Conformity and Dissonance in Generalized Voter Models

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Abstract We generalize the voter model to include social forces that produce conformity among voters and avoidance of cognitive dissonance of opinions within a voter. The time for both conformity and consistency (which we call the exit time) is, in general, much longer than for either process alone. We show that our generalized model can be applied quite widely: it is a form of Wright's island model of population genetics, and is related to problems in the physical sciences. We give scaling arguments, numerical simulations, and analytic estimates for the exit time for a range of relative strengths in the tendency to conform and to avoid dissonance.

Keywords Voter model · Exit time · Epistasis · Diversity · Genetic drift · Culture

The voter model describes one of the simplest statistical processes [15]. In this scheme there are N agents ('voters') that live on a graph, and can take on several values ('opinions'). In the simplest case there are two opinions which we denote by +1, -1. The dynamics are that a voter is chosen at random, and then a neighbor on the graph is chosen at random and 'influences' the first—that is, the chosen voter adopts the opinion of his neighbor. The dynamics continue until all of the voters are in *conformity*, i.e. all opinions are the same; then there can be no further change. In this paper we will be interested in the mean time to arrive at this state for a finite number of voters. We will refer to this as the exit time, T.

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The voter model provides a conceptual description of and provides insights into a variety of social, biological, and physical phenomena. In the social realm, the individual level tendency to conform has implications for macro levels of criminal activity [11], drug use, cultural behavior [1], altruistic behavior, technological adoption, and participation in political and social movements [20]. This same underlying phenomenon—the matching of one entity's state to that of another—arises in biology in the form of genetic drift [17] and in ecology as Hubbell's neutral theory [5, 12]. In the genetic models, the opinions take the form of two or more possible allele values, whereas in neutral theory opinions denote distinct species. The applications to physics are, if anything, more direct. The model captures the coarsening of an alloy in the small-surface tension limit [7] and is very closely related to certain catalysis models for $A + B \rightarrow 0$ [6, 21].

A limitation of the voter model when applied to social and biological settings is that it fails to include a force for *consistency* among opinions on various issues. In social settings, that force has psychological underpinnings. While individuals do alter their behavior so as to conform with the majority as captured in the voter model, they also try to avoid cognitive dissonance [9]. In the biological setting, the consistency force arises from epistasis in the genetic code: different genes work together.

In this paper, we generalize the standard voter model so as to include both a force for external conformity and a force for internal consistency (avoidance of dissonance) [2]. We accomplish this by endowing each site with a vector of values of length M. For each coordinate of this vector, the site engages in a voter model with a fixed probability p. With probability q = 1 - p the site considers the dissonance in its vector of values, and engages in a voter model with itself, i.e. it changes the value at different coordinates to match the values at other positions. In figurative language, a voter may have opinions about a political party, the war in Iraq, gun control, etc. He can be influenced (with probability p) by his neighbors on any of these issues. With probability q he tries to change his own opinions to be consistent within himself. See Fig. 1 for a picture of this geometry. We assume, for the purposes of the model, that there is a fixed relationship between opinions on these different issues, e.g., given "cares about" and "apathetic about" as the two possible states, a person apathetic about trade tariffs will be apathetic about farm subsidies, if he thinks about it.

The resulting model neatly captures a range of social phenomena from cultural formation—where individuals want to coordinate but also remain consistent—to the formation of political party platforms—party members want to agree with one another but also



take consistent positions across issues. It may also be thought of as version of the wellknown Wright Island model of population genetics [19]. In this model islands have a certain frequency of an allele which can be changed by migration from other islands. The migration probability is analogous to our p. In the limit of small p the two models are the same.

The results of applying these dynamics is surprising. Note that the only equilibria are for all voters to have the same opinion for each issue, i.e. complete conformity *and* consistency. These are absorbing states, since dynamics cease when either state is achieved. What is interesting is the time required for that convergence to occur, namely the exit time T(N, M, p). The generalized model takes much longer to converge than the standard model. We will show that when p is very near to 0 or 1, T increases without bound with respect to p. One implication of this is that if the conformity effect is much larger than the consistency effect, which could well be the case in some settings, then we might not expect convergence in a reasonable time. The model may partly explain persistent cultural heterogeneity, fractiousness of political parties, and genetic diversity of populations that we see in the world.

