Evolution in Spatial Predator-Prey Models and the "Prudent Predator": The Inadequacy of Steady-State Organism Fitness and the Concept of Individual and Group Selection

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Abstract

We review recent research which reveals: (1) how spatially distributed populations avoid overexploiting resources due to the local extinction of over-exploitative variants, and (2) how the conventional understanding of evolutionary processes is violated by spatial populations so that basic concepts, including fitness assignment to individual organisms, are not applicable, and even kin and group selection are unable to describe the mechanism by which exploitative behavior is bounded. To understand these evolutionary processes a broader view is needed of the properties of multiscale spatiotemporal patterns in organism-environment interactions. We discuss measures that quantify the effects of these interactions on the evolution of a population, including multi-generational fitness and the heritability of the environment.

1. Overview

One of the longstanding controversies in studies of evolution is traditionally understood to revolve around group selection and altruistic behavior. Original studies by Wynne-Edwards [1] suggesting that predators executed restraint in reproduction in order to avoid overexploitation of resources were later dismissed [2,3] as inadequate since any such restraint appears to require group selection. Individual selection of a predator could not reflect the implications of over-reproduction that, by the individual predator's standards, has an evolutionary advantage. While the original rejection of the "prudent predator" concept was based on an overall rejection of group selection, recent research [4-8] has built a more solid case for the relevance of group selection in various evolutionary contexts. Nevertheless, the fundamental perspective that the average number of surviving offspring of an individual is the correct measure of evolutionary success continues to guide evolutionary literature, whether it includes individual or group selection, since group selection directly affects the reproductive fecundity of members of a group.

In this paper, our objective is not to discuss group selection directly, but rather to discuss the implications of spatially distributed populations, their properties, and the relationship of these properties to the conventional understanding of evolution, with significant implications for the controversy surrounding group selection and altruism. We will show that, within the context of a simple model, there is theoretical justification for a self-consistent limitation of reproduction by predators. This self-consistent process arises due to the local extinction of strains that over-exploit their environment. However, this process does not directly correspond to the picture of group selection. The primary reason for this problem is that conventional evolutionary models assume that competition among individuals or groups occurs within a particular generation. Since the local extinction of over-exploitative strains we will describe arises from an organism-environment interaction over many generations, it does not fit within this approach, and thus not within the group selection perspective. It also does not fit within the more specific kin selection concept. Instead, what is breaking down is an often-unstated quasi-steady-state assumption that organismal fitness as measured by reproductive success is relatively

constant from generation to generation; that it is the same for individuals and their descendants of the same type. This reflects the assumption that fitness (as measured by reproductive success) is linked to hereditary genotypic/phenotypic traits and therefore is transmitted along with these traits, essentially unchanged, for many generations.

To appreciate these comments, the inadequacy of the conventional understanding of fitness must be more fully understood. The assignment of organismal fitness as given by the average number of surviving offspring of an organism type is one of the most basic concepts of evolutionary theory. The mathematical formulation of genetic heredity by Fisher, Haldane and Wright [9-11] established the generation-to-generation change in frequency of genotypes as the measure of fitness characterizing the role of natural selection in evolution. The centrality of this characterization [12] has not been diminished by recognized observational difficulties due to sampling error, the intricacies of the genotype-phenotype relationships, and the possibility of population and environmental changes impacting on fitness. Using the rate of change in frequency of a type as a measure of fitness quantifies the concept that types whose individuals leave more offspring come to dominate a population, and are therefore more fit [13].

However, a more general approach would suggest that the direct relevance of reproductive success only applies when the generational change in frequency is sufficient to determine the long-term composition of the population; that is, systems for which the reproductive success of an organism does not systematically differ from that of the organism's more distant descendants. This quasi-steady-state assumption, in which what happens at one time is characteristic of what happens at every time, and therefore of the long-term behavior of the system, is violated by the simple spatial models of predator-prey or host-pathogen systems we will describe.

A review of the traditional approach to evolution and group selection leads us to conclude that in order to accommodate our results, a new concept of environmental inheritance should be introduced. Environmental inheritance is to be contrasted with genetic inheritance, and reflects the likelihood that offspring will inherit the environment that progenitors left to them, including its effects on their reproductive success or even their viability. The importance and even revolutionary nature of the role of environment inheritance on evolutionary dynamics has recently been discussed using the term “niche construction.” [14-16] Significantly, the formalization provided in these discussions uses conventional averaging approximations which limit its validity, because they do not reflect the role of distinct spatial locations, thus eliminating distinctions between niches that are made by different local types. We point out these limitations below and introduce a formalism that does not have such severe limitations. In order to avoid some confusion, we also note that due to overlapping terminologies there might be confusion between what is discussed here and a different topic: environmental influence on biological organisms in ways that are subsequently inherited, epigenetics. [17] The practical implications of our review are important in bringing attention to the failure of conventional evolutionary concepts in understanding basic features of biological communities, i.e. responding to the question: What are the processes that set or limit the reproductive fecundity of evolving populations?

Conventional approaches to representing evolutionary processes are based upon quantities averaged over organisms and their environments distributed in space, eliminating the role of explicit spatial variation. This approximation leads to convenient simplifications, including the Neo-Darwinian gene-centered view [9-11, 18-20], that guide the conceptual framework in which evolution is currently understood. Spatial aspects of the distribution of populations have been invoked for important processes including speciation [21], the evolution of social behaviors [22], evolution by group selection [3, 23, 24], and models of evolution of virulence in parasites (reviewed in [25]). However, these inquiries have been guided by the framework that uses averaging, and spatial variation that is self-generating rather than imposed externally has not been included in a consistent manner. Recent studies [26-44] have emphasized the importance of self-generated patterns of spatial variation that dramatically alter the characteristic properties and behavior of evolutionary processes. These studies also formalize conceptual aspects of Wright's Shifting Balance Theory [10, 45], which suggested local groups of organisms (demes) could differ from each other as part of the process of significant shifts in population genetic types. Previous efforts at formalization that have been found lacking [46] did not sufficiently incorporate the effects of spatial heterogeneity.

The relationship between averaging approximations used in evolutionary biology and the mean-field approximation used in physics has been formally demonstrated. [19, 20] The insights that have been developed in the study of the violation of mean-field approximations due to self-organization of spatial patterns (often called symmetry breaking) provides a framework in which the study of spatial patterns in biology can be clarified through scaling behaviors describing the rate of change of the population, its diversity, and the role of environmental context. [33-36, 38, 43, 44] Additional discussions of the limitations of the mean-field approximation in application to ecology can be found in the literature. [47]

Space can be taken into account in essentially three different ways: patch models, continuous partial-differential equations, and lattice models. The first class is reflected in an extensive literature on island, patch, stepping stone, meta-population, or structured population models that assume an *a priori* spatial distribution of the population into well-mixed clusters, or demes, that weakly interact via migration or other types of contact. [48-54] Due to the assumption of weak interactions, many of the more interesting dynamic spatial effects were not studied in this context. The second class includes reaction-diffusion partial differential equations, used to model pigment patterns in animal skins [55] and ecological processes [56]. Finally, lattice models [26-44] treat space as a discrete set of sites, or regions, whose states are determined by local interaction with nearby points. These interactions are generally not limited to weak interactions, and the types of behavior that can be studied are similar to those of partial differential equations. Spatial patterns of inhomogeneity may form spontaneously in lattice models, depending on the specifics of the model and parameters.

This paper is organized as follows: Section 2 is a review of the behavior of spatial models of predator-prey dynamics, and describes the inadequacy of conventional fitness and the need for a time-scale dependent fitness. Section 3 relates these studies to the conventional Neo-Darwinian concepts and group selection, and introduces the concept of environmental heredity. Section 4 relates these studies to kin selection, and Section 5 provides our conclusions about the importance of wider studies of evolving spatial populations.

2. Spatial predator-prey/host-pathogen models

Recent research on spatially distributed predator-prey or host-pathogen models [30, 39, 40, 57] has revealed essential properties of the dynamics of such systems, and especially their spatial and temporal heterogeneity. When the predator evolves, the evolutionarily stable type is out-competed in the short term by seemingly fitter mutants, which have the highest numbers of offspring for many generations but go extinct in the long term (e.g., after 200 generations).[39, 40] The rapidly reproducing types modify their local environment, depleting resources in a way that is detrimental to their survival, but this environmental modification and its feedback to population growth require many generations. The distinct fates of the different types are made possible by self-organized spatial segregation.

The feedback of local environmental exploitation to the extinction of higher reproducing mutants violates the assumption that reproductive fecundity is a measure of long-term success of a mutant strain. Indeed, we will quantify the time-inhomogeneous nature of the evolutionary process using a more general measure of fitness that acknowledges that descendents may have different reproductive success than their ancestors of the same genotype. This measure indicates the evolutionarily stable type in such cases, and it can be used to quantify the time scale at which selection acts against mutants with short-term advantage.

We will present the model in terms of a parasite or pathogen spreading through a host population [26, 30, 57], but it can also be thought of as a predator-prey system, with the pathogens as predators and the hosts as prey, or local groups of predators and herds of prey [29, 58]. Such systems exhibit interesting spatial dynamics that are not present in models that average over the population distributed in space; hence, space is fundamental to their dynamics, a property believed to be shared by many real biological systems [31].

The model. The model is a probabilistic cellular automaton with possible states at each site of a two dimensional lattice given by *0* (empty), *S* (susceptible host), and I_τ (host infected with pathogen of transmissibility τ). It has three parameters. At each time step, susceptible hosts reproduce into each neighboring cell (taken to be the four closest sites with periodic boundary conditions) with probability g if that cell is not yet occupied; the probability of reproduction is independent for each neighbor. An infected host dies with probability v (virulence) along with its infecting pathogen. Finally, an infected host I_τ causes a neighboring uninfected host to become infected with probability τ. In the

language of predator-prey systems, g is the prey reproductive rate. For a site that has been attacked by a predator, v is the rate at which the predator catches and consumes prey. As long as predators consume prey, they can reproduce, sending offspring to neighboring sites. When the local prey is consumed, the local predator population expires. We will leave v fixed because lower values are always beneficial to the predator (lower values of v imply that predators can survive while eating fewer prey); instead we will focus on the evolutionary changes in τ, which describes the rate at which new prey sites are attacked by the offspring of reproducing predators. The subscript τ allows more than one type to be present on the lattice.

