PHYSICAL REVIEW LETTERS

Fixation and Consensus Times on a Network: A Unified Approach

G. J. Baxter,[1,*] R. A. Blythe,[2] and A. J. McKane[3]

[1]*School of Mathematics, Statistics and Computer Science, Victoria University of Wellington, P.O. Box 600, Wellington, New Zealand*
[2]*SUPA, School of Physics and Astronomy, University of Edinburgh, Mayfield Road, Edinburgh EH9 3JZ, United Kingdom*
[3]*Theory Group, School of Physics and Astronomy, University of Manchester, Manchester M13 9PL, United Kingdom*

We investigate a set of stochastic models of biodiversity, population genetics, language evolution, and opinion dynamics on a network within a common framework. Each node has a state $0 < x_i < 1$ with interactions specified by strengths m_{ij}. For any set of m_{ij}, we derive an approximate expression for the mean time to reach fixation or consensus (all $x_i = 0$ or 1). Remarkably, in a case relevant to language change, this time is independent of the network structure.

Mathematical models predicting biological and social change are becoming increasingly commonplace, with the past few years having seen an explosion of activity among statistical physicists in cultural dynamics [1]. One aspect of this work which is not widely appreciated is that several seemingly distinct phenomena can be described by very similar models: In some cases, they can even be exactly mapped into each other [2]. Examples include biodiversity [3], population genetics [4], opinion dynamics [1], and language change [5]. The common thread is that objects that come in different variants are copied from one place (an "island") to another according to some stochastic rule. If no new variants are created in the process (e.g., by mutation) and the number of objects does not grow without bound, one variant is eventually guaranteed to take over an entire population, or go to fixation in the genetics parlance. Changes in the network structure connecting different islands, and the stochastic rules used to choose the source and target islands, lead to a variety of scaling laws relating the number of islands and time to reach fixation (see, e.g., [6–8]). In this Letter, we present a theoretical treatment of a very general stochastic-copying model that includes many previously studied cases and unifies the diverse fixation time results obtained so far. We also discuss a mapping to a particle-reaction system from which it can be shown that our prediction for the fixation time, obtained by making various approximations, can in many cases be stated as a bound that simulations show is often saturated. We also discuss a key application of our findings—to a current theory of new-dialect formation [9].

To establish the basic features of the large class of models that we consider, we describe a prominent special case, Hubbell's model of biodiversity and biogeography [3]. Here there are only two islands: a metacommunity or mainland (island 1) and a local community (island 2). The objects are individuals which compete for a common resource (e.g., trees competing for space, sunlight, and nutrients [10]), and the variants are different species. At regular time intervals, an individual in island 2 is picked at random to die and to be replaced by a copy of either (a) another individual picked at random from island 2 or (b) a *migrant* from island 1. Process (b) is assumed to happen less frequently than (a), and, as mentioned above, if (b) is absent, then the final state of the system is one which contains individuals of only one species. The number of individuals on island 2 is a constant n, and new species are created on island 1, but not island 2, by mutationlike events. This model is a *neutral* theory; no one species is assumed to be "fitter" than another.

The relationship between this model and simple neutral models of population genetics is well known [3]: Individuals are analogous to genes, and species are types of genes (alleles). A more general model comprises a set of islands labeled $i = 1, \ldots, N$, each of which contains n genes (in reality, n individuals each containing one copy of the gene of interest). For simplicity, we assume that there is no mutation, so that no new alleles may be created. The alleles are labeled by $\alpha = 1, \ldots, M$. The dynamical processes, illustrated in Fig. 1, are as before: a death on island i followed by (a) a birth on island i or (b) a migrant offspring from island j arriving on island i. There are various ways to parametrize these dynamics. As in Ref. [2], we let the parent (copied object) be taken from island j with probability f_j. In process (b), the probability that the offspring (copy) lands on island i is taken to be proportional to m_{ij}, which specifies a *migration rate* within
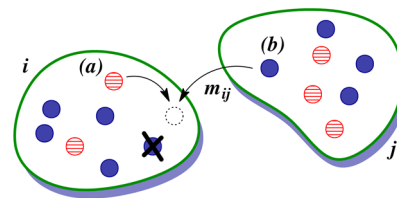

FIG. 1 (color online). Stochastic-copying dynamics between two islands i and j forming part of a larger network. After a death on i, an object is replaced either with a copy from (a) the same island i or (b) a different island j (rate m_{ij}).

a standard continuous-time limit described in Ref. [2] but whose details are unimportant here. At any time t, the state of the system can be given in terms of the fraction $x_{i\alpha}(t)$ of genes on island i that are allele α. Then the islands can be represented as nodes on a network, which in the opinion dynamics and language change models are individuals i with opinions or language variants α expressed with frequency $x_{i\alpha}$. In these social contexts, fixation is sometimes called consensus.

