Review

Evolution in structured populations: beyond the kin versus group debate

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Much of the literature on social evolution is pervaded by the old debate about the relative merits of kin and group selection. In this debate, the biological interpretation of processes occurring in real populations is often conflated with the mathematical methodology used to describe these processes. Here, we highlight the distinction between the two by placing this discussion within the broader context of evolution in structured populations. In this review we show that the current debate overlooks important aspects of the interplay between genetic and demographic structuring, and argue that a continued focus on the relative merits of kin versus group selection distracts attention from moving the field forward.

> It's like what Lenin said... you look for the person who will benefit, and, uh, uh...
>
> –The Dude

Kin versus group selection

Recent years have seen a revival of interest in the evolution of structured populations, with a strong emphasis on the evolution of social traits such as altruistic and cooperative behaviours [1–5]. This has reignited the debate on kin versus group selection and has generated much discussion about the processes underlying the evolution of such traits, as well as the most appropriate modelling formalism [6–9]. Much of this recent discussion has diverted attention from important biological issues, and our goal here is therefore to place this debate within the broader context of evolution in structured populations. In so doing we highlight the fact that in a structured population, virtually all traits can be thought of as social, including dispersal [10], life-history traits such as reproductive effort, senescence and sex allocation [11], and virulence or resistance traits in host–parasite interactions [12,13]. Within this broader perspective we point out possible avenues for future research.

What is the debate about?

The current debate seems to stem, in part, from a failure to clearly distinguish between the biological interpretation of processes occurring in real populations and the mathematical methodology used to describe these processes. The two are necessarily intertwined, but it can sometimes be useful to distinguish between them. To this end, we use the terms kin selection (KS) and multilevel selection (MS) to describe two different biological interpretations of the evolutionary processes occurring in structured populations, and the terms inclusive fitness (IF) methodology and multilevel selection methodology to describe the mathematical approaches typically used with each.

General background

Whenever an individual's reproductive success is affected by traits expressed by other individuals, we need to account for the way in which genotypes are distributed among individuals to predict evolutionary change. The IF and MS methodologies are different ways by which theoreticians account for this genetic structure.

As an example, consider a case in which all individuals in the population provide some level of help to n other individuals, and suppose that a mutant allele arises that causes its bearer to provide an increased level of help at a cost to itself. To determine if the allele will spread, we need to calculate the selection coefficient, which is the difference between the average reproductive outputs of individuals carrying the mutant versus wild-type alleles. The average reproductive outputs are difficult to calculate because of the spatial structure of the population. In fact, this difficulty arises for two reasons: (i) when calculating the average reproductive outputs for bearers of either allele, we need to know the probability that its neighbours carry the same allele; and (ii) the probability that its neighbours carry the same allele will typically depend on the action of the allele. For example, if the allele causes a higher local level of reproductive output, then its neighbours might be very likely to carry this allele as well. These complications typically preclude analytical progress unless further simplifying assumptions are made.

IF and MS methodologies

The IF methodology (Box 1 and online appendix S1) partitions the selection coefficient into a direct and an indirect selection component [14–17]. The direct selection component accounts for differences in the direct effects of the allele on its bearers' reproductive success. In our example this is negative because the mutant allele causes its bearer to provide more help than that of the wild-type, at a cost to itself. The indirect selection component accounts for differences between mutant and wild-type individuals in the

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Box 1. Inclusive fitness from allele frequency change

Consider an asexual organism with a trait, z, that is determined by a single diallelic locus (alleles A and a). Individuals are identified by their genotype x, which is 0 for a individuals and 1 for A individuals. We can write $z = \hat{z} + \delta x$, where $\hat{z}$ is the phenotype of a carriers and δ is the phenotypic difference between A and a. The dynamics of the frequency of allele A (which is the average genotype value $\bar{x}$) under mutation selection is [20,25,27,37,38]:

$$\frac{d\bar{x}}{dt} = \bar{x}(1-\bar{x})S - uM \quad (1a)$$

where S is the selection coefficient, u is the mutation rate and M is a mutation term that depends in general on the correlation between mutation and reproduction. Social evolution theory usually assumes low mutation rates (gradual evolution), and much of the debate has revolved around how best to express the selection coefficient S. In general, S can be expressed either as the slope of the regression of an individual's fitness, w, against its genotype, across all individuals in the population (i.e. $S = \mathrm{cov}(w,x)/\mathrm{var}(x)$); or as the difference in expected fitness between the two alleles [17,27,37].

We now assume that each individual interacts with n other individuals (without being more explicit about population structure at this stage) and that z represents the amount of help provided to others, at a cost to self. The fitness (reproductive output) of the i th individual depends on its own phenotype z_i and on the phenotype of n other individuals, and is given by $w_i(z_i; z_{i1}, \ldots, z_{in})$. The first argument indicates the level of help provided by the focal individual, and z_{ij} indicates the level of help received from its jth interactant.