The state transition probabilities are:

$$P(0 \to S) = 1 - (1 - g)^n$$
$$P(S \to I_\tau) = 1 - (1 - \tau)^{m_\tau}$$
$$P(I_\tau \to 0) = \nu$$

where n is the number of uninfected host neighbors, and m_τ is the number of infected neighbors of transmissibility τ. The lattice is updated synchronously, as the dynamics are not significantly different when updating asynchronously [30]. For synchronous updating, if more than one pathogen sends offspring to the same site, the parent is chosen at random. This model is used in [30,39,40] and differs only in details from the one used in [29,57].

Fitness and invasibility. To quantify the fitness of an organism we begin by considering the conventional approach that reproductive success is the most direct measure. Quite generally, two very similar measures, R and r, are used to quantify reproduction [13, 59, 60]. R, the net reproduction ratio, measures the expected number of surviving offspring produced per organism over its lifetime[1]. In a non-mutating population of constant size, R is equal to one. In a population of constant size with mutation, the maximum R may be greater than one to balance the mutant types which have a value of R less than one (though the average value of R is one). The differential analogue of R is the "Malthusian parameter" r [9, 60], which measures the per capita instantaneous rate of increase of the population of a type per unit time. These quantities are normally referred to simply as "fitness."

The concept of invasibility is another approach to the question of what types will come to dominate a population. One considers a population dominated by a phenotype p and asks whether a mutant phenotype p' can invade. An evolutionarily stable strategy [61] is one

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[1] A different measure, the *basic* reproduction ratio R_0, measures the expected offspring when there are no other organisms present. In epidemiology, R_0 is defined as the expected number of other individuals infected by an individual in a completely susceptible population. R, the *net* reproduction ratio, is therefore sometimes referred to as the "density-dependent" measure.

for which no mutant can invade. Under the assumptions normally used, the evolutionarily stable strategy is the one that maximizes *R* [62-64].

In many evolutionary models the average population composition changes over time and therefore, in such a context it is readily understood that the reproduction rate in a particular generation is not predictive of the eventual evolutionary success over many generations. This behavior is treated mathematically by considering the reproductive success to be "frequency" or "density" dependent, i.e. dependent on the population composition (frequency and density refer to the concentration of a particular trait/allele in the population). [65, 66] However, as we will show in the spatial model given in this paper, the conventional treatment does not have the ability to represent the necessary relationship of short-term reproduction and long-term success even in a system that has reached steady-state conditions for the population as a whole. This occurs because the variation of the population composition as a whole is not related to the local variation of the population in the vicinity of a particular type, which controls the fitness. Therefore, the use of measures that consider reproductive success to be density-dependent are not adequate. Discussion of the inadequacy of traditional measures, various implications, and new measures that can be effective have been described in the literature. [40-42, 47] The key to this understanding is related to the inhomogeneous local behavior of the model and its changes over time in response to local changes of the population. Conventional treatments that average over contexts do not capture these effects. [62-66] What is most important and not generally understood is that the conventional mathematical treatment (of density-dependent fitness and other averaging approximations) has been used to infer conclusions (via mathematical proof using averaging assumptions) that are not valid in the case of systems with collective spatiotemporal behaviors. These consequences are clarified by mathematical correspondence to the breakdown of the mean-field approximation due to symmetry breaking and pattern formation. The implications appear here in their relevance to the controversy over individual and group selection, and altruism.

Our objective is to identify the evolutionarily stable strategy in the host-parasite system and to understand this strategy in terms of reproductive success and invasibility. We can then demonstrate explicitly the ultimate limitations of the conclusions obtained from the conventional approach, and show how these limitations arise from spatial averaging. Making this connection is necessary to refute the claims based upon proofs that rely upon averaging assumptions. We start from a population-averaged treatment, which does not provide the correct results for this model, and point out some of the limitations of this approach.

Spatially averaged (mean field) treatment. An approximate solution to this problem can be obtained by thinking of all infected hosts as experiencing the same local environment so that each of them has the same average number of nearby susceptible hosts, vacant sites, and other infected sites; in other words, by averaging the local environment over all infected sites. This spatially averaged solution is the mean field approximation of the model that has been shown to be [41, 42]

$$s_{t+1} = s_t + (1 - s_t - n_t)[1 - (1 - g s_t)^{\xi}] - s_t[1 - (1 - \tau n_t)^{\xi}]$$
$$n_{t+1} = n_t + s_t[1 - (1 - \tau n_t)^{\xi}] - v n_t$$

where s is the density of susceptible hosts and n of infected hosts, and ξ the number of neighbors of a single lattice site. To simplify the discussion, it is sufficient to consider these expressions for small values of g and τ [30, 41, 42]:

$$s_{t+1} = s_t[1 + \xi g(1 - s_t - n_t) - \xi \tau n_t]$$
$$n_{t+1} = n_t(1 + \xi \tau s_t - v)$$

Consider the question of whether a competing strain with transmissibility τ', with density n', can invade:

$$s_{t+1} = s[1 + \xi g(1 - s_t - n_t - n'_t) - \xi \tau n_\tau - \xi \tau' n'_\tau]$$
$$n_{t+1} = n_t(1 + \xi \tau s_t - \nu)$$
$$n'_{t+1} = n'_t(1 + \xi \tau' s_t - \nu)$$

The growth rate of the strain population is $\xi\tau s$-v and hence monotonically increasing in τ. In such systems, the strain with the highest growth rate excludes those with lower growth rates [67]. Thus, in homogeneous systems with competing strains, higher-τ strains dominate. If the full equations are considered, for arbitrary g and τ, there is a possibility of coexistence for τ and τ' very close together.[41, 42] However, the strain with the highest τ dominates and if it is more than a little bit higher the lower τ value strain disappears.

Spatial simulations. The spatially averaged, mean-field approximation does not capture important aspects of the spatial variation in this model. The system is spatially inhomogeneous, with host and pathogen distributed patchily. If we consider a single type of pathogen and simulate the behavior of this host-pathogen system, the overall behavior can have one of the following outcomes: the pathogen dies out but the host survives, host and pathogen coexist, or the pathogen drives the host to extinction (causing its own extinction as well). Parasite-driven extinction occurs above a threshold of τ which depends on the values of the other parameters [68]. Thus, there is a minimum and maximum transmissibility at which the pathogen and host can coexist. Fig. 1 shows snapshots of simulations after the long-term behavior is established, revealing how the geometry changes with differing transmissibility and host reproduction rate.

In order to investigate the evolutionary dynamics, mutation can be introduced directly into the dynamics of the model [57, 69, 70]. The transmissibility becomes a quantitative trait associated with an individual pathogen instead of a parameter of a population. When a pathogen of transmissibility τ reproduces, its offspring has probability μ of having transmissibility $\tau \pm \varepsilon$:

$$P(0 \to S) = 1 - (1-g)^n$$

$$P(S \to I_\tau) = [1 - \prod\nolimits_{\tau'} (1-\tau')^{m_{\tau'}}] \left[\frac{\frac{\mu}{2}\pi_{\tau-\varepsilon} + \frac{\mu}{2}\pi_{\tau+\varepsilon} + (1-\mu)\pi_\tau}{\sum_{\tau''} (\frac{\mu}{2}\pi_{\tau''-\varepsilon} + \frac{\mu}{2}\pi_{\tau''+\varepsilon} + (1-\mu)\pi_{\tau''})} \right]$$

$$P(I_\tau \to 0) = \nu$$

where $\pi_\tau = 1 - (1-\tau)^{m_\tau}$ and m_τ is the number of infected neighbors of transmissibility τ. For suitably large lattice sizes, the system evolves to an evolutionarily stable average value of τ [57]. When high values of τ lead to extinction, τ does not increase to the point of extinction; rather, the system reaches an evolutionarily stable value that is lower than the extinction limit (Fig. 2a). This is the case for the entire region of parameter space where parasites and hosts coexist. A population of pathogens above the evolutionarily stable value, but able to coexist with the host, evolves to a lower transmissibility (Fig. 2b). Figure 3 shows an evolving system at intervals of 20 generations after it has reached the evolutionarily stable average transmissibility, showing patches of susceptible hosts growing and being depleted by pathogens of various types. We show in Fig. 4 snapshots of evolving populations with different combinations of parameters. Each snapshot is taken after 10,000 generations, a time long enough to allow the evolved transmissibility to reach a stable value, aside from fluctuations.

Relationship of pathogen type and spatial structure. The characteristics of the pathogen shape the characteristics of host patches in which they find themselves. [39] Fig. 5 shows a mutant strain 50 generations after it arose, with a value of τ that is significantly above the evolutionarily stable type. This strain has arisen from a single ancestor at time T_0 which mutated from a lower value of τ. By time T_0+250, the strain has become extinct. The figure suggests that the local environment is significantly altered by the mutant type. We study the local environment directly in Figure 6, which shows how the local configuration of hosts in which a pathogen finds itself changes with τ. Strains that arise by mutation are generally located in an area with a local environment determined by the strain from which it mutated. After the first mutant arises, however, the new strain changes the local environment. When measured by the local contact rate, we see that the local environment is transformed to that characteristic of the mutant's value of τ. Fig. 6a shows the local contact rate of susceptible hosts as a function of the time since the strain arose, where the change can be seen to take about 40 generations. Fig. 6b shows an average over time of the local contact rate for the evolving system and compares it with a system having only one type. We see that, for all values of τ, the local contact rate for mixed systems (with mutation) is the same as that for homogeneous systems (without mutation), even though in the mixed system many strains exist on the same lattice and individuals are constantly mutating. This indicates that pathogens of different types are spatially segregated.

