$, we have $x_i = 1$ in the territories where its propagules land, and so its growth comes entirely from territories which deviate appreciably from l_i . To account for this, we separate Eq. (2) into $x_i = 1$ and $x_i > 1$ parts. Our more general mean field approximation only requires that there are no large discrepancies in competitive ability (i.e. we do not have $c_i/c_j \gg 1$ for any two genotypes). We obtain (details in Appendix B)

$$\Delta_+ n_i(t) \approx b_i n_i \left[e^{-L} + (R_i + A_i) \frac{c_i}{\bar{c}} \right], \quad (4)$$

where

$$R_i = \frac{\bar{c} e^{-l_i} (1 - e^{-(L-l_i)})}{c_i + \frac{L-1+e^{-L}}{1-(1+L)e^{-L}} \frac{\bar{c} L - c_i l_i}{L-l_i}}, \quad (5)$$

and

$$A_i = \frac{\bar{c} (1 - e^{-l_i})}{\frac{1-e^{-l_i}}{1-(1+l_i)e^{-l_i}} c_i l_i + \frac{1}{L-l_i} \left(L \frac{1-e^{-L}}{1-(1+L)e^{-L}} - l_i \frac{1-e^{-l_i}}{1-(1+l_i)e^{-l_i}} \right) \sum_{j \neq i} c_j l_j}. \quad (6)$$

To supplement our analytical mean field derivation, we did numerical simulations of our exact density-dependent lottery model, and verified that Eq. (4) is a good approximation (Appendix B). Thus, Eq. (4) describes how type abundances change over time in a lottery model where population density can itself vary with time.

Comparing Eq. (4) to Eq. (1), the classic lottery per-propagule success rate $c_i/\bar{c}L$ has been replaced by three separate terms. The first, e^{-L} , accounts for propagules which land alone on unoccupied territories; these territories are won without contest. The second, $R_i c_i/\bar{c}$ represents competitive victories when the i genotype is a rare invader in a high density population: from Eq. (5), $R_i \rightarrow 0$ when the i genotype is abundant ($l_i \gg 1$), or other genotypes are collectively rare ($L - l_i \ll 1$). The third term, $A_i c_i/\bar{c}$, represents competitive victories when the i genotype is abundant: $A_i \rightarrow 0$ if $l_i \ll 1$. The relative importance of these three terms varies with both

the overall propagule density L and the relative propagule frequencies m_i/M . If $l_i \gg 1$ for all genotypes, we recover the classic lottery model (only the $A_i c_i / \bar{c}$ term remains, and $A_i \rightarrow 1/L$).

Coexistence in constant and cyclical environments

In the previous section we only considered how b , c and d should respond to selection in Grime's environmental extremes, based on invasion fitness. Here we further explore the low frequency behavior of Eq. (4) to determine which types can coexist in a constant environment, and then consider the full time-dependent behaviour of Eq. (4) in a cyclical environment.

In a constant environment, stable coexistence is possible in our extended lottery model. A b -specialist i and c -specialist j ($b_i > b_j$, $c_j > c_i$) can co-exist because then propagule density L is frequency-dependent, and so is the importance of competitive ability (Appendix D). This is a version of the classic competition-colonization trade-off [Levins and Culver, 1971, Tilman, 1994]; the competitor (c -specialist) leaves many territories unoccupied (low L) due to its poor colonization ability (low b), which the colonizer (b -specialist) can then exploit. A similar situation holds for coexistence between high- c and low- d specialists; a "competition-longevity" trade-off [Tilman, 1994]. These forms of co-existence require density dependence (being mediated by L), and are not present in the classic lottery model. Coexistence is not possible between b - and d -specialists in a constant environment (Appendix D).

Now suppose that birth and death rates vary periodically with amplitude sufficient to cause large changes in population density. This example is inspired by natural *Drosophila* populations, which expand rapidly in the warmer months when fruit is abundant, but largely die off in the colder months. Along with this seasonal population density cycle, hundreds of polymorphisms exhibit frequency cycles that are in phase with the seasons [Bergland et al., 2014]. Some of these polymorphisms may be adaptive and potentially millions of years old, suggesting stable coexistence [Bergland et al., 2014, Messer et al., 2016]. Selection on allele frequencies thus occurs on the same time scale as population demography, a situation vastly more complicated than classical sweeps in demographically stable populations [Messer et al., 2016].

The classical population genetic treatment of fluctuating selection suggests that environmental fluctuations do not promote coexistence. Allele frequencies are successively multiplied by relative fitness values for each environmental iteration, and so two alleles favored in different environments can only stably coexist if the product of fitnesses for one type exactly equals the product for the other [Dempster, 1955]. Thus, stable coexistence still requires frequency-dependent selection or heterozygote advantage (as is required in a constant environment).

This classical argument overlooks two general mechanisms that promote coexistence in fluctuating environments [Messer et al., 2016]. The first is the classic version of the storage effect, which occurs when part of the population is protected from selection (due to overlapping generations in the lottery model; Chesson and Warner 1981). The second is the bounded population size effect of Yi and Dean [2013], which occurs when each environmental cycle involves growth from low to high density, with the time spent growing each cycle dependent on the fitness of the types present.