Using the formalism first developed for these systems in population genetics [4], we describe the evolution in terms of a Fokker-Planck equation. Suppose, first of all, that there is only one island and no mutation. Then the only dynamical process is *random genetic drift* in which the frequencies $x_\alpha(t)$ diffuse on the interval $[0, 1]$ due to the random sampling in the death-birth process. For simplicity, we will assume that there are only two alleles which have frequencies x and $(1 - x)$, so the state of the system is described by the single stochastic variable $x \in [0, 1]$. The probability that the system is in the state x at time t $[P(x, t)]$ satisfies the Fokker-Planck equation $\partial_t P(x, t) = \partial_x^2[D(x)P(x, t)]$ where the diffusion constant is state-dependent: $D(x) = x(1 - x)/2$ [4]. Moving to the case of N islands, with migration rate m_{ij} from j to i, the Fokker-Planck equation for $P(x_i, t)$ now reads [2]

$$\frac{\partial P}{\partial t} = \sum_{\langle ij \rangle}\left(m_{ij}\frac{\partial}{\partial x_i} - m_{ji}\frac{\partial}{\partial x_j}\right)[(x_i - x_j)P]$$
$$+ \frac{1}{2}\sum_{i=1}^{N} f_i \frac{\partial^2}{\partial x_i^2}[x_i(1 - x_i)P], \quad (1)$$

where $\langle ij \rangle$ means sum over distinct pairs i and j. This may be generalized to $M > 2$ and to include mutation [2], but Eq. (1) will be sufficient for our purposes.

Analysis of Eq. (1) is, on the face of it, a hopeless task since it has many degrees of freedom x_i interacting with arbitrary strengths m_{ij}. However, much of the macroscopic dynamics is captured by the first and second moments of $x_i(t)$. The mean $\alpha_i(t) = \langle x_i(t) \rangle$ can be found from Eq. (1) to evolve according to

$$\frac{d\alpha_i}{dt} = \sum_{j \neq i} m_{ij}(\alpha_j - \alpha_i) \equiv \sum_{j=1}^{N} m_{ij}\alpha_j, \quad (2)$$

where the equivalence holds if the diagonal elements m_{ii} are defined to be $-\sum_{j \neq i} m_{ij}$. This matrix has a zero eigenvalue, which we will assume is nondegenerate. The associated right eigenvector has all elements equal to one, and the left eigenvector we denote Q_i, so that $\sum_i Q_i m_{ij} = 0$, and normalized such that $\sum_i Q_i = 1$. Then we find from Eq. (2) that the ensemble (noise-history) average of the collective variable

$$\xi(t) = \sum_{i=1}^{N} Q_i x_i(t) \quad (3)$$

is conserved by the dynamics. Decomposing $\alpha_i(t)$ in terms

of its right eigenvectors, we see that it approaches a constant independent of i as $t \to \infty$. Since all $x_i(t)$ tend to 0 or 1 as $t \to \infty$, this is the probability of the allele fixing. From (3) we see that $\langle \xi(t) \rangle$ also approaches this value in this limit and, since ξ is conserved, the fixation probability is $\xi(0)$ [6,11].

Numerical studies suggest that convergence of the ensemble average $\alpha_i(t)$ to its asymptote $\xi(0)$ occurs on a much shorter time scale than the ultimate fixation of a variant, which in turn governs the rate of change of the second moments $\beta_{ij}(t) = \langle x_i(t)x_j(t) \rangle$; see Fig. 2. Equation (1) implies for the latter

$$\frac{d\beta_{ij}}{dt} = \sum_k m_{ik}\beta_{kj} + \sum_\ell m_{j\ell}\beta_{i\ell} + \delta_{ij}f_i(\alpha_i - \beta_{ii}), \quad (4)$$

while the mean time to fixation T is given by the solution of a backward version of the Fokker-Planck equation (1) [12]

$$-1 = -\sum_{\langle ij \rangle}(x_i - x_j)\left(m_{ij}\frac{\partial T}{\partial x_i} - m_{ji}\frac{\partial T}{\partial x_j}\right)$$
$$+ \frac{1}{2}\sum_{i=1}^{N} f_i[x_i(1 - x_i)]\frac{\partial^2 T}{\partial x_i^2}. \quad (5)$$