Time inhomogeneity of reproductive success. The distribution of τ during evolution has significant features that hint at the time-inhomogeneous nature of the evolutionary

process. Figure 7 is a density plot showing the distribution of τ over time. In this figure, it is apparent that some pathogens continue to evolve higher τ, but these strains go extinct. These offshoots are genetically related pathogens, or strains.

To shed light on the evolutionary dynamics of the system, it is instructive to examine the reproduction ratio for pathogens of different types when mutations are to a random transmissibility rather than a fixed increment. Figure 8a shows the net reproduction ratio $R(\tau)$ for such mutants when they first arise; it increases monotonically with τ. However, Fig. 8b shows $R(\tau)$ for all pathogens, averaged over time; it peaks at the evolutionarily stable value. Thus, selection initially favors high-τ mutants. [40] The selection on initial mutants is thus consistent with a spatially homogeneous treatment. The difference between these two plots shows that selection against high-τ mutants does not act when a new strain first arises, but only on longer time scales; evolutionary dynamics are different at different time scales.

Extended view of fitness. We now discuss more general measures of fitness that can handle cases where the short-term reproductive success of a mutant type does not correspond to long-term success [40], and illustrate their use by applying them to the model. In order to explicitly contrast the fitness over time, we must consider the reproductive success not only of the mutant, but also of its descendants, which can vary as a function of time since the beginning of the strain. We define a strain as the descendants of a particular individual. The reproductive success of the strain over time can be quantified using the average population size of a mutant strain, as a function of the time T since it arose. For a general evolving system, the *time-dependent invasion fitness* $F_i(T,q)$ is defined to be the expected number of descendants at time t_0+T of a mutant of type q introduced at time t_0. T can be measured as time or in generations; here we use the number of generations. Note that $F_i(1,q)$ is the net reproductive ratio R for mutants. In general, F_i should include environmental factors in its arguments. When, however, the local environment of type q is shaped by q itself, as in the model [40], one may write it as a function of only time and type. In order to make a more explicit comparison with the reproduction ratio R, one can calculate the normalized reproduction ratio as a function of time $R(T,q) = F_i(T,q)^{1/T}$. The evolutionarily stable types q_{es} are given by q such that the long time value of $F_i(T,q)$ is greater than zero, $\lim_{T\to\infty} F_i(T,q) > 0$. No other value of q can successfully invade in the long term.

In our model, the type q of the evolving species corresponds to the transmissibility τ. Figure 9 shows $F_i(T,\tau)$, obtained numerically for the host-pathogen model. Strains where τ is less than the evolutionarily stable value τ_{es} have both a short-term and long-term disadvantage, and decline immediately. Strains with $\tau > \tau_{es}$, by contrast, initially grow much more quickly than those of the evolutionarily stable type, but begin declining after an average of about 30 generations. They remain more successful than the evolutionarily stable type for a large number of generations, however. Selection begins to act against strains of a given non-evolutionarily stable type when its curve drops below that of the evolutionarily stable type.

Using time-dependent fitness, one can determine which types dominate at each time scale. For a given time scale T, the most successful type for that time scale $q_{opt}(T)$ is the value of q such that $R(T,q)$ is maximized. Systems for which $q_{es}(T) = q_{opt}(1)$ have no contrast between short-term and long-term fitness. Figure 10a shows that, for the model, one type dominates for short time scales, and another dominates for long time scales, with a sharp transition between the two scales.

Since selection acts differently on a given type at different time scales, one can determine the relevant time scales for a particular type. For all $q \neq q_{es}$ we can define the time scale $T_s(q)$ at which selection acts against q as:

$$T_s(q) = \text{minimum of } T \text{ such that for all } t > T,\ F_i(T,q) < F_i(T,q_{es}),$$

Thus for some $T < T_s(q)$, mutants of phenotype q have more descendants than those of q_{es}. The time scale at which the evolutionarily stable type begins to dominate is given by T_L = minimum of T such that $q_{opt}(T)=q_{es}$. For the host-pathogen system ($q=\tau$), Fig. 10b shows $T_s(\tau)$. For values of τ less than τ_{es}, $T_s(\tau) = 0$ since these low-transmissibility types have a disadvantage on all time scales. For values of τ greater than τ_{es}, $T_s(\tau)$ approaches a constant number of generations (about 200 for the parameters used in Fig. 10b), but is larger when τ is close to τ_{es}. Thus, for τ greater than τ_{es}, on time scales significantly shorter than T_s, the dynamics of the relative frequencies of different types can be determined from conventional fitness measures such as the net reproduction ratio R; on longer time scales, other mechanisms are essential to the dynamics, such as the feedback between the population and the environment. In general, when a type has a short-term advantage ($R(q)<R(q_{es})$), $T_s(q)$ is a quantitative measure of the time scale in which instantaneous change in frequency dominates the evolutionary dynamics for that type.

Finally, one can measure the long-term invasibility by a particular strain. Define the *limiting invasion fitness* $F_l(q)$ of type q to be the long time limit of $F_i(T,q)$, $\lim_{T\to\infty} F_i(T,q)$. F_l can be thought of as a fitness measure of a mutant strain of type q. Similarly to R averaged over time, F_l peaks at the evolutionarily stable value. However, considering fitness to be a function of time, rather than a single number, allows one to characterize the time-inhomogeneous nature of evolutionary systems in which short-term and long-term fitness are different. The populations of such systems can be considered to contain a mixture of strains, each of which has high fitness on a particular time scale.

Because some of the individuals in the population can be of rapidly reproducing types that have high short-term fitness but low long-term fitness, the long-term composition of types in the population may differ from that derived by considering only the strain fitness F_l plus mutation-selection balance. Instead, the distribution $P(q)$ of types, $q \neq q_{es}$, is given for low mutation rates by [40]:

$$P(q) = \frac{m(q)\int_{T=0}^{\infty} F_i(T,q)}{n_{es} + \sum_{q' \neq q_{es}} m(q')\left[\int_{T=0}^{\infty} F_i(T,q')\right]}$$

where $m(q)$ is the rate at which mutants of type q arise, and n_{es} is the average number of individuals of the evolutionarily stable type. $P(\tau)$ measured numerically agrees with the above (except for types which are within 0.1 of the evolutionarily stable type, since these strains take a long time to decline and were not tracked longer than 1000 generations).

Implications. The contrast between long-term and short-term fitness may occur generally in populations that depend on, and can deplete, local resources, (see, for example, [71]). The initial reproductive rate of types does not reveal their long-term fates. The model suggests that mutant strains continually arise and persist for many generations before going extinct through resource depletion. The composition of the population cannot be predicted from either the initial reproductive rate, or the long-term average rate. In particular, such systems observed in nature would on average contain a significantly larger fraction of organisms of non-evolutionarily-stable types than would be expected from the long time average reproductive rate. It is more appropriate to view the composition of types in such systems as a mixture of types, each of which is adapted to a particular time scale.

At the same time, the feedback between exploitation and extinction is seen to have the effect originally proposed [72] as the "prudent predator" concept. Considering the population as a whole in a phenomenological way, the population would appear to moderate the degree to which it exploits the resource. The origin of this moderation can be understood through the spatiotemporal dynamics of populations and the effect of local extinctions. This perspective on local extinctions replaces the concept of group selection mechanisms that were the subject of controversy for many years.

More generally, we believe that many natural evolutionary systems have a contrast between short-term and long-term fitness. In such systems, the long-term distribution of types in a stable population cannot be determined solely from the generation-to-generation change in frequency of the types. Studying the evolutionary biology of such systems thus requires one to look for mechanisms that allow phenotypes to persist that have a short-term disadvantage. Since organisms often greatly affect their own environment, the feedback between the environmental change caused by the organism and selection may be substantial The model we studied demonstrates one possible mechanism for this feedback: the local reproduction and depletion of the resource (hosts) makes it possible for some types to change their environment locally in a way that is ultimately detrimental to their survival. This is an organismal version of allelic frequency-dependent selection but with a local dependence on population density of the type, rather than a global population density.

An alternate perspective can be provided by recognizing the dynamics of a mutant strain as akin to a transition between single celled and multi-cellular organisms, or to insect colonies from individualistic progenitors. A multi-cellular organism has a developmental process and a senescence. If we consider the life span of a mutant strain, many features of such a dynamical process are present through the initial rapid replication followed by decay. Thus the spatiotemporal pattern of mutant strains could be considered a prototype

for the appearance of such larger scale systems. The concept of formation of aggregate organisms out of individuals, as in the formation of multicellular organisms out of individual cells, is relevant to the topic of group selection. The strain growth and senescence shows the role of larger collections of organisms, yet there is no direct correspondence to the group selection concept as we now show.

3. Group selection

Group selection has been defined as the differential extinction and proliferation of groups [73]. In a typical model a set of individuals are divided into subsets. Within each group, individual selection (acting through the differential survival and reproduction of individuals) may be acting to change gene frequencies within populations. In many models group selection occurs because some groups grow larger than other groups, and therefore contribute differentially to groups in the next generation (e.g., Maynard Smith's haystack model [2]). There are many variants on this general scenario, including differential group extinction and differential migration. Variations in the scenarios also include the methods in which new groups are founded and the strength of individual selection acting within groups (reviewed in [74]).

Modern discussion of this process dates to Wynne-Edwards [1] who introduced group selection to explain the tendency of many organisms to apparently withhold reproduction for the good of the group. Behavior in which an individual sacrificed its own fitness to the benefit of others is referred to as altruism. This view was criticized as being an evolutionarily implausible situation. Rather, it was suggested that these apparently altruistic traits were either not truly altruistic or that the altruism was specifically directed toward related individuals [2, 3, 75]. The latter scenario, termed kin selection [2], is considered plausible since an "altruist" can potentially increase the fitness of a relative and therefore the spread of its own genes. As a result of these criticisms, group selection fell out of favor as an important evolutionary force. More recent experimental (reviewed in [6]) and theoretical work (e.g., discussed in [76, 77]) has brought group selection back into the spotlight, although its importance in evolution remains controversial.