To go further, we make two assumptions: (i) the reproductive output of an individual is independent of the demographic state of the population (see Box 5 for an extension); and (ii) fitness is approximately (or exactly) linear in the phenotype and genotype of interactors, so we can write $w_i = -Cz_i + B_1 z_{i1} + \ldots + B_n z_{in}$ (assuming all individuals have the same number and types of interactions, so that the B_j values are the same for each focal individual; see [39,101] for an extension). Then, the difference in expected fitness between the two alleles can be written as:

$$S = [-C + B_1 R_1 + \cdots + B_n R_n]\delta, \quad (1b)$$

which leads to a form of Hamilton's rule when $S > 0$. The term $-C$ is referred to as the direct fitness effect of the allele, and expresses the cost to an individual of providing help. The remaining terms B_j and R_j are referred to as indirect fitness effects, and express the benefit of receiving help from others. Importantly, R_j measures the assortment between alleles for the jth interaction (Box 3). Note that the IF methodology usually considers mutations of small effects (weak selection, i.e. δ is small), in which case $-C$ and B_j are the partial derivatives of w with respect to the phenotype of the individual and its n social partners.

Equation (1b) shows that if fitness is approximately (e.g. under weak selection) or exactly linear, we need only know the first moments (R_j) of the distribution of different genetic interactions to calculate S. In Box 3, we discuss the relatedness interpretation of the R_j values.

indirect effects of the allele as a result of the phenotype of its neighbours. In our example, this will often be positive because mutant individuals will have a higher average number of mutant neighbours than wild-type individuals, and thus will receive more help.

The MS methodology (Box 2 and online appendix S1) uses a different partitioning of the selection coefficient, but one that is applicable only when there is some form of hierarchical structure to the population, such that distinct groups of individuals can be identified. The selection coefficient is then partitioned into two components representing within-group and between-group selection. The within-group selection component accounts for differences among individuals within a group in their reproductive success, averaged over all groups in the population. In our example, assuming that the $n + 1$ interacting individuals form such groups, this component of the selection coefficient would typically be negative because selfish individuals tend to do better than those who provide help within a group. The between-group selection component accounts for differences in average group productivity as a function of group composition. In our example, this would typically be positive because groups with more helpers have higher overall productivity. The mutant allele then spreads if the balance of within- and between-group selection is positive.

So which methodology is best?

Part of the current debate revolves around the relative merits of the IF and MS methodologies, but this oversimplifies the issue. First, even if both the IF and MS methodologies yield significant conceptual insight, neither provides a complete solution for the actual analytical calculation of the selection coefficient. To do so, theoreticians typically need to make further assumptions, as described below.

Second, for some types of population structure one methodology can be more applicable than the other. For instance, the MS methodology can be applied only to group-structured populations, because there is a requirement to unambiguously identify the different levels of biological organization. In populations with a more fluid spatial

Box 2. Group-structured populations and multilevel selection

A special case of interest for Equation (1b) is when all n interactants have the same relationship to the focal individual (e.g. group-structured populations), giving:

$$S = (-C + nBR)\delta. \quad (2a)$$

For such situations, the MS methodology can then also be applied because we can view the $n + 1$ interacting individuals as members of a group. Using the regression formulation for the selection coefficient, we can then decompose the covariance term to give [16,17]:

$$S = \frac{\mathrm{E}[\mathrm{cov}_g(w,x)]}{\mathrm{var}(x)} + \frac{\mathrm{cov}(\bar{w}_g, \bar{x}_g)}{\mathrm{var}(x)} \quad (2b)$$

where the first term is the covariance of individual fitness, w, with genotype within each group, g, averaged over all groups, and the second term is the covariance of mean group fitness, $\bar{w}_g$, with mean group allele frequency, $\bar{x}_g$, across all groups. Thus, the first term represents within-group selection and the second represents between-group selection.

The relationship between the IF and MS methodologies can now be better understood if we use the same two assumptions as in Box 1. The selection coefficient can then be written as a sum of four components, corresponding to the different combinations of direct or indirect and within- or between-group effects. Each methodology simply differs in how these four components are grouped, according to the following table, where y is the genotype of a randomly selected group member for the focal individual.