1 Background: The Mean Field Voter Model

The simplest graph for the voter model is the complete graph or mean field, i.e. all N voters are neighbors of each other. In this case a well-known connection to coalescing random walks makes solving for many properties straightforward [16]. To get a qualitative picture of the results, note that the system can be characterized by the number of plus opinions, denoted by n_1 . We now have the problem of a random walker at site n_1 on a line of length N. The probability of a move to the left or right is the probability of randomly selecting two sites with differing opinions. For large N this is $(n_1/N)(1 - n_1/N)$. The mean exit time starting from $j = n_1$, T_j , obeys a well-known equation [18]:

$$-1 = \frac{j}{N} \left(1 - \frac{j}{N} \right) (T_{j+1} - 2T_j + T_{j-1}).$$
(1)

The right hand side is the discrete second derivative of T. Letting x = j/N be the density of plus opinions, for large N we have:

$$-N^{2} = x(1-x)\frac{d^{2}}{dx^{2}}T(x)$$
(2)

on the unit interval, subject to T(0) = T(1) = 0. Therefore:

$$T(x) = -N^{2} \left(x \log(x) + (1-x) \log(1-x) \right).$$
(3)

This is the first passage time to the boundaries for a one dimensional random walk with spatially varying jump rate [13]. It should be noted that some authors define a unit of time to be a number of time steps equal to the system size, corresponding to the time it would take for all sites to update, which reduces T by a factor of N.

2 Scaling

We now return to the generalized voter model. Let there be N voters, each with an opinion on M issues; the opinions take values ± 1 . We can think of the graph as having M layers



with N points which are all coupled to each other (i.e. mean-field coupling). Each column corresponds to a voter. Let p be the probability of an opinion change between voters in a layer, and q = 1 - p be the probability of an internal change. These dynamics can conflict and slow the time to agreement.

For M = 1 or N = 1 we have the simple voter model with N or M voters, respectively. From the previous section, $T(N = 1, M) \propto M^2$. Similarly $T(N, 1) \propto N^2$. However, for $p = \frac{1}{2}$, $T(N, M, p = \frac{1}{2})$ must be symmetric in N and M. A reasonable guess is:

$$T\left(N, M, p = \frac{1}{2}\right) \propto N^2 M^2.$$
⁽⁴⁾

Simulations confirm this guess, as shown in Fig. 2. In fact, this scaling holds pretty well for p up to 0.8. We should note for comparison that if we are not concerned with consistency, but find the time for M uncoupled layers to be in conformity, we would get $T \propto N^2 M$.

If $p \approx 1$, the fast dynamics are between voters. Each issue is almost always in conformity, and acts like a single issue in the simple model, namely $T \propto \tau M^2$, where τ is the time to flip a whole layer of voters. To find τ first note that we must wait 1/q time steps to have a change between layers. However, in most cases, the intralayer dynamics will simply eliminate the foreign opinion. The probability of a single introduced +1 changing a whole layer of -1 can be gotten by considering a random walk whose position is the number of +1's in the layer. We need to know the probability of a walker located adjacent to an adsorbing trap reaching a spot N spaces to its right before hitting the trap immediately to its left. This probability is 1/N [16], so that there need to be, on average, N introductions of a minority opinion before the layer flips. Thus τ , the time scale to flip the layer is N/q and $T \propto NM^2/q$. We expect the approximation to be valid if the time to generate a dissenting opinion, 1/q, is bigger than the time to reach conformity, N^2 . That is $q < 1/N^2$.

Exchanging $M \leftrightarrow N$ and $p \leftrightarrow q$ gives the result for $p \rightarrow 0_+$. This leads to:

$$T(N, M, p) \propto \begin{cases} NM^2/q, & p \to 1_-, \\ MN^2/p, & p \to 0_+. \end{cases}$$
(5)

The overall behavior with p is shown in Fig. 3. Note the increase for p near 0 or 1. Figure 4 shows a scaling plot which confirms (5).



3 Analysis Using Network Theory

We now think of the graph on which the voters lie as a network with weighted bonds. Denote by **s** the vector of all opinions and $\langle \mathbf{s} \rangle$ its ensemble average. The components of **s** are denoted σ_i . Their averages lie in the interval [-1, 1]. The network structure is encoded in an $NM \times NM$ matrix **A** such that A_{ij} is the probability that, having selected a node *i*, the opinion at *i* takes on the value of node *j*. Thus we have

$$A_{ij} = \begin{cases} q/(M-1), & \text{if } i \text{ and } j \text{ are in the same voter,} \\ p/(N-1), & \text{if } i \text{ and } j \text{ are of the same issue,} \\ 0, & \text{otherwise.} \end{cases}$$
(6)

Note that the sum of the rows and columns is 1.