The dynamic behavior of mutant strains in the host-pathogen model appears to have relevance to the concept of group selection in that we could consider the process as due to a competition among strains. However, the strains that are rapidly growing in one generation eventually drive themselves to extinction essentially independently of the existence of other strains. Thus the notion of strain competition does not appear to apply; a more direct notion of environmental feedback seems to better characterize the behavior of these strains.

More significantly, a review of the subject of group selection reveals that the essential concept of sufficiently well defined groups that are competing with each other is a single-generational process. To make this clear, we adopt a pedagogical approach and review the subject of group selection as a process of evolution of groups. This will also enable us to show how the temporal properties of fitness through environmental feedback can be

incorporated in a more standard evolutionary perspective by introducing a notion of environmental heritability. This heritability arises through the likelihood that offspring will inherit the effects of progenitors on the environment. This contextual inheritance plays a distinct role from the usually treated genetic inheritance of an organism but is no less real.

A key conceptual foundation for evolution (regardless of whether this applies to organisms or groups) was established by the general arguments of Lewontin [78], who identified three properties of a population that are necessary and sufficient for evolution by natural selection to occur. First, there must be phenotypic variation, that is, there must be some differences among organisms in their appearance, physiology, or behavior. Second, these differences in phenotype must be correlated to differences in fitness. That is, some phenotypic variants must have higher fitness than other variants. As discussed previously, in this context fitness is usually defined as the number of offspring produced by an individual. Third, differences in fitness must be heritable. That is, high fitness individuals must produce offspring that on average also have high fitness.

Thus, natural selection occurs whenever there is variation in phenotypes affecting fitness, and this will lead to evolutionary change whenever those phenotypes have a heritable basis. Most commonly this is considered to occur for selection among individuals, but any biological structure that has the properties of phenotypic variation, differential fitness and heritability will evolve by natural selection [78]. This is the context in which group selection can be formalized, since groups are a level at which selection can potentially act. The identification of a group of organisms associated in some way can lead to the consideration of whether group selection operates upon them. There is little controversy as to whether there is variation among groups; however there is considerable question as to whether there will generally be an association between group-level phenotype and fitness. More seriously, there is a question as to whether groups have sufficient multigenerational cohesiveness for the group level phenotypes to be heritable; that is whether groups persist long enough for group selection to lead to evolutionary change. Experimental evidence clearly shows that laboratory populations that have all these properties can be established; however, whether populations with all three of the requirements for evolution by group selection occur in nature remains to be examined [6]. For this discussion we will return to the simple definition of fitness as the number of offspring produced by an individual. It is convenient to translate the fitness of an individual into "relative fitness".[2] Relative fitness of the *i*th individual is defined as the number of offspring produced relative to the population mean:

[2] In some works relative fitness is defined in relation to the maximum fitness in the population. Such an approach, while perhaps formally equivalent and giving the same conclusions, is likely to be poorly behaved in application to realistic models where small subpopulations may have transient large reproduction rates. Thus we do not adopt it here. We use notation that is standard in evolutionary biology in this section.

$$\tilde{w}_i = \frac{N_i}{\overline{N}}$$

where $\tilde{w}_i$ is the relative fitness of the *i*th individual, N_i is the number of offspring produced by the ith individual, and $\overline{N}$ is the mean number of offspring produced in the population. Individuals with a relative fitness greater than 1 will produce more offspring than average, and those with a relative fitness less than 1 will produce fewer offspring than average. Realizing that the mean relative fitness is one, $\overline{\tilde{w}} = 1$, a basic measure of interest is the variance in relative fitness,

$$Var(\tilde{w}) = \sum_i p_i \left(\tilde{w}_i - \overline{\tilde{w}_i}\right)^2 = \sum_i p_i (\tilde{w}_i - 1)^2$$

where p_i is the frequency of the *i*th phenotype. This variance is of sufficient importance that it has been referred to as the "opportunity for selection" [79], and it provides a measure of the variation in fitness that is available for selection. By itself, this measure cannot be considered evolution (defined for our purposes as change in gene frequency) since this provides no insight into the causes of differences in number of offspring produced. Indeed, even random mating will produce variance in relative fitness, since the number of offspring will have a binomial distribution.

For selection to occur there must be a relationship between relative fitness and phenotypic traits, i.e., differences in phenotype must be correlated to differences in fitness. This can be quantified using the covariance between a trait, Z, and relative fitness [79]:

$$Cov(Z, \tilde{w}) = \sum_i p_i \left(Z_i \tilde{w}_i - \overline{Z}\overline{\tilde{w}}\right) = \sum_i p_i Z_i \tilde{w}_i - \overline{Z}\overline{\tilde{w}}$$

Remembering that $\overline{\tilde{w}} = 1$, and realizing that $p' = p_i \tilde{w}_i$ is the frequency of the of the ith phenotype after selection, the change in phenotype as a result of selection is:

$$\Delta\overline{Z}^* = Cov(Z, \tilde{w}) = \sum_i p_i' Z_i - \overline{Z}$$

If we make the assumption that change in Z is the result of selection acting on Z, an assumption that in many circumstances is not valid, we can use regression to write relative fitness in terms of phenotype:

$$\tilde{w}_i = b + aZ_i + e_i$$

where b is the intercept and a is the slope of the regression equation given by:

$$a = \frac{Cov(Z, \tilde{w})}{Var(Z)}$$

and e_i is an error term. This approach can be extended to include multiple traits using partial regression rather than simple regression [80]. In this case:

$$\tilde{w}_i = b + a_1 Z_{i1} + \cdots + a_n Z_{in} + e_i$$

where a_1 etc. are now the partial regression coefficients of relative fitness on the appropriate trait.

This description of selection only refers to the within-generation change as a result of selection. Between-generation change, that is, evolution by natural selection, requires the third necessary and sufficient condition, that the traits be heritable. Heritability in a quantitative genetic sense can be described by the regression of offspring traits on parent traits. The slope of this regression is half of the heritability. For historical reasons the standard symbol for heritability is given by h^2 (note that the square root of h^2 is never used) (see [81] for a careful description of heritability). Heritability is primarily used to describe the response to selection using the "breeder's equation." To attain the traditional form of this equation define R to be the intergenerational response to selection, $\Delta\overline{Z}' = \overline{Z}' - \overline{Z}$, where $\overline{Z}'$ is the mean of the population after selection and reproduction, and S is the within generation change due to selection, $\Delta\overline{Z}^*$ then [81]:

$$R = \Delta\overline{Z}' = h^2 S = h^2 \Delta\overline{Z}^*$$

Group selection has been defined as the differential proliferation and/or extinction of groups [82]. Group selection can be incorporated into this model of selection if group selection is defined in terms of what is called "contextual analysis" [6, 82, 83]. Contextual analysis is a regression approach in which both group-level and individual-level traits are simultaneously included in a multiple regression model. It was developed in the social sciences to analyze situations where social behaviors and opinions of individuals are influenced simultaneously by characteristics of individuals and society [84]. The model is identical to the individual selection model described above, except that "contextual" traits are also included. Contextual traits are traits measured on the group and may include both summary measures, such as the mean of an individual trait, and traits that can only be measured on the group, such as population size. Note that the "group" need not be a discrete entity, but can be any collection of individuals that influence the fitness of the focal individual. Thus the regression becomes [82]:

$$\tilde{w}_i = b + a_1 Z_{i1} + \cdots + a_n Z_{in} + a_{(n+1)} C_{i1} + \cdots a_{(n+m)} C_{im} + e_i$$

where:

w is relative fitness,
b is the intercept,
$a_1 - a_{(m+n)}$ are partial regression coefficients,
$Z_{1i} - Z_{ni}$ are individual level traits,
$C_{1i} - C_{mi}$ are contextual traits, and
e_i is an error term.

Using this model of selection, group selection occurs when there is a significant partial regression of relative fitness on a contextual trait. By this definition, group selection

occurs when the fitness of an individual is influenced by interactions with other individuals.[3] In traditional models of group selection the individuals have been organized into discrete groups, with selection occurring through differential extinction and recolonization, and through differential migration. However, contextual analysis works equally well with spatially structured or poorly mixed continuous populations when neighbors have sustained interactions influencing fitness.

It must be emphasized that contextual analysis only describes within-generation change. Many situations that may show up as group or contextual selection will not lead to any adaptive change (i.e., a response to selection) because the population structure is not sufficiently stable to provide heritability, the third component necessary and sufficient for evolution by natural selection identified by Lewontin. For example if new groups are founded by individuals from several different groups, high fitness groups may not reliably pass on their characteristics when new groups are founded.

Importantly, multilevel selection as it is currently formulated is a within-generation phenomenon. That is, multilevel, or contextual, selection results when the fitness of an organism is influenced by interactions with other contemporaneous organisms. The environment as influenced by previous generations does not figure into the calculation of fitness. Nevertheless, in the model presented in this paper, it is the modification of the environment that will ultimately cause the extinction of lineages with high transmissibility. This means that in this case, selection is a multigenerational phenomenon in which high transmissibility mutant strains progressively modify their environment resulting in the extinction of the lineages over several generations. This is clearly similar to multilevel selection: it involves interactions among organisms, and the fitness of an organism is a function of these interactions; however these interactions of an organism with its predecessors are mediated through changes in the environment. While conceptually similar to within-generation multilevel selection, it is nevertheless a distinct phenomenon.