Fig. 2a-c shows the behavior of Eq. (4) for an example where b and d cycle between zero and positive values (“summers” with rapid growth and no mortality, and “winters” with mortality and no growth). Both the storage effect (adults are sheltered from selection during the summer growth phase) and the bounded density effect (expansion to high density occurs every cycle) are operating. Two types are present, a b -specialist, which is better at rapidly growing in the summer (higher b), and a d -specialist which is better at surviving the winter (lower d). Neither type has an advantage over a full environmental cycle, and they stably coexist. This is due to a combination of the storage and bounded density effects (recall that stable coexistence between b and d specialists was not possible in a constant environment).

The classic lottery model (Eq. 1) fails to give co-existence for these parameters because expansion to carrying capacity occurs immediately at the start of the summer (Fig. 2d-f). As a result, coexistence requires that the winter survivor’s b must be about 5 times smaller than required when we properly account for the growth in the abundance of each type using Eq. (4) (keeping the other parameters the same; Fig. 2g-i). Previous models of the promotion of genetic variation

via the storage effect [Ellner and Hairston Jr, 1994] similarly assume that the total number of offspring per iteration is constant, and would produce a similar error.

Discussion

It is interesting to compare the predictions of the extended lottery model with earlier approaches, such as the r/K scheme, where $r = b - d$ is the maximal, low-density growth rate [Pianka, 1972]. Confusingly, the term “ K -selection” sometimes refers generally to selection at high density [Pianka, 1972], encompassing both selection for higher saturation density [MacArthur and Wilson, 1967] and competitive ability [Gill, 1974]. Contrary to predictions of an r/K trade-off, empirical studies have shown that maximal growth rate at low density and the high density at which saturation occurs (measured by abundance) are positively correlated, both between species/strains [Fitzsimmons et al., 2010, Hendriks et al., 2005, Kuno, 1991, Luckinbill, 1979], and as a result of experimental evolution [Luckinbill, 1978, 1979]. From the perspective of our model, this positive correlation is not surprising since the saturation density, which is determined by a balance between births and deaths, increases with b .

There is support for a negative relationship between competitive success at high density and maximal growth rate [Luckinbill, 1979], consistent with a tradeoff between r and the competitive aspect of K . This could be driven by a tradeoff between individual size and reproductive rate. To avoid confusion with other forms of “ K -selection”, selection for competitive ability has been called “ α -selection” after the competition coefficients in the Lotka-Volterra equation [Case and Gilpin, 1974, Gill, 1974, Joshi et al., 2001]. However, competitive success as measured by α (i.e. the per-capita effect of one genotype on another genotype’s growth rate) is only partly determined by individual competitive ability — in the presence of age-structured competition and territoriality, it also includes the ability of each genotype to produce contestants i.e. b in our model. Our c is strictly competitive ability only — as such, changes in c do not directly affect population density (the total number of territories occupied per iteration is $\Delta_+ N = U(1 - e^{-L})$, which