	Direct	Indirect	
Within-group	$-C\,\frac{\mathrm{E}[\mathrm{var}_g(x)]}{\mathrm{var}(x)}$	$nB\,\frac{\mathrm{E}[\mathrm{cov}_g(x,y)]}{\mathrm{var}(x)}$	$\Rightarrow \frac{\mathrm{E}[\mathrm{cov}_g(w,x)]}{\mathrm{var}(x)}$
Between-group	$-C\,\frac{\mathrm{var}(\bar{x}_g)}{\mathrm{var}(x)}$	$nB\,\frac{\mathrm{cov}(\bar{x}_g,\bar{y}_g)}{\mathrm{var}(x)}$	$\Rightarrow \frac{\mathrm{cov}(\bar{w}_g,\bar{x}_g)}{\mathrm{var}(x)}$
	$\Downarrow$	$\Downarrow$	
	$-C$	nBR	

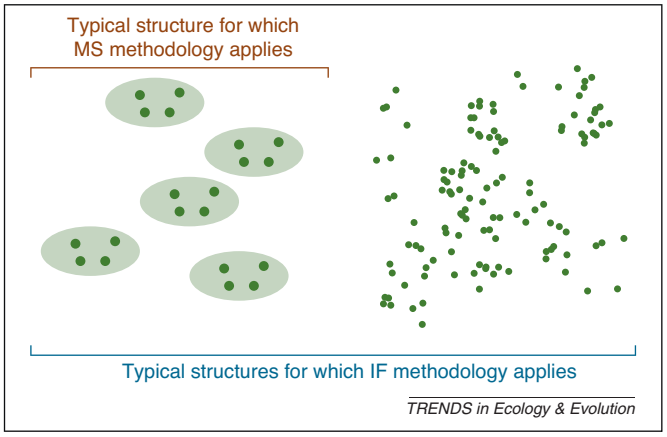

Figure 1. The MS methodology requires a clear hierarchical structure, but the IF methodology can be applied to populations with a fluid structure.

structure in which simply occasional local clustering occurs but no clearly predefined groups, an IF approach is often more manageable (Figure 1) [18]).

Third, a fair comparison of the two approaches can only be made by examining each under a common set of assumptions. For example, assuming that mutations have small effects and that the population is group-structured, it is easy to show that the selection coefficient can be partitioned into four separate components corresponding to within-group direct, within-group indirect, between-group direct and between-group indirect effects (Box 2). The two approaches simply differ in the grouping of these four terms. In other words, provided the same assumptions are used, the same result must necessarily be obtained whether calculation is carried out at the individual or at the group level.

Biological assumptions

The parallel between the MS and IF methodologies is sometimes obfuscated because many practitioners of the IF methodology in fact make two additional, interrelated simplifying assumptions as a routine part of the IF partitioning. In such cases, the IF partitioning not only yields conceptual insight, but also provides a means of making analytical progress. These assumptions are that: (i) fitness is linearly related to genotype; and (ii) selection is weak (i.e. mutations have small phenotypic effects).

If the reproductive output of an individual is a linear function of genotype, then calculating the average reproductive output for the mutant and wild-type alleles is simplified because the fitness effect of a neighbour providing more help is constant. Therefore, we need only know the expected genotypes of neighbours rather than the entire distribution of genotypes in the population (Boxes 1 and 3).

However, the selection coefficient is often still too difficult to calculate analytically because the expected value of a neighbour's genotype will depend on the action of the mutant allele [complication (ii) mentioned above]. If we further assume that selection is weak, however, then these expected genotypes can be calculated under the assumption that the mutant allele is neutral (Box 1). Note that if mutations have small effects, as typically assumed in IF methodology, fitness will be approximately linear in the genotype [19,20]. Hence, these two assumptions are distinct, but interrelated.

Box 3. Kin selection and relatedness

In Equation (1b), the population genetic structure is fully characterized by the coefficients $R_j = \rho^j_{A/A} - \rho^j_{A/a}$, where $\rho^j_{A/A}$ ($\rho^j_{A/a}$) denotes the probability that the neighbour involved in the jth interaction of an A (a) individual carries the A allele. R_j can also be expressed as $R_j = (\rho^j_{A/A} - \bar{x})/(1 - \bar{x})$ [40]. Equivalently, using the regression formulation for S, we can also write $R_j = \mathrm{cov}(x, x_j)/\mathrm{var}(x)$. Under weak selection, the R values can be calculated assuming allele A is neutral. Then these neutral measures of genetic associations can be determined, or measured, independent of the mutation process [20,25], and can be interpreted as the genealogical relatedness between individuals [23,24,26,27]. For mutations of large effect, selection will affect the genetic associations R, and characterizing genetic structure is less straightforward.

A common source of confusion is that different interpretations of kin selection exist. If interacting individuals share a more recent common ancestor than a randomly chosen individual, then interacting individuals are truly kin in the genealogical sense. This is the strict interpretation of kin selection. Such situations arise, for instance, through limited dispersal or through kin recognition. Thus, all instances of evolution in structured populations with limited dispersal can be interpreted as resulting from a kin selection process, although this does not mean that shared genetic ancestry is the sole process at work.