While conventional group selection does not incorporate intergenerational effects, we can expand the conventional formalism to include intergenerational influences. In the model presented here, prior generations influence the fitness of an individual because they have killed potential hosts. Thus, they have modified the environment. In conventional formulations, environment cannot contribute to evolution by natural selection because it is not heritable. Recent discussions of environmental inheritance, niche construction, allow for the concept of environmental change by organisms. [14-16] In their discussions environmental changes become heritable and should be included in the fitness of genotypes due to their aggregate role similar to all other effects of individual organisms, alleles. However, the application of averaging in mathematical formulation removes the distinctive dynamical role of local changes on the individual lineages we discuss here. Intuitively, we can recognize that the specific history of a particular location in space at a

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[3] Under this definition many forms of frequency- and density-dependent selection are forms of multilevel selection. This broad definition is appropriate because under contextual analysis they are mathematically the same process.

particular time influences the local environment, and subsequently the effective fitness of a particular type at that location. While this is intuitive, what is ultimately important is that this effect changes the overall dynamical behavior of the evolutionary process as demonstrated by comparing the results of an averaged treatment of the model with that of the direct simulation. We can capture this in a formalism that appears similar to the traditional one but has essential differences.

In the case of a spatial environment where averaging does not apply, because the environmental conditions are generated by predecessors that occupied the same or nearby physical locations the environment does become heritable and distinctive for different organisms at the same time or at different locations in space, and can be legitimately included in the equation for relative fitness. Thus, this multiple generational effect on fitness can be modeled as:

$$\tilde{w}_i = b + a_1 Z_{i1} + \cdots + a_n Z_{in} + a_{(n+1)} C_{i1} + \cdots + a_{(n+m)} C_{im} + a_{(n+m+1)} E_i + e_i$$

Where E_i is the environmental effect generated by the predecessors that lived at the same or nearby physical location. In the model presented here, E_i will primarily be a measure of the number of hosts available to the ith individual (the contact rate, ρ, see Fig. 6). During the early (e.g. first 30) generations this number will be similar for all pathogen strains. In later generations the contact rate will change to a value that is characteristic of the transmissibility, τ, of the ith individual's predecessors. For low mutation rates, the transmissibility of the predecessors will be the same as that of the individual; however, in general this need not be true. The contact rate will be increased by low values of τ in the predecessors, and decreased by high values of τ.

We can show that spatial location is heritable by demonstrating that offspring are located near their parents. This heritability is equivalent to the correlation of genealogical relatedness in space. By way of example, we show in Fig. 11 a representation of the spatial structure of genealogical distance. In this picture, the colors show the degree of genealogical relatedness to a particular pathogen. The left and right panels show this for two different individuals at the same time in an evolving population, simulated using incremental mutations. Figure 12 shows the average genealogical relatedness as a function of spatial distance.

4. Kin Selection

There are specific, widely recognized cases where the reproductive fitness of an individual organism does not necessarily predict its reproductive success over many generations. A key mechanism for this is the process of kin selection, since an individual's reproduction can be diminished (or even zero) while its effective reproduction is larger because of the benefit that arises to other genetically related individuals that it is helping. It is clear that the notion of kin selection is closely related to traditional discussions of the mechanism by which "altruism" (the reduction of an individual's reproductive success to help others') arises.

The term kin selection was introduced by Maynard-Smith [75] to explain the evolution of altruism that is directed towards relatives. Kin selection is based on Hamilton's rule [23],

$$\frac{Cost}{Benefit} < relatedness$$

This equation states that an altruistic behavior should evolve if the ratio of cost of performing the behavior to benefit to the recipient (or recipients) is less than the relatedness between the altruist and the recipient. It is reasoned that under these circumstances, because the beneficiaries of altruistic behavior are also likely to carry the genes controlling altruistic behavior, the behavior should spread. Kin selection is widely accepted as an important evolutionary force, and is frequently invoked as an explanation for the evolution of altruistic traits [85]. Kin selection (or the related concept of inclusive fitness) provides a specific view of how altruism can enter and even dominate an evolving population [2, 23]. The mechanism assumes that the selection of heritable traits can promote a behavior in which one individual sacrifices its own reproductive capacity in order to help a relative reproduce at a higher rate. The benefit to the sacrificing individual from this arrangement arises from the existence of shared alleles among relatives. If there is a large enough increase in the offspring of the beneficiary compared to the loss of the altruist, then there will be a greater number of alleles that promote this behavior in the following generation. Specifically, if the relatedness is that of identical twins, the benefit must be greater than the deficit. If the relatedness is that of sisters, the benefit must be over twice as much as the deficit, and so on. Experimental cases that are often quoted as examples indicative of kin selection include cases where neither individual would be able to have offspring without the altruistic behavior, whereas only one would have offspring in the case of the altruistic behavior.

Since we have shown that the moderation of transmissibility can be understood as a kind of altruism, we can ask whether the notion of kin selection has something to do with the moderation of transmissibility that is observed in the model we are describing here. To address this question it is essential to realize that the process of environmental feedback through many generations does not correspond to the notion of altruism within a generation: one individual helping other individuals by sacrificing reproduction does not occur.

If we consider the effect of lowered transmissibility of one pathogen on the possibility of reproduction of other pathogens, we realize that this is not a case of kin selection as it is normally defined. Specifically, if one pathogen were to reduce its transmissibility from τ to τ-$d\tau$, the likelihood of its infecting a particular adjacent host would go down. At most, this would enable one other pathogen to infect that host. If the host was indeed infected, and this infection were by an identical twin of the original pathogen, then the outcome would be for the original pathogen the same as a direct infection. Thus, the best-case scenario is only a case of equal benefit and there is no scenario in which a pathogen can increase the likelihood of infection by its own genotype through reducing its transmissibility.

We see from this argument that kin selection, as it is normally defined, does not apply in the case we are concerned with here. Suitably generalized to account for the dynamics of the growth and death of strains, we can account for the model behavior using standard evolutionary processes that also can be discussed in terms of kin selection – where kin are separated in time. Thus if a pathogen were to calculate the benefit to its ultimate descendents for the choice of a transmissibility, then the highest fitness would be trivially related to the average R(t) over time rather than the instantaneous R(t) of a mutant. Kin selection is an attempt to project the longer-term effects of reproduction onto the fitness of a single generation through memory that is encoded genetically. This genetic encoding is not part of the model discussed here. Instead, the limitation on transmissibility occurs as a dynamic process that explicitly occurs in the environment of the system. *If* there were a mechanism of memory for the long-term effects of mutation on the ultimate outcome of the strain, this limitation could be attributed to the genotype as an evolutionary strategy to *choose* the transmissibility that is evolutionarily stable. The simulation shows how this occurs as a dynamic phenomenon instead.

Importantly, without such a genomic memory, the limitation of the transmissibility is explicitly due to the environmental feedback of physical parameters (phenotype). More specifically it is not due to the genotype relatedness. To demonstrate this explicitly we studied the effect of genotype relatedness of nearby individuals on the evolutionary stable value of the transmissibility. Nominally, in a kin selection model, the evolutionary stable value of the transmissibility would manifest the level of altruism in the population [75]. If the level of altruism depended on the genotype relatedness of nearby individuals, the evolutionary stable value of the transmissibility would be sensitive to the genotype relatedness. We show in Fig. 13 the effect of varying the mutation rate on the evolutionarily stable value of the transmissibility. We contrast this with the effect of the reproduction rate of the host organisms on the transmissibility. The latter has a significant effect, while the former, which more directly affects the local relatedness of individuals, has a very small effect.

The role of relatedness should be understood as relatedness of individuals to whom altruistic behavior is performed compared to the relatedness to the population of competing organisms. Specifically, if an organism is closely related to all of the organisms that are present, then there is no reason for it to act in an altruistic way, because benefiting in a relative way one individual (compared to the rest of the population) does not change the relative success of the trait or genome of that individual. In the context of this model, the local relatedness of individuals by genotype and the long-range relatedness of individuals do not have a major influence on the evolutionarily stable value of the transmissibility.

We can reinterpret altruism in kin selection to be a genetic learning of the multigenerational consequences of behavior. Our reasoning is that in a single generation it is not possible for the effect of altruism to be manifest, but over several generations this is possible.

Analogously, one of the main problems in the context of the discussion of group selection is the heritability of group traits. We can address this problem in the context of our model by noting that what would be normally ascribed to a group, here is ascribed to the interaction between the group and its environment. Moreover, our discussion suggests that there is a possibility of the incorporation (learning) of the interplay of environment and strains into the genomes of organisms. The selection of traits that enable strains to better survive could occur. Thus, the longer time survivability of strains leads to the possibility of group traits becoming inherited and this can be thought of as the incorporation of the patterns of interplay of environment and groups into the genomes of organisms. Such learning would reflect the spatiotemporal patterns of behavior that occur over multiple individuals and generations.

6. Conclusion

Real populations are distributed spatially. Organisms are located at different points in space and thus they experience different environments, and interactions among organisms are local. The spatial distribution of organisms in nature, and the varied local environments in which they exist, are not directly represented in conventional models of evolution. Instead, in conventional studies of evolutionary and ecological systems, these and other complicated spatial and temporal distributions are averaged over. Indeed, in the gene-centered view, such systems are represented as the frequencies of various genes or types in the entire population. In this formulation, the environment experienced by a particular individual is, by definition, the average over all environments. Such averaging reflects the assumption that fluctuations and patterns of spatial inhomogeneity become unimportant in the limit of large populations or over long times. Populations with subdivision, in which locality is relevant, have been treated as an ensemble of homogeneous populations with some migration between them [49-54]. However, each of the subpopulations is treated in the conventional way, and the outcomes of these systems are evaluated by comparing generation-to-generation changes in frequency of the types.

The essential dynamical nature of evolutionary processes has also been relegated to that of a gradual process in a quasi-steady state approximation, i.e. where incremental changes of the population composition are gradual enough to enable other system characteristics to settle down to reach equilibrium at each moment so they have no independently specified or coupled dynamics (this is called in physics the adiabatic approximation, and is termed a “quasi” steady-state assumption because the population may vary over time). While predator-prey Lotka-Volterra type equation oscillations, as well as the punctuated equilibrium concept [86] and the related concept of cascades in networks of co-evolving systems [87] suggest that quasi-equilibrium treatments are inadequate, the influence of these concepts on the understanding of the long term evolutionary dynamics of species still remains limited. Standard approaches average over time-varying quantities, as they assume that the effects of this variation are unimportant on all but the shortest time scales. In the presence of spatial inhomogeneity, conclusions of such models can be systematically violated. This can occur when parts of the system undergo change over the course of many generations even when the population has

reached a steady state, for example when some organisms gradually modify their own environment so that the environment encountered by descendants is systematically different from that encountered by their ancestors. Thus, both space and time heterogeneity lead to substantial differences in the evolutionary behavior of populations as compared to homogeneous ones.