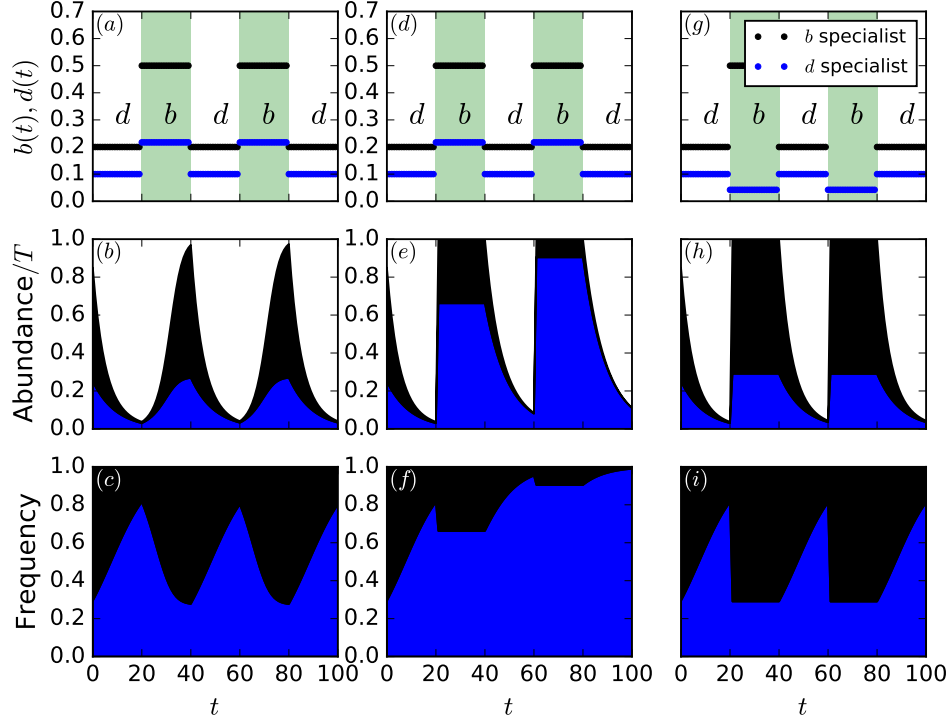


Figure 2: Stable coexistence between b and d specialists in a fluctuating environment requires a much greater b advantage in the classic lottery model compared to our density-dependent extension of it when population density is seasonally cyclical. (a) Birth and death rates seasonally alternate being nonzero (white for winter, green for summer). The b -specialist (black) has higher b and d ($b = 0.5$, $d = 0.2$) than the d -specialist ($b = 0.217$, $d = 0.1$) (blue). (b) Both types grow during the positive b phase, and decline during the positive d phase, but the d -specialist does so at a lower rate. Total height (blue+black) is population density N/T . (c) Summer favors the b specialist, winter the d -specialist, and they stably coexist. (d-f) Same as (a-c) for the classic lottery model; the types no longer coexist. (g-i) Same as (d-f) where now $b = 0.0421$ for the d specialist and the types coexist. For illustration, the propagule abundances are assumed to have the form $m_i = b_i(1 - N/T)n_i$, reflecting non-directed dispersal.

does not depend directly on the c_i). The clean separation of a strictly-relative c parameter is particularly useful from an evolutionary genetics perspective, essentially embedding a zero-sum relative fitness trait within a non-zero-sum fitness model. This could have interesting applications for modeling the impacts of intra-specific competition on species extinction, for example due to clonal interference [Desai and Fisher, 2007, Gerrish and Lenski, 1998] between c -strategists on the one hand, and b - and d - strategists on the other.

K -selection in the narrow logistic sense of selection for a greater environmental carrying capacity for given r , sometimes referred to as “efficiency” [MacArthur and Wilson, 1967], could be represented in our model by smaller individual territorial requirements. To a first approximation, two co-occurring genotypes which differ by a small amount in their territorial requirements only should have the same fitness, since the costs or benefits of a change in the amount of unoccupied territory is shared equally among genotypes via the propagule density per territory L . The situation is more complicated when the differences in territorial requirements become large enough that territorial contests can occur on different scales for different genotypes. We leave these complications for future work.

Nevertheless, it is interesting to note that ruderals, which are typically thought of as high fecundity dispersers (b -specialists), may also be strongly d -selected, which while unintuitive, is consistent with our findings. An effective way to reduce d in the face of unavoidable physical destruction is to shorten the time to reproductive maturity — short life cycles are a characteristically ruderal trait. Moreover, a recent hierarchical cluster analysis of coral traits did find a distinct “ruderal” cluster, but high fecundity was not its distinguishing feature. Rather, ruderals used brood- (as opposed to broadcast-) spawning, which could plausibly be a mechanism for improving propagule survivorship in disturbed environments [Darling et al., 2012].

One potential limitation of our model as a general-purpose model of density-dependent selection is its restriction to interference competition between juveniles for durable resources (lottery recruitment to adulthood), analogous to the ubiquitous assumption of viability selection in population genetics [Ewens, 2004, p. 45]. In some respects this is the complement of consumable

resource competition models, which restrict their attention to indirect exploitation competition, typically without age structure [Tilman, 1982]. In the particular case that consumable resources are spatially localized (e.g. due to restricted movement through soils), resource competition and territorial acquisition effectively coincide, and in principle resource competition could be represented by a competitive ability c (or conversely, c should be derivable from resource competition). The situation is more complicated if the resources are well-mixed, since, in general, resource levels then need to be explicitly tracked. It seems plausible that explicit resource tracking may not be necessary when the focus is on the evolution of similar genotypes that use identical resources rather than the stable co-existence of widely differing species with different resource preferences [Ram et al., 2016]. We are not aware of any attempts to delineate conditions under which explicit resource tracking is unnecessary even if it is assumed that community structure is ultimately determined by competition for consumable resources. More work is needed connecting resource competition models to the density-dependent selection literature, since most of the former has to date been focused on narrower issues of the role of competition at low resource availability and in the absence of direct interactions between organisms at the same trophic level [Aerts, 1999, Davis et al., 1998, Tilman, 2007].

While our model can be applied to species rather than genotypes (e.g. ecological invasions), our focus is genotype evolution i.e. the change in allele frequencies over time. Our assumption that there are no large c discrepancies (section “Mean field approximation”) amounts to a restriction on the amount of genetic variation in c in the population. Since beneficial mutation effect sizes will typically not be much larger than a few percent, large c discrepancies can only arise if the mutation rate is extremely large, and so the assumption will not be violated in most cases. However, this restriction could become important when looking at species interactions rather than genotype evolution.