The assumption that the time over which all of the α_i converge (T_0) is much less than T (see Fig. 2) leads to the following approximate treatment of this equation. We assume that T depends *only* on the state of the system at time T_0 and principally through $\xi(0)$. Changing to the $\xi(0)$ variable using Eq. (3), we find that the first term on the right-hand side of Eq. (5) vanishes [6] giving

$$-2 = \sum_{i=1}^{N} f_i Q_i^2 x_i(T_0)[1 - x_i(T_0)]\frac{d^2 T}{d\xi(0)^2}. \quad (6)$$

This equation still depends on the variables x_i at time T_0. We can estimate these by assuming that correlations between the nodes are absent, i.e., $\beta_{ij} = \alpha_i\alpha_j = \xi(0)^2 i \neq j$, and that the rate of change of the variance of x_i is sufficiently slow that the time derivative in Eq. (4) when $i = j$ can be neglected (see again Fig. 2). Then β_{ii} at time T_0 can be estimated from Eq. (4).
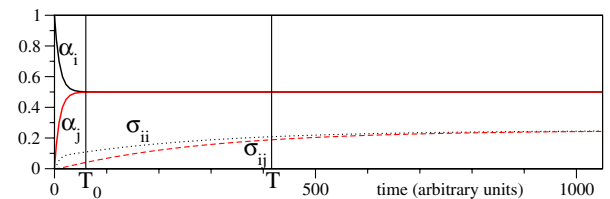

FIG. 2 (color online). Numerical solution for means α_i and α_j and (co)variances $\sigma_{ij} \equiv \beta_{ij} - \alpha_i\alpha_j$ on a fully connected network of $N = 20$ sites. Note the α's converge at a time T_0 much less than the mean fixation time T and at time T_0, $\sigma_{ij} \approx 0$ for $i \neq j$. These features become more pronounced as N is increased.

By replacing $x_i(1 - x_i)$ in Eq. (6) by $\alpha_i - \beta_{ii}$ at time T_0, we find $\{\xi(0)[1 - \xi(0)]\}d^2T/d\xi(0)^2 = -2/r$, where

$$r \approx \sum_i Q_i^2 f_i \frac{2\sum_{j\neq i} m_{ij}}{2\sum_{j\neq i} m_{ij} + f_i}. \qquad (7)$$

The mean fixation time is obtained by integrating the equation for $T[\xi(0)]$ with the boundary conditions $T(0) = T(1) = 0$ to give

$$T[\xi(0)] = -\frac{2}{r}\{\xi(0)\ln\xi(0) + [1 - \xi(0)]\ln[1 - \xi(0)]\}, \qquad (8)$$

which in tandem with (7) is our main result, derived for a large class of stochastic-copying processes on any network and arbitrary migration rates. It should be emphasized that the reduction from a system with $(M - 1)$ degrees of freedom to a system with only one degree of freedom is not imposed but instead emerges from the dynamics.

For orientation and as a check of these results, we verify that specific choices of the parameters f_i and m_{ij} give expressions which have been previously obtained. As a first check, we examine the case of voter dynamics on heterogeneous graphs described in [6,7]. The voter model proper has each node chosen uniformly to be the recipient of a new opinion; hence, all $f_i = 1/N$. This opinion is selected randomly from the node's neighbors, giving $m_{ij} = A_{ij}/(2Nk_i)$, where $A_{ij} = 1$ if nodes i, j are connected, k_i is the degree of node i, $k_i = \sum_{j\neq i} A_{ij}$, and the factor of $2N$ is a consequence of the continuous-time limit described in [2]. To calculate r, one needs Q_i, the normalized zero left eigenvector of the matrix m_{ij}. One finds that this eigenvector equals $Q_i = k_i/(N\bar{k})$, where $\bar{k}$ is the mean degree and is included to normalize the Q_i. Putting all of this together, we find from (7) that $r = \overline{k^2}/2(N\bar{k})^2$. This corresponds with the results of Refs. [6,7] after taking into account the different choice of time units made in those works.