The study of spatial models of predator-prey and host-parasite systems has been undertaken in recent years because of the direct relevance of such models to understand natural processes. In this paper we have reviewed recent research that shows how the evolutionary dynamics of a spatial population of predators or pathogens cannot be understood using conventional spatial averaging. More significantly, we show that the concept of fitness as a property of an organism at a particular time is violated through the failure of quasi-steady state assumptions. Instead, the breaking of temporal homogeneity leads to a dynamics of mutant strains that appears at first glance to be like group or kin selection. However, conventional formulations of kin or group selection, which rely both upon quasi-steady state approximations and spatial averages turn out not to encompass the spatiotemporal behavior of strains found in this model.

More specifically, standard measures of fitness, which are based on the generation-to-generation change in frequency of organism types, contain the assumption that temporal heterogeneity in the interaction between the organisms and their environment is unimportant, and can be averaged. The key to understanding the failure of this approach in the spatial predator-prey model is that the organisms modify their local environment by exploitation so that descendents may experience systematically different environments than their ancestors. If spatial averages over the environment are assumed, then these local spatial differences appear to affect all organisms identically, rather than preferentially affecting the offspring of highly exploitative individuals, and therefore the importance of this effect is lost. The differences in the effect of spatial populations, as compared to a homogeneous approximation, do not disappear even in the large population limit. While existing definitions of group selection and kin selection do not allow for the effects of spatiotemporal inhomogeneity and therefore do not encompass the range of possible forms of multi-level selection, we showed that one way to overcome this problem is to introduce the notion of environmental inheritance. The concept of environmental inheritance is a major modification of conventional evolutionary thought. It is also appealing as a practical approach to studying models of evolutionary change.

The importance of spatial and temporal inhomogeneity and the role of environment modification and feedback are potentially relevant to several areas of biological inquiry. In recent times the importance of spatial inhomogeneity on the dynamics, stability, and diversity of ecological [32] and epidemiological [22, 27] systems has begun to be recognized. The research reviewed here may be directly relevant to models of ecological processes influencing the distribution and abundance of organisms. For example, the persistence of organisms in their habitats can be dominated by feedback between the organism and its environment, and the distribution of organism types can be significantly different from that estimated using spatially and temporally averaged environments. Perspectives on the viability of spatially limited habitats that are reserved for endangered

species may also be impacted by such research. Similarly to ecology, the dynamics of infectious pathogens can also be governed by feedback between the organism and its environment (in this case, the distribution of susceptible or infected hosts). In this case evolution is of particular relevance because pathogen generation times are short, and the dynamics of the infection may be changed by evolution of the pathogen (for example, resistance to drugs) over the course of a single epidemic, or in their year-to-year variations. Thus, the dynamics of an infection can be significantly different than that predicted by studies using averages of the distribution of susceptible and infected hosts over space and time. When previously spatial systems become more highly connected, as is currently happening to our world through globalization, substantial changes that threaten evolutionary stability may arise. Intimations of such effects in the behavior of invasive species and pandemics are matters of global concern. [88]

Finally, inhomogeneity in space or time can also be a determining factor in the evolutionary history of species. Both survival and extinction of types can be fundamentally different from the outcome predicted using standard approaches, which predict outcomes by comparing the generation-to-generation change in frequency of different types (normally called fitness). We have also shown how existing definitions of group selection and kin selection, since they do not allow for the effects of spatial and temporal inhomogeneity, do not encompass the range of possible forms of multi-level selection. This raises significant new challenges to developing alternate formulations of evolution that can accommodate the effects of spatiotemporal patterns.

The significant role of space in the dynamics of evolution opens the door to new inquiries in understanding altruism and other collective behaviors in evolution. In this regard, it is significant that social signaling of the scarcity of resources (i.e., predators signal to each other the scarcity of prey) was an essential coordinating mechanism of the reproductive restraint described by Wynne-Edwards. [1] Recent research has shown that social signaling-based reproductive restraint is indeed evolutionarily favored in spatial environments. [89] This research shows that social behaviors, including signaling and altruism based upon signaling, is a robust property of evolving populations in spatial environments. As in the case of individual reproductive restraint, social altruism arises because the local environment is inherited: altruistic individuals have environments shaped by the altruism of their ancestors, while selfish individuals have environments shaped by the selfishness of their ancestors. This is surely a lesson of wide relevance.

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Figures

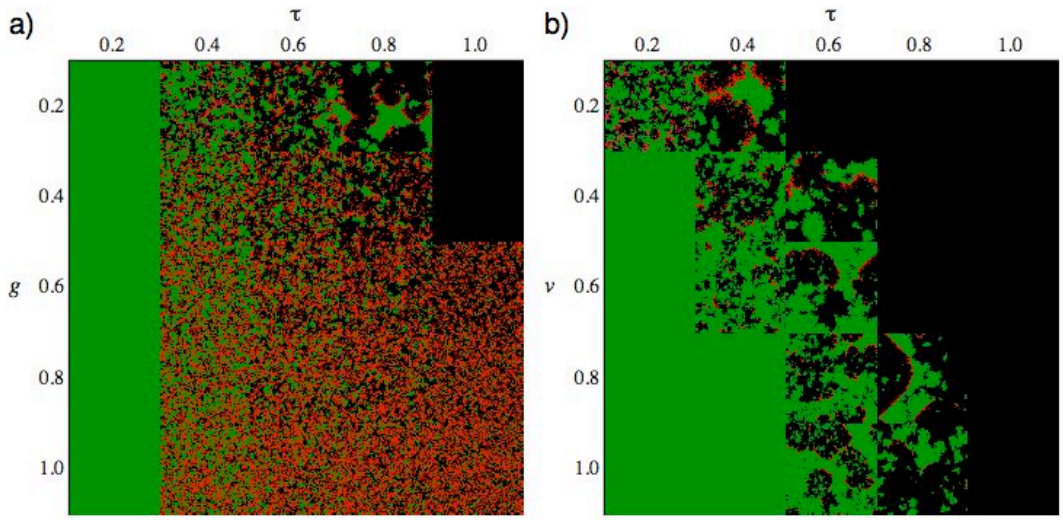

Figure 1: Snapshots of the host-pathogen model with no mutation. For (a) each of the 25 blocks is from a simulation with distinct values of transmissibility τ and host reproduction rate g, with virulence v held at 0.5. For (b) each of the 25 blocks has distinct values of transmissibility τ and virulence v, with host reproduction rate g held at 0.05. Green represents healthy hosts, red represents infected hosts, and black represents empty sites. The snapshots for those parameters for which there are no surviving pathogens after 100 generations appear completely green. For those that appear black, the outcome is uncertain and can be either pathogen extinction or extinction of both pathogen and host. The lattice size L is 80. We use an $L \times L$ square lattice with periodic boundary conditions and a von Neumann neighborhood (north, south, east and west neighbors).

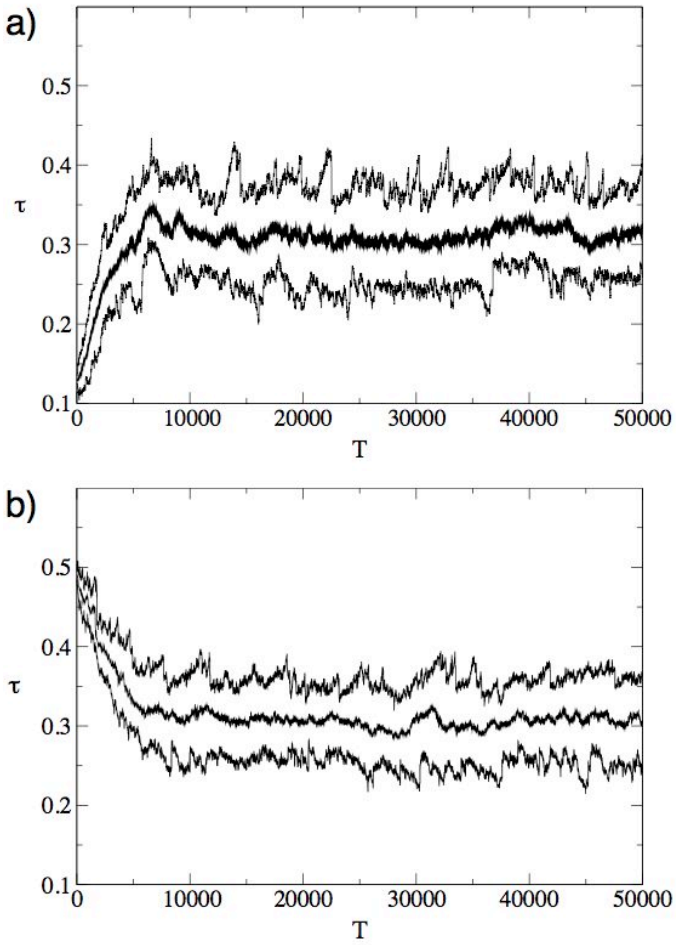

Figure 2: Time series of transmissibility, τ, in an evolving population, showing average, maximum, and minimum values. (a) τ started at 0.15, below the evolutionarily stable value of 0.3. τ evolves upward to reach the evolutionarily stable value within 7,000 generations. (b) τ started at 0.49. τ evolves downward to the evolutionarily stable value, again within 7,000 generations. The virulence v is .2, host reproduction rate g is .05, mutation rate μ is .15, and mutation increment ε is .005. These parameters will be used in subsequent figures unless otherwise noted. The lattice size L is 250.