In the introduction we mentioned the recurring difficulties with confounding selection and demography in population genetic inference. It seems that Eq. (4) or something similar (and hopefully more analytically tractable) is unavoidable for the analysis of time-course genetic data

because, fundamentally, selective births and deaths affect both abundances and frequencies, not one or the other in isolation. Moreover, some aspects of allele frequency change are intrinsically density-dependent. In the classic lottery model, which as we have seen is essentially the Wright-Fisher model with overlapping generations, b_i and c_i are equivalent in the sense that the number of territorial victories only depends on the product $b_i c_i$ (see “Model”). This is no longer the case in our extension, where b and c specialists can co-exist. This “colonization-competition trade-off” is well known in the co-existence literature [Tilman, 1994]. It and similar forms of “spatial co-existence” in stable environments have previously been modeled either with Levin’s qualitative representation of competition [Levins and Culver, 1971, Tilman, 1994], as opposed to the quantitative c of lottery competition, or with a more sophisticated treatment of space (non-uniform dispersal; Bolker and Pacala 1999, Shmida and Ellner 1984). In cyclical environments, polymorphisms can be stabilized by the bounded density effect, which is completely lost if there is an exclusive focus on allele frequencies [Yi and Dean, 2013]. We leave the details of how our model might be applied to inference problems, including the crucial issue of its genetic drift predictions (providing a null model for neutral sites), for future work.

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Appendix A: Poisson approximation

For simplicity of presentation, we have assumed a Poisson distribution for the x_i as our model of dispersal. Strictly speaking, the total number of i propagules $\sum x_i$ (summed over unoccupied territories) is then no longer a constant m_i , but fluctuates between generations for a given mean m_i , which is more biologically realistic. Nevertheless, since we do not consider the random fluctuations in type abundances here, and for ease of comparison with the classic lottery model, we ignore the fluctuations in m_i . Instead we focus, on Poisson fluctuations in propagule composition in each territory.

420 In the exact model of random dispersal, the counts of a genotype's propagules across un-
 421 noccupied territories follows a multinomial distribution with dimension U , total number of trials
 422 equal to m_i , and equal probabilities $1/U$ for a propagule to land in a given territory. Thus, the
 423 x_i in different territories are not independent random variables. However, for sufficiently large
 424 U and m_i , this multinomial distribution for the x_i across territories is closely approximated by
 425 a product of independent Poisson distributions for each territory, each with rate parameter l_i
 426 [Arenbaev, 1977, Theorem 1]. Since we are ignoring finite population size effects, we effectively
 427 have $T \rightarrow \infty$, in which case U can be only be small enough to violate the Poisson approximation
 428 if there is vanishing population turnover, and then the dispersal distribution is irrelevant any-
 429 way. Likewise, in ignoring stochastic finite population size for the n_i , we have effectively already
 430 assumed that m_i is large enough to justify the Poisson approximation (the error scales as $1/\sqrt{m_i}$;
 431 Arenbaev 1977).

432 **Appendix B: Derivation of growth equation**

433 We separate the right hand side of Eq. (2) into three components $\Delta_+ n_i = \Delta_u n_i + \Delta_r n_i + \Delta_a n_i$ which
 434 vary in relative magnitude depending on the propagule densities l_i . Following the notation in
 435 the main text, the Poisson distributions for the x_i (or some subset of the x_i) will be denoted p ,
 436 and we use P as a general shorthand for the probability of particular outcomes.

437 **Growth without competition**

438 The first component, $\Delta_u n_i$, accounts for territories where only one focal propagule is present
 439 $x_i = 1$ and $x_j = 0$ for $j \neq i$ (u stands for "uncontested"). The proportion of territories where this
 440 occurs is $l_i e^{-L}$, and so

$$\Delta_u n_i = U l_i e^{-L} = m_i e^{-L}. \quad (7)$$

Competition when rare

The second component, $\Delta_r n_i$, accounts for territories where a single focal propagule is present along with at least one non-focal propagule (r stands for “rare”) i.e. $x_i = 1$ and $X_i \geq 1$ where $X_i = \sum_{j \neq i} x_j$ is the number of nonfocal propagules. The number of territories where this occurs is $Up_i(1)P(X_i \geq 1) = b_i n_i e^{-l_i}(1 - e^{-(L-l_i)})$. Thus

$$\Delta_r n_i = m_i e^{-l_i}(1 - e^{-(L-l_i)}) \left\langle \frac{c_i}{c_i + \sum_{j \neq i} c_j x_j} \right\rangle_{\tilde{p}}, \quad (8)$$

where $\langle \rangle_{\tilde{p}}$ denotes the expectation with respect to \tilde{p} , and \tilde{p} is the probability distribution of nonfocal propagule abundances x_j *after* dispersal, in those territories where exactly one focal propagule, and at least one non-focal propagule, landed.

Our “mean field” approximation is to replace x_j with its mean in the last term in Eq. (8),

$$\left\langle \frac{c_i}{c_i + \sum_{j \neq i} c_j x_j} \right\rangle_{\tilde{p}} \approx \frac{c_i}{c_i + \sum_{j \neq i} c_j \langle x_j \rangle_{\tilde{p}}}. \quad (9)$$

Below we justify this replacement by arguing that the standard deviation $\sigma_{\tilde{p}}(\sum_{j \neq i} c_j x_j)$ (with respect to \tilde{p}), is much smaller than $\langle \sum_{j \neq i} c_j x_j \rangle_{\tilde{p}}$.