A broader interpretation of KS, which originates with Hamilton's seminal papers [14,41], includes other causes of genetic similarity and defines relatedness more broadly as a measure of genetic association between partners, and not only as a measure of genealogical relationship (Gardner et al. [31], describe a recent treatment). This is conceptually helpful because it enables evolutionary biologists to take a bird's-eye view of the field. A downside is that in its broad interpretation, relatedness becomes an abstract concept that might be disconnected from empirically assessable measures of population structure, except in rather restrictive ecological scenarios. This leaves empiricists with a puzzle: although genealogical relationships are often the most readily accessible data, they are not necessarily relevant measures of relatedness for their biological system under the broad interpretation of Hamilton's rule. Hence, when trying to generate novel, testable theoretical predictions, we argue that it might be preferable to use methodologies that explicitly derive selective pressures from demographic and ecological processes (as in closed models; Box 4) and to express them in terms of empirical measures of population structure. Where biologically applicable, the weak selection approximation is one way to achieve this goal.

Before moving to the conceptual and empirical advantage of the weak selection assumption, we need to tackle a final technical point. Because much of IF theory typically assume mutations of small phenotypic effects, it has sometimes been argued that IF cannot deal with strong selection while the MS methodology can. However, partitioning of the selection coefficient between within-group and between-group components does not make its analytical calculation any simpler under strong selection. In other words, the MS methodology does not provide a superior characterization of genetic structure under strong selection, and in fact most MS models also typically resort to a weak selection approximation or assume linear fitness to make analytical progress [21]. Hence, the relevant question is not what approach is inherently better, but how to derive analytical approximations to characterize genetic structure under strong selection in an empirically meaningful way.

Is one interpretation better than the other?

The IF and MS methodologies naturally lend themselves to different biological interpretations. Hierarchical structure

Box 4. Open versus closed models

In applying the IF or MS methodology, the usual starting point is to define a fitness function. This facilitates partition of the selection coefficient into components involving quantities such as relatedness that are readily interpreted as measures of population structure. However, this methodology does not provide information on how the population structure depends on the details of survival, reproduction and other ecological interactions, including dispersal. Such models are sometimes referred to as open models because they leave open the connection between the population dynamical processes and the structuring of the population that results [42].

Although open models have conceptual utility, they can also lead to misconceptions about the evolutionary process. For example, open models have been used to reveal that, all else being equal, greater altruism is expected to evolve when interactors are more closely related [17]. This might lead to the conclusion that limited dispersal ought to favour the evolution of altruism because individuals will then tend to interact with close relatives. Numerous results have now revealed, however, that this is not the case, essentially because all else is not equal [1,4,43–45]. For a wide range of demographic assumptions, limited dispersal not only increases the relatedness of interacting individuals, but also affects their fitness through changes in the scale of competition for resources [1,3,4]. Precise insights into how ecological factors affect evolution in structured populations can be obtained with closed models [42], which specify in detail the life cycle and population structure.

is a central component of the MS methodology, and therefore recognising that selection acts at different levels naturally leads to what we call an MS interpretation (i.e. MS refers to 'new' group selection; we do not consider 'old' group selection theory, in which selection occurs at the level of groups only and leads to group-level adaptation [6,22]).

Likewise, neutral measures of genetic associations are central components of the IF methodology, and this naturally leads to a KS interpretation. Indeed, for neutral alleles, the expected value of a neighbour's genotype corresponds exactly to the genealogical definition of relatedness and can be calculated for any type of population structure using standard population genetics techniques (Box 3) [20,23–27]. Therefore, under weak selection, the genealogical relatedness among individuals provides a sufficient description of the population's genetic structure to make evolutionary predictions. This has a clear empirical advantage, because it allows for measurement of genetic structure in populations by means of neutral alleles [28], which has provided a very powerful tool for relating theoretical results to population data. Relatedness measures are routinely used to infer structure in populations and thus population data can be linked to theoretical predictions on gene flow [29].

Even when applied to the same biological problem, the KS and MS interpretations are not necessarily equally useful when it comes to relating theory to empirical studies. The strong empirical record of the KS interpretation is due, in part, to the fact that individuals are often easier to identify and follow than groups. Many populations in nature do not exhibit a clearly defined group structure, and therefore it is somewhat more difficult to connect such populations to an MS interpretation. This might explain why the KS interpretation (and the concepts of relatedness and kin competition) has been highly successful in providing empiricists with testable predictions in organisms as diverse as bacteria, social insects and vertebrates for various topics such as cooperative breeding, dispersal and sex allocation [1,6,11,30]. As we emphasize in Section 2, this does not necessarily mean that empiricists do not need further theoretical progress, nor does it mean that the MS interpretation is not conceptually useful (e.g. when studying evolutionary transitions).

Finally, we have shown under which conditions genetic structure can be characterized by measures of genealogical relatedness, and therefore emphasized a 'strict' interpretation of kin selection, but there exist broader interpretations (Box 3; [31]). Furthermore, in the light of a recent article [9] that gives a misleading representation of current IF theory, we stress that extensions of the theory we have presented exist for fluctuating demography [32–34], nonlinear genotype-phenotype maps [35] and non-pairwise interactions [36]. Although we have focused up to now on the type of simplified models that form the basis of most discussions of KS and MS ([9] being a clear example), we show in the next section that current theory can be used as a conceptual and methodological springboard to discuss open biological problems.