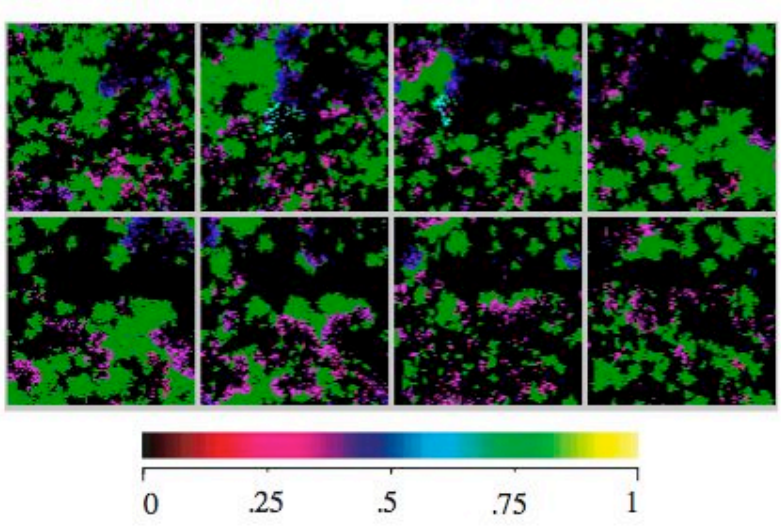

Figure 3: Snapshots of the lattice for the evolving host-pathogen model. 20 generations elapse between frames from left to right, top row then bottom row. Susceptible hosts are shown as green and infected hosts are colored depending on their value of τ, as shown in the legend. In this and all subsequent figures, the system has settled to a stable value of τ. The lattice size *L=100*.

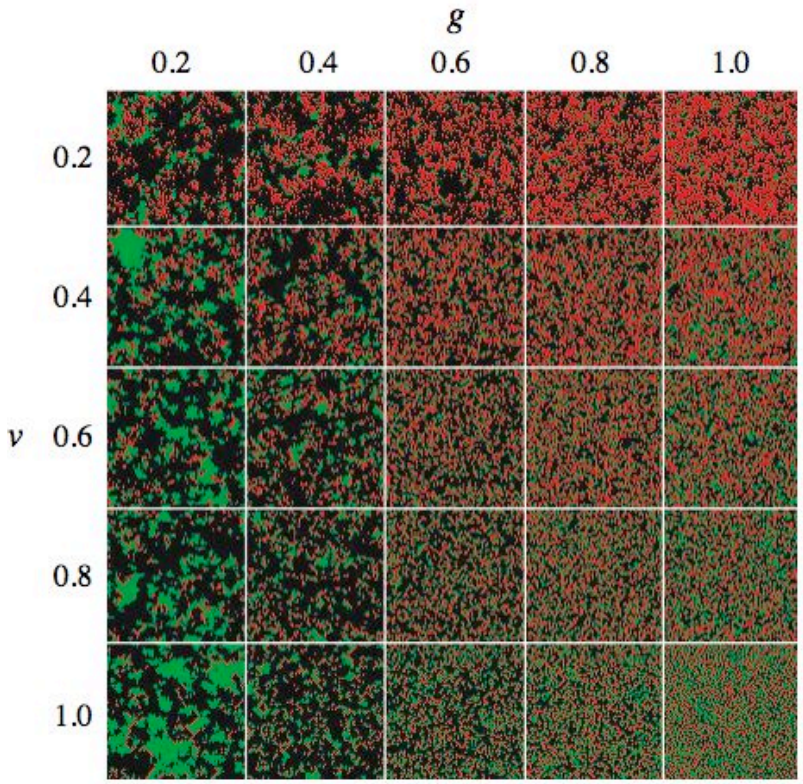

Figure 4: Snapshots of the host-pathogen model with mutation after 10,000 generations. The transmissibility has evolved to an evolutionarily stable value. Each of the 25 blocks represents a simulation with different values of *g* and *v* as indicated. The dimension of the lattice *L* is 175.

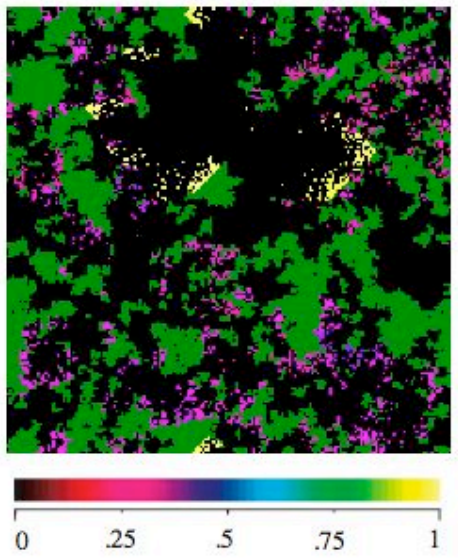

Figure 5: Evolution of a mutant strain. In this snapshot of the lattice, yellow indicates a high transmissibility (τ=0.9) mutant strain which arose 50 generations ago. The lattice size is 175. We see that the mutant strain is spatially clustered and is depleting the hosts from its local environment. This environmental change leads to the eventual extinction of the strain.

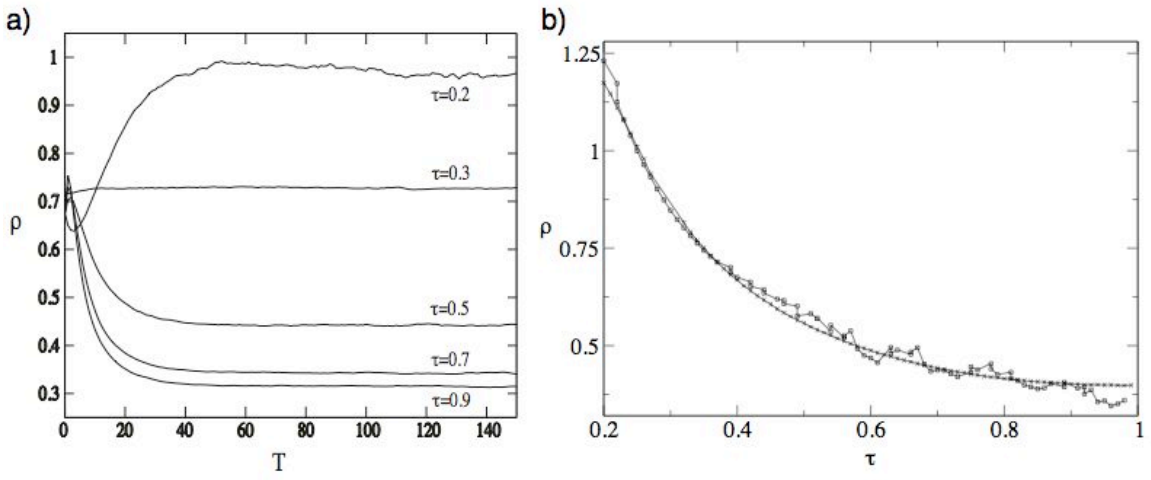

Figure 6: (a) The contact rate, ρ (the number of neighboring susceptible hosts), averaged over all individuals infected with a strain of a particular type, as a function of time since the strain first arose. Within 40 generations, the local environment in the vicinity of the strain has been changed from the value characteristic of the evolutionarily stable type to a value characteristic of the mutant strain. (b) The characteristic contact rate, ρ, as a function of transmissibility τ. Squares represent data measured in non-mutating populations where all pathogens are of the same type, and xs represent data taken in evolving populations, where many other strains with different τ are present.

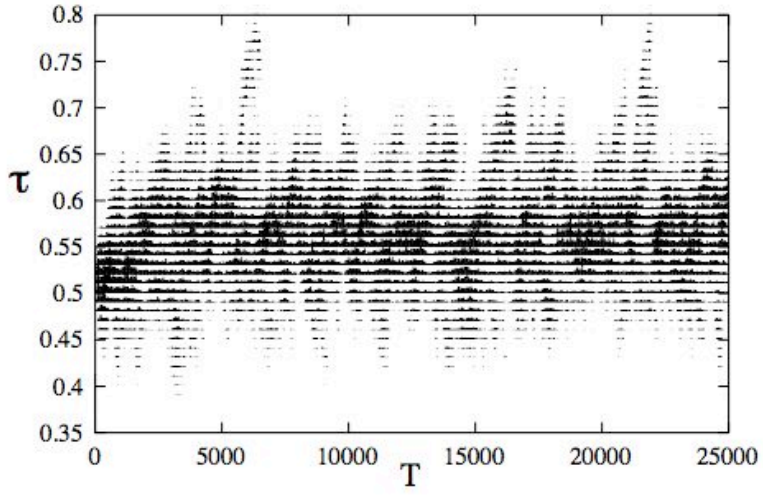

Figure 7: Time series of the distribution of in an evolving population. Each vertical slice represents the distribution of τ at a particular moment in time. Groups of individuals exceed the evolutionarily stable value (most notably at T=6000 and 21000) but then go extinct. The virulence v is 0.5 and the host reproduction rate g is 0.1.

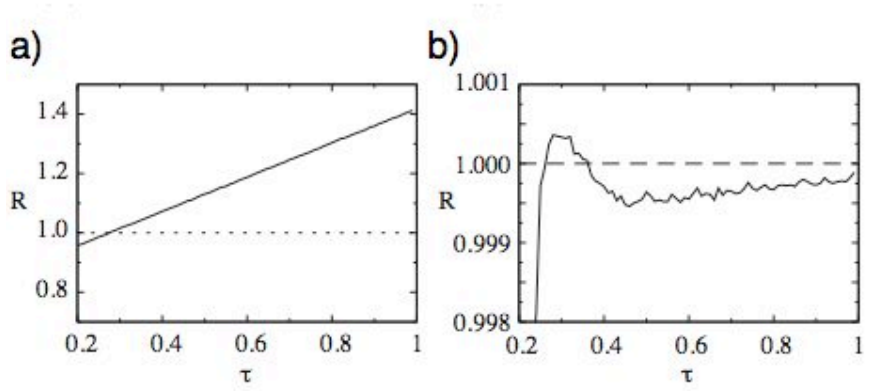

Figure 8: (a) R (the net reproduction ratio) as a function of τ for mutants, showing the expected number of offspring of a mutant one generation after it arises. The dominant phenotype has reached its evolutionarily stable value of $\tau = 0.3$. (b) As on the left, but for all pathogens, averaged over time; R peaks at the evolutionarily stable value of 0.3 and is below one when τ is significantly greater or less than the evolutionarily stable value. In order to collect data for all τ, mutants' transmissibility is set to a random value between .2 and 1 rather than being a small increment. The mutation rate μ is 0.002 and the lattice size L is 175.