We first calculate $\langle x_j \rangle_{\tilde{p}}$. Let $X = \sum_j x_j$ denote the total number of propagules in a territory and $\mathbf{x}_i = (x_1, \dots, x_{i-1}, x_{i+1}, \dots, x_G)$ denote the vector of non-focal abundances, so that $p(\mathbf{x}_i) = p_1(x_1) \dots p_{i-1}(x_{i-1}) p_{i+1}(x_{i+1}) \dots p_G(x_G)$. Then, \tilde{p} can be written as

$$\begin{aligned} \tilde{p}(\mathbf{x}_i) &= p(\mathbf{x}_i | X \geq 2, x_i = 1) \\ &= \frac{P(\mathbf{x}_i, X \geq 2 | x_i = 1)}{P(X \geq 2)} \\ &= \frac{1}{1 - (1 + L)e^{-L}} \sum_{X=2}^{\infty} P(X) p(\mathbf{x}_i | X_i = X - 1), \end{aligned} \quad (10)$$

and so

$$\begin{aligned}\langle x_j \rangle_{\tilde{p}} &= \sum_{\mathbf{x}_i} \tilde{p}(\mathbf{x}_i) x_j \\ &= \frac{1}{1 - (1 + L)e^{-L}} \sum_{X=2}^{\infty} P(X) \sum_{\mathbf{x}_i} p(\mathbf{x}_i | X_i = X - 1) x_j.\end{aligned}\quad (11)$$

The inner sum over \mathbf{x}_i is the mean number of propagules of a given nonfocal type j that will be found in a territory which received $X - 1$ nonfocal propagules in total, which is equal to $\frac{l_j}{L - l_i}(X - 1)$. Thus,

$$\begin{aligned}\langle x_j \rangle_{\tilde{p}} &= \frac{l_j}{1 - (1 + L)e^{-L}} \frac{1}{L - l_i} \sum_{k=2}^{\infty} P(X)(X - 1) \\ &= \frac{l_j}{1 - (1 + L)e^{-L}} \frac{L - 1 + e^{-L}}{L - l_i},\end{aligned}\quad (12)$$

452 where the last line follows from $\sum_{X=2}^{\infty} P(X)(X - 1) = \sum_{X=1}^{\infty} P(X)(X - 1) = \sum_{X=1}^{\infty} P(X)X -$
 453 $\sum_{X=1}^{\infty} P(X)$.

The exact analysis of the fluctuations in $\sum_{j \neq i} c_j x_j$ is complicated because the x_j are not independent with respect to \tilde{p} . These fluctuations are part of the “drift” in type abundances which we leave for future work. Here we use the following approximation to give some insight into the magnitude of these fluctuations and also the nature of the correlations between the x_j . We replace \tilde{p} with \tilde{q} , defined as the \mathbf{x}_i Poisson dispersal probabilities conditional on $X_i \geq 1$ (which are independent). The distinction between \tilde{p} with \tilde{q} will be discussed further below. The \tilde{q} approximation

gives $\langle x_j \rangle_{\tilde{q}} = \langle x_j \rangle_p / C = l_j / C$,

$$\begin{aligned}
\sigma_{\tilde{q}}^2(x_j) &= \langle x_j^2 \rangle_{\tilde{q}} - \langle x_j \rangle_{\tilde{q}}^2 \\
&= \frac{1}{C} \langle x_j^2 \rangle_p - \frac{l_j^2}{C^2} \\
&= \frac{1}{C} (l_j^2 + l_j) - \frac{l_j^2}{C^2} \\
&= \frac{l_j^2}{C} \left(1 - \frac{1}{C} \right) + \frac{l_j}{C},
\end{aligned} \tag{13}$$

and

$$\begin{aligned}
\sigma_{\tilde{q}}(x_j, x_k) &= \langle x_j x_k \rangle_{\tilde{q}} - \langle x_j \rangle_{\tilde{q}} \langle x_k \rangle_{\tilde{q}} \\
&= \frac{1}{C} \langle x_j x_k \rangle_p - \frac{l_j l_k}{C^2} \\
&= \frac{l_j l_k}{C} \left(1 - \frac{1}{C} \right),
\end{aligned} \tag{14}$$

where $C = 1 - e^{-(L-l_i)}$ and $j \neq k$.