Moving beyond

The main message of the previous section is that both the IF and MS methodologies seek to characterize the genetic structure of a population, but they do so differently. We now step back from this debate and focus attention more broadly on open questions in the study of evolution in structured populations. We show that many simplifying ecological or genetic assumptions routinely used in current theory are invalidated to some extent by empirical observations, and identify six key questions for which further work is desirable.

Demography and population dynamics

Genetic versus demographic structuring In the previous section, we considered only genetic structure (i.e. the spatial distribution of genotypes; Figure 2a). This is all we need under the assumption that (local) populations have constant size, which is a classical starting point for population genetics. However, if we relax this assumption and let population size be regulated by population dynamics or fluctuate according to demographic processes, the measure of selection in structured populations needs to account for the interplay between population dynamics (demographic structuring, Figure 2b) and selection. Hence, we need to consider both genetic structuring and demographic structuring (i.e. the spatial distribution of individuals in the population, regardless of genotype; Figure 2c).

A worked example: evolution of helping revisited As an illustration, consider an extension of the earlier model for helping behaviour. We now assume that individuals live on a network of sites, some of which might be empty, and that helpers provide a survival benefit B to their neighbours at a survival cost C to themselves.

As previously, genetic structuring makes the mathematical analysis difficult without further assumptions. The task is even more arduous now, however, because