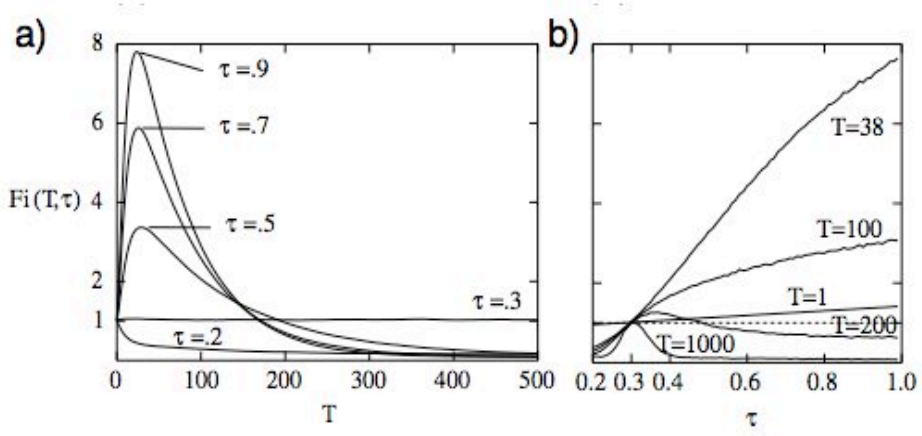

Figure 9: The time-dependent invasion fitness $F_i(T,\tau)$ for the host-pathogen system. (a) As a function of time T, with curves for various transmissibilities τ. (b) The same data as a function of τ, with curves for various time scales T. The lattice size L is 250

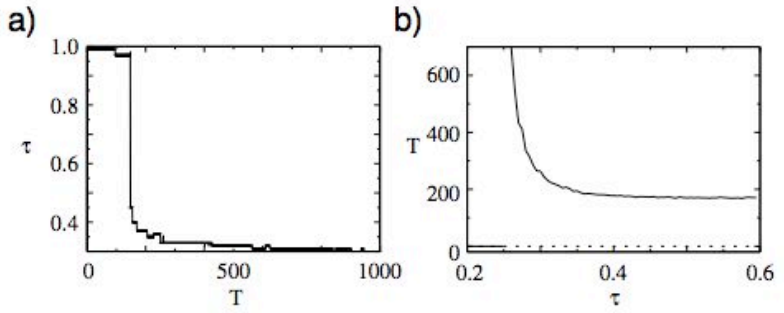

Figure 10: Time scale of selection. (a) The most successful type $T_{opt}(T)$, as a function of time since the beginning of the strain. Types of high transmissibility (those with high values of R in figure 7a dominate for time scales shorter than about T=175, while types close to the evolutionarily stable type (those with high values of time-averaged R in figure 7b dominating on time scales longer than T=250. (b) The time scale $T_s(\tau)$ at which selection acts against strains of pathogens with transmissibility τ. $T_s(\tau)$ is 0 for τ less than τ_{es}, indicating that selection acts against these types instantaneously. For τ greater than τ_{es}, the time scale is very long for values close to τ_{es}, and converges to approximately 180 for high τ.

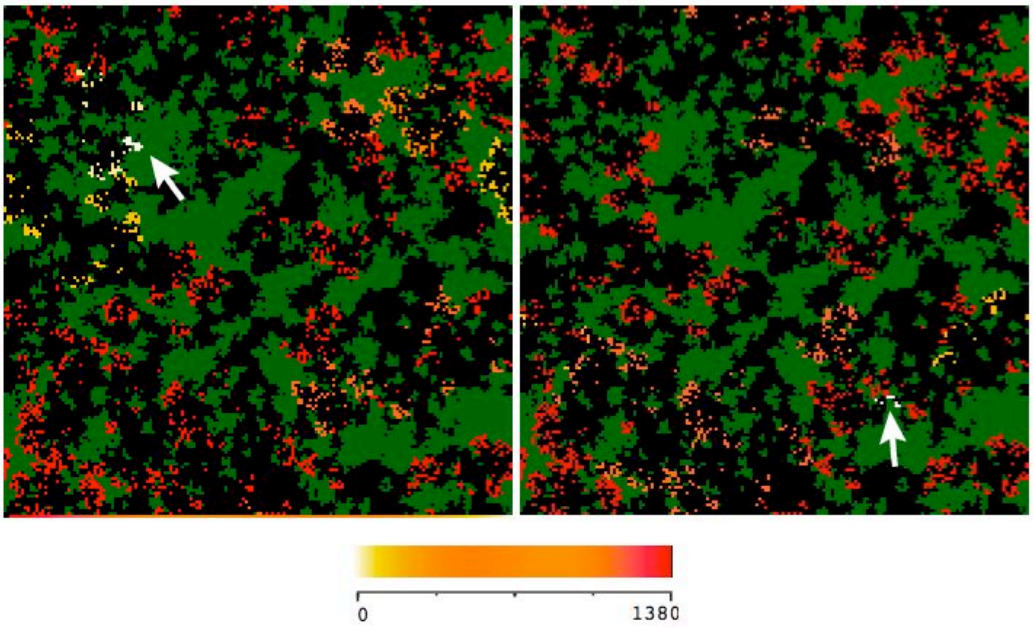

Figure 11: Genealogical distance between individuals in space. Distance from the individual marked by the arrow is shown as color. Yellow indicates pathogens that have a recent ancestor in common with the pathogen indicated by an arrow; red represents those that have the most distant common ancestor (a distance of 1,380 generations). Pathogens of the same color are not necessarily related to each other. The two plots show relatedness from two different individuals at the same time.

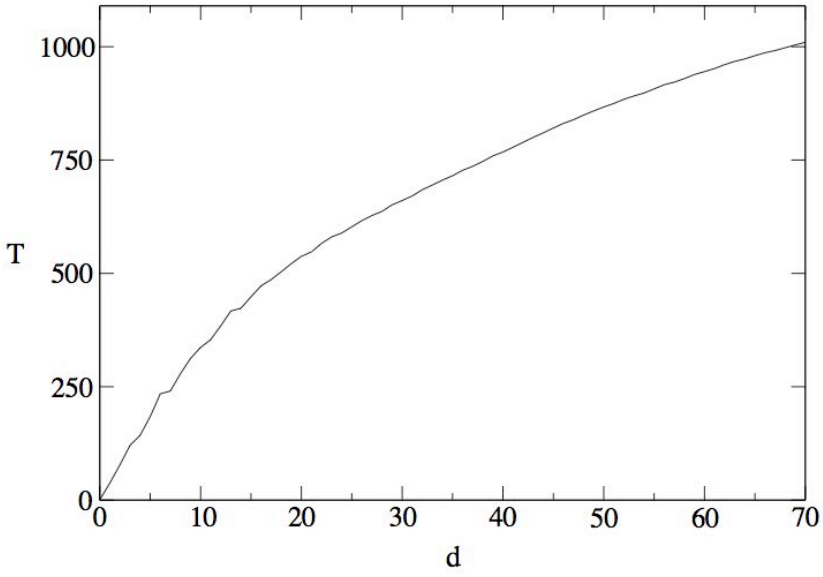

Figure 12: The average genealogical relatedness, or number of generations since a pair of individuals had their most recent common ancestor, as a function of their distance from each other. Since the size of the system being simulated is only 100x100, the leveling off of the curve may be due to the finite system size.

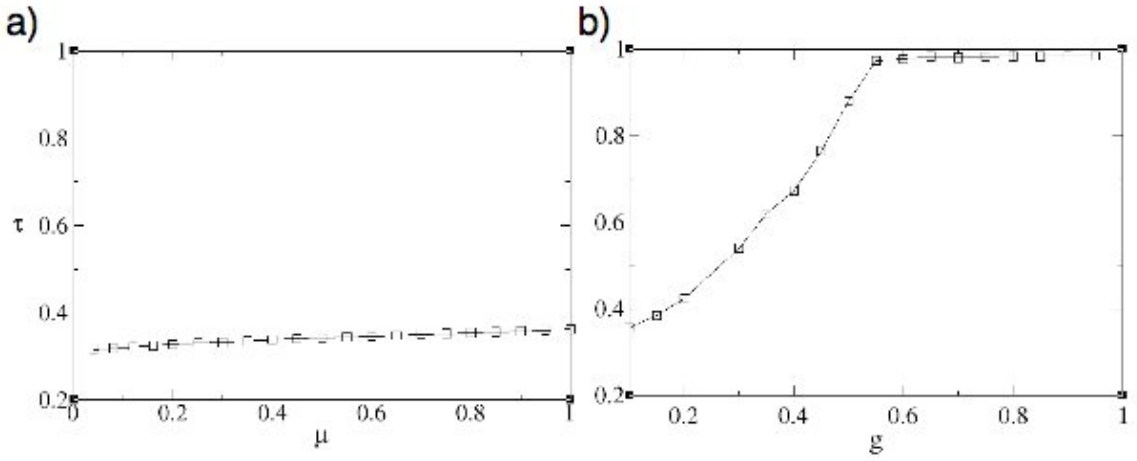

Figure 13: a) τ_{es}, the evolutionarily stable average value of τ, as a function of the mutation rate μ. μ has a very small effect on τ_{es} even when all offspring are mutants. The small increase is mostly due to high-τ mutant strains, which arise more frequently for higher μ and increase the average, but die out, rather than an increase in the evolutionarily stable background. b) τ_{es} as a function of the host reproduction rate g. g has a much more significant effect on τ_{es} than μ.