The exact distribution \tilde{p} assumes that exactly one of the propagules present in a given site after dispersal belongs to the focal type, whereas \tilde{q} assumes that there is a focal propagule present before non-focal dispersal commences. As a result, \tilde{q} predicts that the mean propagule density is greater than L (in sites with only one focal propagule is present) when the focal type is rare and the propagule density is high. This is erroneous, because the mean number of propagules in every site is L by definition. Specifically, if $L - l_i \approx L \gg 1$, then the mean propagule density predicted by \tilde{q} is approximately $L + 1$. The discrepancy causes rare invaders to have an intrinsic rarity disadvantage (territorial contests under \tilde{q} are more intense than they should be). In contrast, Eq. (12) correctly predicts that there are on average $\sum_{j \neq i} \langle x_j \rangle_{\tilde{p}} \approx L - 1$ nonfocal propagules because \tilde{p} accounts for potentially large negative covariances between the x_j “after dispersal”. By neglecting the latter covariences, \tilde{q} overestimates the fluctuations in $\sum_{j \neq i} c_j x_j$; thus \tilde{q} gives an upper bound on the fluctuations. The discrepancy between \tilde{q} and \tilde{p} will be largest

when L is of order 1 or smaller, because then the propagule assumed to already be present under \tilde{q} is comparable to, or greater than, the entire propgaule density.

Decomposing the variance in $\sum_{j \neq i} c_j x_j$,

$$\sigma_{\tilde{q}}^2(\sum_{j \neq i} c_j x_j) = \sum_{j \neq i} \left[c_j^2 \sigma_{\tilde{q}}^2(x_j) + 2 \sum_{k > j, k \neq i} c_j c_k \sigma_{\tilde{q}}(x_j, x_k) \right], \quad (15)$$

and using the fact that $\sigma_{\tilde{q}}(x_j, x_k)$ and the first term in Eq. (13) are negative because $C < 1$, we obtain an upper bound on the relative fluctuations in $\sum_{j \neq i} c_j x_j$,

$$\frac{\sigma(\sum_{j \neq i} c_j x_j)}{\langle \sum_{j \neq i} c_j x_j \rangle} = C^{1/2} \frac{\left(\sum_{j \neq i} c_j^2 l_j + (1 - 1/C) \left(\sum_{j \neq i} c_j l_j \right)^2 \right)^{1/2}}{\sum_{j \neq i} c_j l_j} < C^{1/2} \frac{\left(\sum_{j \neq i} c_j^2 l_j \right)^{1/2}}{\sum_{j \neq i} c_j l_j}. \quad (16)$$

Suppose that the c_j are all of similar magnitude (their ratios are of order one). Then Eq. (16) is $\ll 1$ for the case when $L - l_i \ll 1$ (due to the factor of $C^{1/2}$), and also for the case when at least some of the nonfocal propagule densities are large $l_j \gg 1$ (since it is then of order $1/\sqrt{L - l_i}$). The worst case scenario occurs when $L - l_i$ is of order one. Then Eq. (16) gives a relative error of approximately 50%, which from our earlier discussion we know to be a substantial overestimate when L is of order 1. Our numerical results (Fig. 3) confirm that the relative errors are indeed small.

However, the relative fluctuations in $\sum_{j \neq i} c_j x_j$ can be large if some of the c_j are much larger than the others. Specifically, in the presence of a rare, extremely strong competitor ($c_j l_j \gg c_{j'} l_{j'}$ for all other nonfocal genotypes j' , and $l_j \ll 1$), then the RHS of Eq. (16) can be large and we cannot make the replacement Eq. (9).

Substituting Eqs. (9) and (12) into Eq. (8), we obtain

$$\Delta_r n_i \approx m_i R_i \frac{c_i}{\bar{c}}, \quad (17)$$

where R_i is defined in Eq. (5).

Competition when abundant

The final contribution, $\Delta_a n_i$, accounts for territories where two or more focal propagules are present (a stands for “abundant”). Similarly to Eq. (8), we have

$$\Delta_a n_i = U(1 - (1 + l_i)e^{l_i}) \left\langle \frac{c_i x_i}{\sum_j c_j x_j} \right\rangle_{\hat{p}} \quad (18)$$

where \hat{p} is the probability distribution of both focal and nonfocal propagule abundances *after* dispersal in those territories where at least two focal propagules landed.

Again, we argue that the relative fluctuations in $\sum c_j x_j$ are much smaller than 1 (with respect to \hat{p}), so that,

$$\left\langle \frac{c_i x_i}{\sum_j c_j x_j} \right\rangle_{\hat{p}} \approx \frac{c_i \langle x_i \rangle_{\hat{p}}}{\sum_j c_j \langle x_j \rangle_{\hat{p}}}. \quad (19)$$

Following a similar procedure as for $\Delta_r n_i$, where the vector of propagule abundances is denoted \mathbf{x} , the mean focal genotype abundance is,

$$\begin{aligned} \langle x_i \rangle_{\hat{p}} &= \sum_{\mathbf{x}} x_i p(\mathbf{x} | x_i \geq 2) \\ &= \sum_{x_i} x_i p(x_i | x_i \geq 2) \\ &= \frac{1}{1 - (1 + l_i)e^{-l_i}} \sum_{x_i \geq 2} p(x_i) x_i \\ &= l_i \frac{1 - e^{-l_i}}{1 - (1 + l_i)e^{-l_i}}. \end{aligned} \quad (20)$$