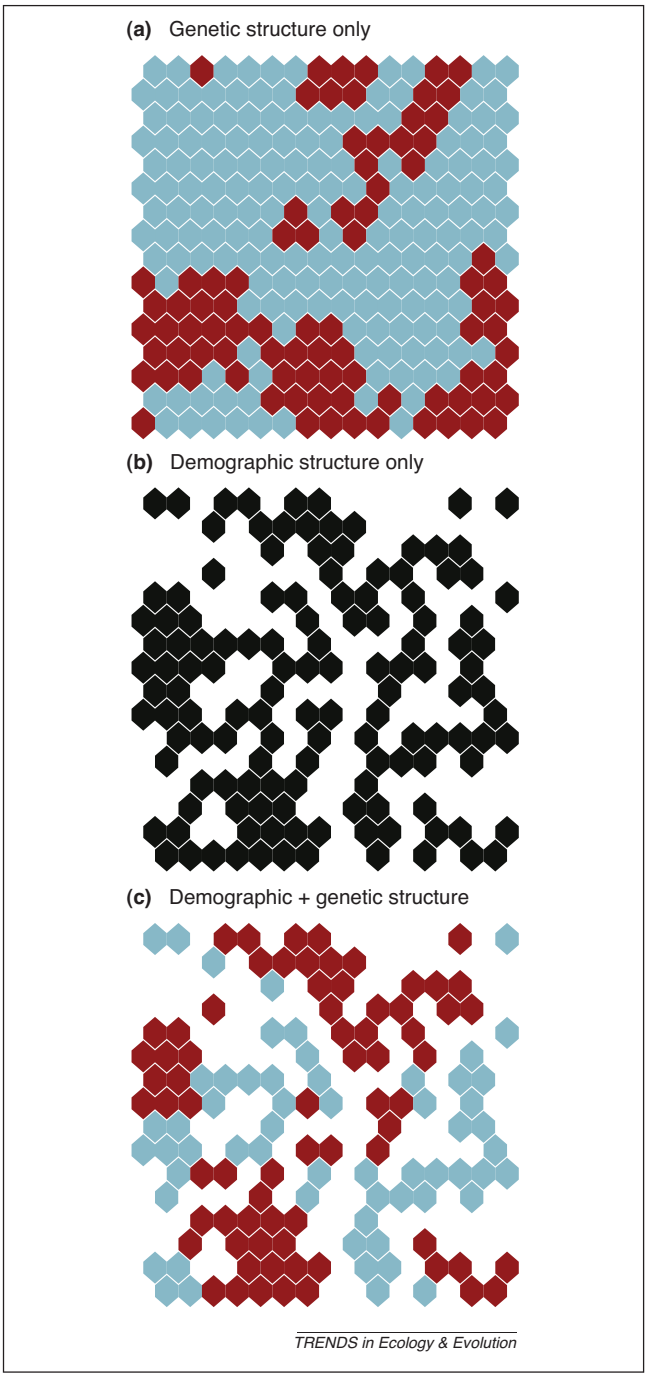

Figure 2. Evolution in structured populations depends on two main forms of structuring. **(a)** Genetic structure refers to the (spatial) distribution of alleles and **(b)** demographic structure refers to the (spatial) distribution of individuals. The genetic structure is visualised by showing a schematic distribution of neutral alleles (here blue and red) in haploid individuals. The alleles are non-randomly distributed because of the viscosity of the population. Therefore, the probability of encountering two neighbours of the same colour is greater than the probability of picking two random individuals of the same colour, a notion captured in the parameter R (Box 1). Demographic structure follows from the occupation and release of space through birth, death and migration, and results in a spatial pattern. In a viscous population the pattern is distinct from random (in the sense that the probability of encountering two neighbouring sites that are both occupied or empty is different from picking two random sites that are both in the same state, a notion that is captured by the measure of habitat saturation $q_{\times/\times}$; Box 5). Population genetics models typically neglect demographic structure, and ecology focuses on the spatial dynamics of populations. In general, population dynamics will lead to **(c)** both demographic and genetic structure simultaneously and evolution will depend on the interplay between the two processes.

not only might mutants experience a difference from the wild-type individuals in terms of the genotypes of their neighbours, but, because some sites are empty, they might also experience different local population densities (i.e. different levels of habitat saturation).

Assuming that social interactions linearly affect the vital rates of individuals, we can calculate the selection coefficient under weak selection and easily obtain a partition into direct and indirect fitness components (Box 5). Now, however, because some neighbouring sites can be empty, the indirect fitness components are weighted not only by relatedness, but also by measures of habitat saturation. This demonstrates an important interaction between genetic structuring and demographic structuring (Box 1 *vs* Box 5 Figure 2c).

The selection coefficient has additional terms arising from the demographic structuring compared with the classical IF expressions (Boxes 1 and 5) see also [5,32]). These terms represent the double-edged effect of empty space: a detrimental effect, because an individual surrounded by empty sites loses the baseline level of help provided by neighbours, irrespective of their genotype; and a beneficial effect, because empty sites decrease competition for breeding spots under density-dependent reproduction (Box 5).

Why does it matter? The analysis in Box 5 leads to a form of Hamilton's rule that depends on measures of genetic structuring (relatedness) and of demographic structuring (habitat saturation). However, this familiarity obfuscates important practical implications. First, relatedness itself depends on habitat saturation because of the feedback between the distribution of individuals and that of genotypes. This is best illustrated by considering a population on the verge of extinction. In this case, clusters of individuals will tend to be further apart, so that genotypes will tend to be segregated. By contrast, in abundant populations, individuals might be more likely to encounter unrelated individuals.

Second, the model results in Box 5 rely on a relatively simple ecological scenario for the organism's life cycle, but assumptions about the life history, density dependence and population dynamics are likely to be critical. For example, in some species of cooperatively breeding birds, it has been found that helping increases adult survival rather than adult fecundity [46], which leads to opposite evolutionary predictions [33,44,45], because competition between relatives can take different forms depending on life cycle assumptions [1,4]. Current theory only provides us with a rough understanding of how population structure affects the evolution of social and life-history traits [5]. Cooperative breeding in birds, for instance, has been explained by an array of demographic and ecological factors, including habitat saturation [47,48]. However, the results derived from across-species comparative analyses are often conflicting and inconclusive. Hatchwell [48] suggested that this might be due to a narrow focus on population viscosity (limited dispersal) to the detriment of other life history and ecological processes. To a large extent, this probably reflects the lack of a theoretical foundation that captures the interplay among life-history traits, habitat saturation, dispersal and social behaviours. This is

Box 5. Demographic and genetic structuring

Consider an extension of the model of Box 1, in which individuals live on a network of sites. Each site of the network can be either empty or occupied by one individual, and is connected to n other such sites. We further assume that the benefit B and cost C of helping linearly affects survival. Fecundity is not affected by social interactions, but is density-dependent: individuals produce offspring at a rate proportional to the number of empty neighbouring sites. This is only one possible form of density dependence, but it is sufficient to illustrate some important points. Using the same notation as in Box 1, the selection coefficient is then:

$$S = [-C + Bn(q_{A/A} - q_{A/a})]\delta - B\hat{z}n(q_{o/A} - q_{o/a}) + b(q_{o/A} - q_{o/a}), \quad (5a)$$

where b is the fecundity rate and $q_{o/i}$ ($q_{A/i}$) is the average local density of empty sites (A individuals) experienced by an individual carrying allele i.