An invasion process, where the source node of an opinion is randomly selected in each time step, was also considered in [7]. This corresponds to the choice $m_{ij} = A_{ij}/(2Nk_j)$, from which Q_i may again be found. However, the resulting expression for r via (7) does not simplify unless one additionally assumes (as in [6,7]) that node degrees are uncorrelated: $\overline{A_{ij}} = k_i k_j/(N\bar{k})$. Taking $f_i = 1/N$ as before, one finds from (7) the result of Ref. [7] in the limit $N \to \infty$. Our treatment, however, also extends to networks with strong degree correlations, e.g., a star network that has a central node connected to all $N - 1$ outer nodes, which in turn are connected only to the central node. For this network, (7) predicts a fixation time proportional to N^3, confirmed by simulation data (not shown). By contrast, the approximation of Ref. [7] predicts a fixation time that increases quadratically with N, in our time units.

We also recover known results for link dynamics [7,13], where an opinion is copied in a randomly chosen direction

along a randomly chosen link in each time step. Here we have $f_i = k_i/N$ and $m_{ij} = A_{ij}/(2N)$, which implies that $Q_i = 1/N$. In this special case it has been noted that the mean time to fixation does not depend on the network structure [7,13]. Furthermore, our general result (7) includes the various scaling forms found in [8].

The generality of our results can be tested more stringently by choosing f_i and m_{ij} from various random distributions in such a way that the numerators and denominators in (7) are of similar magnitudes. Simulation results (not shown) on Erdös-Rényi random graphs of varying densities [14] are consistent with Eqs. (7) and (8), except when T and T_0 turn out to be of a similar order in N.

A concrete application of the model is to an evolutionary model of language change [5]. In fact, it was our experience in applying this model to the emergence of New Zealand English [15] that alerted us to the possibility of a general analysis and to some surprising behavior for a subclass of models. As indicated earlier, in this particular application the index i labels speakers who converse and so affect each other's grammar. The probability that two speakers interact is given by a matrix G_{ij}; this is a reflection of the topology of the network. Another factor H_{ij} accounts for the weight that i gives to the utterances of j. It is the product of the G_{ij} and H_{ij} that is equal to m_{ij}. While G_{ij} is by definition symmetric, H_{ij} need not be. In the application to the formation of New Zealand English, Trudgill [9] has postulated that the large quantity of data that exist on the emergence on this English variant [16] may be explained by assuming that social factors which are modeled by H_{ij} are unimportant, and therefore this factor may be replaced by a constant. If this is so, the m_{ij} is symmetric; if the model is not socially neutral, then m_{ij} will not, in general, be symmetric.

To test Trudgill's theory, we assume m_{ij} is symmetric and using the results (7) and (8) check if the mean time to fixation is in accord with the data. *A priori* one would expect that the precise nature of the speaker network during the formation of New Zealand English would be required. However, remarkably, it turns out that in this case the time to fixation is completely independent of the network structure. This is because the symmetry of m_{ij} im-
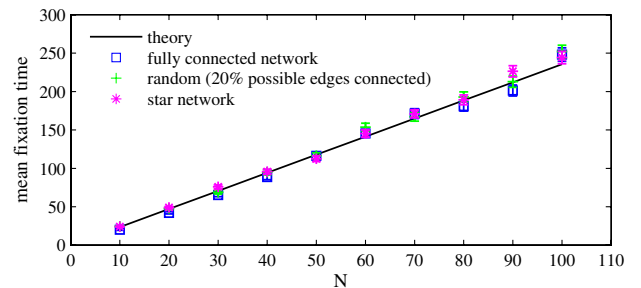
FIG. 3 (color online). Fixation times *per speaker* within the socially neutral utterance selection model (defined in the text) on various networks with N nodes (see legend).

plies that its left and right eigenvectors are proportional to one another, and so $Q_i = 1/N$. This together with $\sum_j m_{ij} \propto f_i$ [5] implies a constant r from Eq. (7), which is confirmed by simulation results shown in Fig. 3 (although see below for some caveats). To evaluate the plausibility of this socially neutral model as a mechanism for new-dialect formation requires in addition to this result detailed consideration of human memory lifetimes that are beyond the scope of this Letter and are discussed elsewhere [15]. Ultimately, we conclude that a purely neutral model is hard to reconcile with available empirical data.