For nonfocal genotypes $j \neq i$, we have

$$\begin{aligned}
\langle x_j \rangle_{\hat{p}} &= \sum_{\mathbf{x}} x_j p(\mathbf{x} | x_i \geq 2) \\
&= \sum_X P(X | x_i \geq 2) \sum_{\mathbf{x}} x_j p(\mathbf{x} | x_i \geq 2, X) \\
&= \sum_X P(X | x_i \geq 2) \sum_{x_i} p(x_i | x_i \geq 2, X) \sum_{\mathbf{x}_i} x_j p(\mathbf{x}_i | X_i = X - x_i) \\
&= \sum_X P(X | x_i \geq 2) \sum_{x_i} p(x_i | x_i \geq 2, X) \frac{l_j(X - x_i)}{L - l_i} \\
&= \frac{l_j}{L - l_i} \left[\sum_X P(X | x_i \geq 2) X - \sum_{x_i} p(x_i | x_i \geq 2) x_i \right] \\
&= \frac{l_j}{L - l_i} \left(L \frac{1 - e^{-L}}{1 - (1 + L)e^{-L}} - l_i \frac{1 - e^{-l_i}}{1 - (1 + l_i)e^{-l_i}} \right). \tag{21}
\end{aligned}$$

492 To calculate the relative fluctuations in $\sum_{j \neq i} c_j x_j$, we use a similar approximation as for $\Delta_r n_i$: \hat{p}
493 is approximated by \hat{q} , defined as the \mathbf{x} dispersal probabilities in a territory conditional on $x_i > 2$
494 (that is, treating the x_j as independent). All covariances between nonfocal genotypes are now zero,
495 so that $\sigma_{\hat{q}}^2(\sum c_j x_j) = \sum c_j^2 \sigma_{\hat{q}}^2(x_j)$, where $\sigma_{\hat{q}}^2(x_j) = l_j$ for $j \neq i$, and

$$\sigma_{\hat{q}}^2(x_i) = \frac{l_i}{D} \left(l_i + 1 - e^{-l_i} - \frac{l_i}{D} (1 - e^{-l_i})^2 \right), \tag{22}$$

496 where $D = 1 - (1 + l_i)e^{-l_i}$, and

$$\frac{\sigma_{\hat{q}}(\sum c_j x_j)}{\langle \sum c_j x_j \rangle} = \frac{\left(\sum_{j \neq i} c_j^2 l_j + c_i^2 \sigma_{\hat{q}}^2(x_i) \right)^{1/2}}{\sum_{j \neq i} c_j l_j + c_i l_i (1 - e^{-l_i}) / D}. \tag{23}$$

497 Similarly to Eq. (16), the RHS of Eq. (23) is $\ll 1$ for the case that $L \ll 1$ (due to a factor of
498 $D^{1/2}$), and also for the case when at least some of the propagule densities (focal or nonfocal) are
499 large — provided that c_i and the c_j are all of similar magnitude. Again, the worst case scenario
500 occurs when l_i and $L - l_i$ are of order 1, in which case Eq. (23) is around 35%, which is again
501 where the \hat{q} approximation produces the biggest overestimate of the fluctuations in \mathbf{x} . Similarly

to Eq. (16), the RHS of (23) will not be $\ll 1$ in the presence of a rare, extremely strong competitor.

Combining Eqs. (18) and (19), we obtain

$$\Delta_a n_i = m_i A_i \frac{c_i}{\bar{c}}, \quad (24)$$

where A_i is defined in Eq. (6).

Comparison with simulations

Fig. 3 shows that Eq. (4) and its components closely approximate our density-dependent lottery model over a wide range of propagule densities (the latter is evaluated by direct simulations of uniform random dispersal and lottery competition). Two genotypes are present, one of which is at low frequency. The growth of the low-frequency genotype relies crucially on the low-density competition term $R_i c_i / \bar{c}$, and also to a lesser extent on the high density competition term $A_i c_i / \bar{c}$ if l_1 is large enough (Fig. 3b). On the other hand, $R_i c_i / \bar{c}$ is negligible for the high-frequency genotype, which depends instead on high density territorial victories (Fig. 3d). Fig. 3 also shows the breakdown of the classic lottery model at low propagule densities.

Appendix C: Mutant invasion and coexistence in a constant environment

Here we evaluate the initial growth or decline of mutants in a population with a single resident type, which is in equilibrium. To determine whether coexistence is possible, we check for “mutual invasion”, that is, we check that type j will invade an i -dominated population, but type i will also invade a j -dominated population.