The quantity $q_{A/A} - q_{A/a}$ measures the extent to which A allele carriers are more abundant in the neighbourhood of other A allele carriers than of a allele carriers, and has a long history ('difference in subjective frequencies' [53] or 'assortment' [54]). When selection is weak, we only need to calculate this measure under neutrality, which gives [34,55]:

$$q_{A/A} - q_{A/a} = q_{\times/\times}R, \quad (5b)$$

where $R = (\rho_{A/A} - \bar{x})/(1 - \bar{x})$. Equation (5b) separates two effects: a demographic effect ($q_{\times/\times}$ is the local density of occupied sites experienced by an individual of any genotype and is therefore a measure of habitat saturation) and a genetic effect, because R is the measure of genealogical relatedness defined in Box 3. Hence, under weak selection, the selection gradient reduces to:

$$S = [(-C + nq_{\times/\times}BR) + (b - nB\hat{z})\Delta q_o]\delta, \quad (5c)$$

where Δq_o is the first-order effect of selection on $q_{o/A} - q_{o/a}$. This separates the selection coefficient into conceptually distinct components representing genetic structuring (R), demographic structuring ($q_{\times/\times}$) and a demographic effect (Δq_o) that will generally depend on the interplay between genetic and demographic structuring (in particular on measures of genetic structure such as relatedness [5,32,34,45]).

As discussed in the main text, the first term of Equation (5c) has a similar form to that of Equation (2a), but the second term of Equation (5c) represents two additional selective effects due to the effect of mutation on demographic structuring. The first selective effect, $b\Delta q_o$, is due to the density dependence of reproduction and measures the difference in availability of empty sites between A and a alleles (in other words, the differential competition between the two alleles for empty space). The second selective effect, $-B\hat{z}\Delta q_o$, accounts for the net loss in helping opportunities for individuals surrounded by many empty sites, and measures the differences between the two alleles in this demographic effect. Together, these two effects can be interpreted as the net cost of competition for open breeding sites, and therefore quantify kin competition.

problematic when empirically testing theory: certain measures of population structure (e.g. genealogical relatedness) might be sufficient for some populations yet irrelevant for others. Ideally it might be possible to categorize different types of populations in terms of the relevant quantities to measure, but we are still a long way from this.

From a more applied perspective, conservation biology would also benefit from integrating social evolution theory and population dynamics. The fact that social behaviour can be critical in shaping extinction risk, for instance through Allee effects in small populations of social species [49], is well established [50,51]. More fundamentally, selection can increase the risk of evolutionary suicide [52]. In an endangered social species of magpie robins, for example, it has been shown that conflict over reproductive status delays population recovery [51].

Mutation and strong selection

Selection in structured populations will depend on the interplay between genetic and demographic structuring and this will in turn be affected by the frequency and nature of mutations. When mutations are rare and have a small phenotypic effect (weak selection), genetic and demographic structuring tend to be decoupled. Then demographic structuring can be computed from the ecological dynamics and genetic structuring can be computed using standard techniques based on two-allele population genetic models (Box 5) [34]. Moreover, in this case the relevant measure of genetic structuring coincides with the strict genealogical interpretation of relatedness. However, when selection is stronger, demographic and genetic structuring will tend to be more tightly coupled, meaning that genealogical measures of relatedness are no longer sufficient descriptors of population structure.

As an example, the evolution of host–parasite interactions is affected by the distribution of susceptible and infected hosts, and by the distribution of parasitic strains. Recent theory has demonstrated that the evolution of reduced parasite virulence in structured populations can be understood as a form of altruism among genetically related parasites, and thereby falls under the scope of social evolution theory [13,56,57]. However, these results typically rely on the assumption that mutation rates are low and that selection is weak. Many parasites (such as RNA viruses) are characterized by high mutation rates and therefore display high levels of genetic polymorphism [58–60]. There is also strong evidence that human activities lead to rapid changes in the dynamics and evolution of pathogen populations through habitat fragmentation, climate change and environmental pollution [61]. Furthermore, pathogens can cause rapid and important shifts in the genetic structure of host populations, as illustrated by long-term field studies of the interaction between wild flax and flax rust in Australia [62]. For such systems the assumptions of weak selection and rare mutations are clearly inappropriate, and theoretical predictions that explicitly consider high mutation rates and large phenotypic effects are required. Non-linear effects in the genotype–phenotype map (resulting e.g. from dominance [35,63] or escape from immunity in pathogens [64]) can complicate matters even further.

More fundamentally, this affects the way we envisage the feedback between ecology and evolution. Broadly speaking, most of the models in social evolution theory rely implicitly on the assumption that mutation rates are low. Thus, evolution is mutation-limited and occurs on a slower time scale than ecological dynamics (i.e. ecological and evolutionary time scales do not overlap). It is now well appreciated that for many organisms, evolution can occur more rapidly than previously envisioned [61,65,66]. Hence, theoretical models need to be extended to account for the transient dynamical structuring that can occur in such populations, and its effect on evolutionary predictions. Likewise, empiricists must be critical of how well model

assumptions about the relative time scales of ecological and evolutionary processes match their study systems.