We remark that our main result [Eq. (7)] can also be obtained and interpreted within a *backwards-time* formulation. Consider, for example, two objects of the same type; by asking which objects these were copied from at some earlier time, one can reconstruct their ancestral lineages, which will hop between nodes as one goes back in time. Eventually, both objects will have been copied from the same "parent," causing a merger of the lineages. This process is called the *coalescent* in population genetics [17], but, by viewing the lineages as particle trajectories, one can also recognize it as the $A + A \rightarrow A$ particle coalescence reaction of nonequilibrium statistical mechanics [18] on a network.

In this picture, the quantity r in Eq. (7) is the asymptotic rate at which the last two unreacted particles coalesce. The specific expression quoted above can be in fact obtained as a bound by means of a variational principle. Most usefully, this approach—whose details will be presented elsewhere [19]—yields physical insight into when the approximations we have made to obtain (7) are valid. The key assumption is that the last two unreacted particles must each typically have been able to explore a large number of the sites of the network before the final coalescence takes place. Then we regard the particles as *well-mixed*: The asymptotic probability of finding a particle on site i relative to finding it on site j is assumed to be independent of the location of the other particle *unless* both particles are on the same site (since then they may react). In practice, we have found that the presence of sufficient long-range connections in the network gives rise to a well-mixed two-particle state at late times in the particle-reaction process. On the other hand, a bottleneck that dramatically extends the time taken to reach one subset of sites from another would likely lead to this assumption of well-mixedness breaking down. Although (7) would then cease to be valid, the variational approach of Ref. [19] could, in principle, be refined to take such network structures into account, a task we leave for future work. Finally, we remark that the pivotal assumption $T_0 \ll T$ corresponds to taking the longest time scale in the backward-time dynamics to be that associated with the final coalescence reaction, that is, that the subsequent relaxation of the one particle state to its equilibrium occurs on a much shorter time scale. If the last two particles are well-mixed, we would expect this as-

sumption to hold, since each particle would be close to the single-particle equilibrium state.

In summary, we have provided an approximate theory, validated numerically on a range of networks, for calculating the fixation time within a general model that has features shared by physical, biological, and social systems. Since in reality specific applications will contain additional processes, it is of interest to extend the general approach we have described to cater for these. We have also briefly discussed how a particularly striking result—that fixation time is independent of network structure—is of direct relevance to current linguistic theory [9,15] and hope that the trend whereby mathematical results for formal models of social behavior are applied in empirical contexts will continue, and increase, in the future.

*Present address: Departamento de Física da Universidade de Aveiro, 3810-193 Aveiro, Portugal.

[1] C. Castellano, S. Fortunato, and V. Loreto, arXiv:0710.3256 [Rev. Mod. Phys. (to be published)].

[2] R. A. Blythe and A. J. McKane, J. Stat. Mech. (2007) P07018.

[3] S. P. Hubbell, *The Unified Neutral Theory of Biodiversity and Biogeography* (Princeton University Press, Princeton, NJ, 2001).

[4] J. F. Crow and M. Kimura, *An Introduction to Population Genetics Theory* (Harper & Row, New York, 1970).

[5] G. Baxter, R. A. Blythe, W. Croft, and A. J. McKane, Phys. Rev. E **73**, 046118 (2006).

[6] V. Sood and S. Redner, Phys. Rev. Lett. **94**, 178701 (2005).

[7] V. Sood, T. Antal, and S. Redner, Phys. Rev. E **77**, 041121 (2008).

[8] R. A. Blythe, Theor. Popul. Biol. **71**, 454 (2007).

[9] P. Trudgill, *New-Dialect Formation* (Edinburgh University Press, Edinburgh, 2004).

[10] R. Condit *et al.*, Science **295**, 666 (2002).

[11] K. Suchecki, V. M. Eguiluz, and M. San Miguel, Europhys. Lett. **69**, 228 (2005).

[12] C. W. Gardiner, *Handbook of Stochastic Methods* (Springer, Berlin, 2004).

[13] C. Castellano, AIP Conf. Proc. **779**, 114 (2005).

[14] P. Erdös, and A. Rényi, Publ. Math. Debrecen **6**, 290 (1959).

[15] G. Baxter, R. A. Blythe, W. Croft, and A. J. McKane (to be published).

[16] E. Gordon *et al.*, *New Zealand English: Its Origins and Evolution* (Cambridge University Press, Cambridge, England, 2004).

[17] J. Wakeley, *Coalescent Theory: An Introduction* (Roberts & Co., Englewood, 2006).

[18] U. Täuber, M. Howard, and B. Vollmayr-Lee, J. Phys. A **38**, R79 (2005).

[19] R. A. Blythe (to be published).