Solving for equilibrium when i is the resident ($\Delta n_i = 0$), we have $R_i = 0$, $\bar{c} = c_i$, $A_i = (1 - (1 + L)e^{-L})/L$, and Eq. (4) becomes

$$b_i(1 - e^{-L})/L - d_i = 0. \quad (25)$$

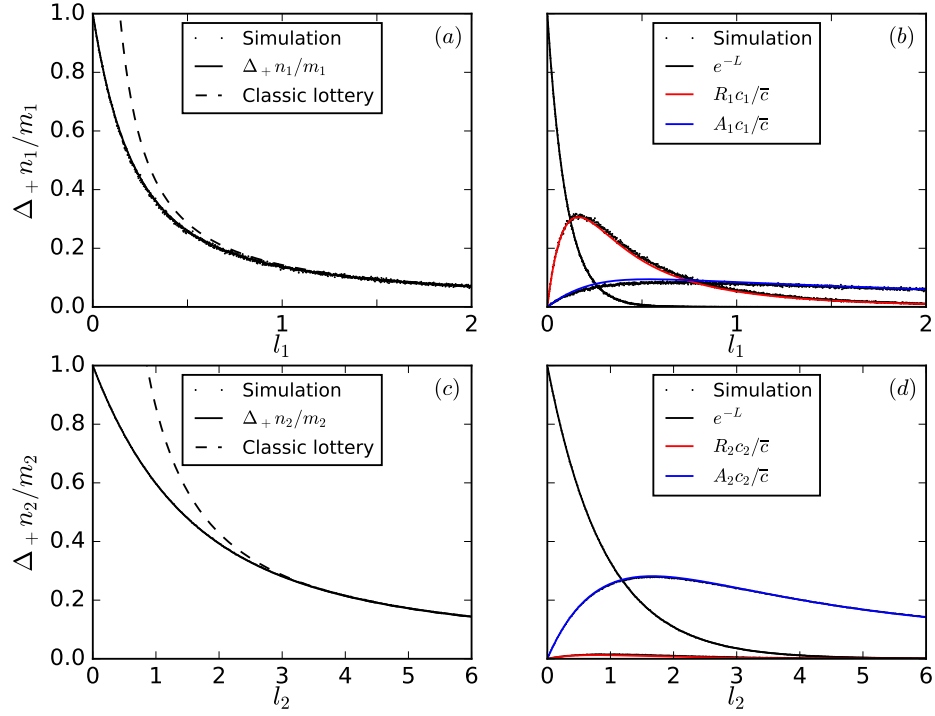


Figure 3: The change in genotype abundances in a density dependent lottery model is closely approximated by Eq. (4). $\Delta + n_i/m_i$ from Eq. (4) (and its separate components) are shown, along with direct simulations of random dispersal and lottery competition over one iteration over a range of propagule densities (U is varied between 5×10^3 and 10^6 with $m_1 = 10^4$ and $m_2 = 9 \times 10^4$). Two genotypes are present. (a) and (b) show the low-frequency genotype with c -advantage ($c_1 = 1.5$), (c) and (d) show the high-frequency predominant genotype ($c_2 = 1$). Simulation points are almost invisible in (c) and (d) due to near exact agreement with Eq. (4). Dashed lines in (a) and (c) show the breakdown of the classic lottery model.

522 This implies $L \approx b_i/d_i$ if $b_i/d_i \gg 1$ and $L \ll 1$ if $b_i/d_i \approx 1$.

523 Now suppose that a novel mutant j , which is initially rare, appears in the population. Then
 524 $A_j/R_j \ll 0$, $l_j \approx 0$ and $\bar{c} \approx c_i$, and so, from Eq. (4), the mutant lineage's fitness is

$$\Delta n_j/n_j \approx b_j \left(e^{-L} + R_j \frac{c_j}{c_i} \right) - d_j \quad (26)$$

525 where $R_j \approx (1 - e^{-L}) / \left(\frac{c_j}{c_i} + \frac{L-1+e^{-L}}{1-(1+L)e^{-L}} \right)$.

526 We consider the case of coexistence between a b -specialist i and a c -specialist j ($b_i > b_j$, $c_j > c_i$
 527 and $d_i = d_j$). Suppose that b_i is so large that $L \gg 1$ when i is dominant, and b_j is so small that $L \ll$
 528 1 when j is dominant. Then, when j is dominant, we have $\Delta n_i/n_i = b_i - d_i = b_i - d_j = b_i - b_j > 0$.
 529 When i is dominant, Eq. (??) applies, where Eq. (25) implies $d_j = d_i = b_i(1 - e^{-L})/L \approx b_i/L$, and
 530 so

$$\Delta n_j/n_j \approx \frac{b_j}{L} \frac{c_j}{c_i} - \frac{b_i}{L}. \quad (27)$$

531 Therefore, coexistence occurs if c_j/c_i is sufficiently large. The analogous argument for d - and
 532 c -specialists ($d_i < d_j$ with $L \gg 1$ when i dominates, $L \ll 1$ when j dominates, and $b_i = b_j$) gives
 533 $\Delta n_j/n_j \approx d_i \frac{c_j}{c_i} - d_j$, which again implies coexistence if c_j/c_i is sufficiently large.

534 For b - and d -specialists ($c_i = c_j$), we have $\Delta n_j/n_j \approx b_j d_i/b_i - d_j$ when i dominates and
 535 $\Delta n_i/n_i \approx b_i d_j/b_j - d_i$ when j dominates. Thus, either i or j grows when rare, but not both,
 536 and stable coexistence is not possible in a constant environment.