Interspecies interactions

Most real populations are not isolated but embedded in a network of trophic interactions (interspecies competition, consumer–resource dynamics, predator–prey and host–parasite interactions). Ecologists are well aware that this can lead to complex dynamics, but we still have an incomplete understanding of how this will affect evolutionary processes, and in particular the coupling between demographic and genetic structuring. Although some models have looked at the effect of interspecies competition on the evolution of social traits (e.g. communal foraging [21]), current theory tends to focus on populations in isolation. The recent interest in the evolution of parasite life history traits in structured populations we mentioned above provides a clear exception. However, despite its clear practical implications for the management of human, plant and animal infectious diseases [67–69] and for conservation biology [61,70], current theory tends to neglect the fact that interacting populations are often characterised by non-equilibrium population dynamics, either because of some inherent non-linearities or because of environmental fluctuations (e.g. seasonal forcing of epidemics). For instance, as a result of global changes, many species shift their biogeographic ranges, and it has been shown that such dynamical processes have important evolutionary consequences [71,72]. Understanding the evolutionary role of non-equilibrium population dynamics is therefore a crucial avenue of research [38,73]. How to define and – importantly – measure fitness in structured non-equilibrium trophic interactions remains an open question.

Evolutionary diversification

Theoreticians (and discussions about KS and MS) often focus on the direction of selection (i.e. the selection coefficient S), but the dynamics of population variance and the emergence of diversity are also questions of great interest. Both the IF and MS partitions of S can be used to predict the direction in which a trait will evolve [25,27,40,74–76], but it is more difficult to determine whether this will result in an evolutionarily stable strategy or in evolutionary diversification [40,77–79]. In particular, some models suggest that population structure could limit the opportunity for sympatric speciation [3,80,81]. Although extensions of the IF methodology to explore these phenomena exist [27,40,80,81] (to the best of our knowledge, no such attempt has been made using MS methodology), an explanation of empirical patterns of diversity in structured populations requires additional analyses [27,40,80–83]. Apart from the fundamental interest, this is important in agriculture and conservation biology. For instance, host genetic diversity can buffer populations against epidemics and affect the evolution of virulence and anti-drug resistance in pathogens [61].

Small population sizes

Many models consider populations that are far from extinction, because they assume either that all local populations have constant population sizes [27] or that the population is large enough (as in Section 2.1, for instance). For small populations, however, the consequences of demographic or environmental stochasticity are likely to play an important role through genetic drift or population extinction. Fragmented populations on the verge of extinction generally display high levels of inbreeding as a result of local drift, which decreases the amount of genetic variability available to respond to selection [61]. In such a context, relatedness effectively quantifies the amount of local drift [84], but how population structure, dispersal and drift interact to shape the selective pressures on a population under threat is still poorly understood. Again, this has important applications not only in conservation biology (evolutionary rescue; [85]), but also in evolutionary epidemiology for predicting the evolutionary extinction of parasite populations.

Spatial heterogeneity

Most populations are heterogeneous in resource availability or habitat quality. Variation can be generated by the physical environment (temperature, altitude), biotic interactions (competitors, parasites, predators, alternative hosts), human interventions (e.g. limited vaccination coverage) or asymmetric dispersal rates between interacting species [86,87]. This can give rise to a mosaic of selective pressures that can create patterns of local adaptation and maladaptation [88–95]. In a review of 29 field studies, Laine [95] demonstrated that coevolutionary trajectories can greatly vary across space, at scales ranging from intercontinental distance to a few kilometres. In some cases, coevolutionary trajectories can be reversed, as in the interaction between the pollinating parasitic moth *Greya politella* and its host plant *Lithophragma parviflorum*, which can be either antagonistic or mutualistic depending on ecological conditions [96]. An explanation of these empirical patterns requires a theoretical framework for structured populations that ties together population dynamics, mutation, trophic interactions, stochasticity and spatial heterogeneity. Although theoreticians have started to independently address these limitations of current theory [25,32,39,57,97–101], we are still a long way from a synthetic framework for the co-evolution of traits in realistic, heterogeneously structured populations.

Conclusion

Although the kin versus multilevel selection debate has been useful in clarifying some important aspects of social evolution, we suggest that it is now time to step back from the details of specific arguments and to consider the question of evolution in structured populations more generally. Ecological processes mould the genetic and demographic structure of populations, and this structure in turn shapes the selective pressures on all traits. We believe that this ecological perspective is helpful because it reveals that most of the debate between kin and multilevel selection is implicitly cast in very simplified ecological scenarios. From an empirical point of view, however, a debate between theoreticians over how best to interpret these simplified models is of little interest when trying to detect and understand patterns of evolutionary change in the laboratory or in the field. Moreover, although the debate generally revolves

around traditional social traits such as cooperation and altruism, the broader perspective advocated here shows that this has relevance to other fields, including more applied fields such as evolutionary epidemiology and conservation biology. The study of evolution in structured populations has the potential to generate insights beyond areas in which it has been traditionally applied, provided theoreticians and empiricists are willing to adopt a more ecological perspective on the field.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.tree.2011.01.006.

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