We use a method adopted from studies of the voter model on a lattice [10]. If the state of the voters is **s**, let \mathbf{s}'_i be the same state as **s**, but with $\sigma_i \rightarrow -\sigma_i$. The probability of being in

state **s** is $P(\mathbf{s})$. The transition rate for $\sigma_i \rightarrow -\sigma_i$ is:

$$W_i(\mathbf{s}) = \frac{1}{2} \left(1 - \sigma_i \sum_j A_{ij} \sigma_j \right).$$
⁽⁷⁾

The master equation for $P(\mathbf{s})$ is:

$$\frac{dP(\mathbf{s})}{dt} = \sum_{i} \left[W_i(\mathbf{s}'_i) P(\mathbf{s}'_i) - W_i(\mathbf{s}) P(\mathbf{s}) \right].$$
(8)

Using $\langle \sigma_i \rangle = \sum_{\{S\}} \sigma_i P(S)$, we can write an equation for the evolution of the average of σ_i :

$$\frac{d\langle \mathbf{s} \rangle}{dt} = -\frac{1}{\mathcal{N}} (\mathbf{I} - \mathbf{A}) \langle \mathbf{s} \rangle, \tag{9}$$

where $\mathcal{N} = NM$ is the effective system size and **I** is the $\mathcal{N} \times \mathcal{N}$ identity matrix. The matrix **I** – **A** is a weighted version of the graph Laplacian. For this matrix all the eigenvalues are nonnegative and when a path exists between any two nodes, there is a zero eigenvalue whose eigenvector has all components equal.

The averages do not give the exit time directly. For this purpose we need two-point correlations. To see this, note that the density of edges along which there is a disagreement is $(1 - \langle \sigma_i [\mathbf{As}]_j \rangle)/2$ [3]. As the correlation function approaches unity, the system approaches conformity and consistency. In a way similar to the derivation of (9), we can show:

$$\frac{d}{dt}\langle\sigma_i\sigma_j\rangle = -\frac{1}{\mathcal{N}} \Big(2\langle\sigma_i\sigma_j\rangle - \langle [\mathbf{As}]_i\sigma_j\rangle - \langle\sigma_i [\mathbf{As}]_j\rangle \Big), \quad i \neq j.$$
(10)

For our network there are only four independent correlation functions since all nodes are equivalent. The autocorrelation is trivially 1 for all time. There are nodes within a voter that are connected by a function we will call r_v , and nodes in the same layer whose correlation we call r_h , and nodes that are not directed connected to one another which we call r_d . The \mathcal{N}^2 equations above thus reduce to three equations:

$$\frac{d}{dt}r_v = \frac{2}{\mathcal{N}} \left(\frac{q}{M-1} - \left(p + \frac{q}{M-1} \right) r_v + pr_d \right),\tag{11}$$

$$\frac{d}{dt}r_h = \frac{2}{\mathcal{N}} \left(\frac{p}{N-1} - \left(q + \frac{p}{N-1} \right) r_h + qr_d \right),\tag{12}$$

$$\frac{d}{dt}r_d = \frac{2}{\mathcal{N}}\left(\frac{p}{N-1}r_v + \frac{q}{M-1}r_h - \left(\frac{q}{M-1} + \frac{p}{N-1}\right)r_d\right).$$
(13)

Define:

$$\mathbf{r} = \begin{pmatrix} r_v \\ r_h \\ r_d \end{pmatrix},\tag{14}$$

$$\mathbf{v} = \begin{pmatrix} q/(M-1)\\ p/(N-1)\\ 0 \end{pmatrix},\tag{15}$$

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$$\mathbf{B} = \begin{pmatrix} p + \frac{q}{M-1} & 0 & -p\\ 0 & q + \frac{p}{N-1} & -q\\ -\frac{p}{N-1} & -\frac{q}{M-1} & \frac{q}{M-1} + \frac{p}{N-1} \end{pmatrix},$$
(16)

then

$$\frac{d}{dt}\mathbf{r} = \frac{2}{\mathcal{N}}(\mathbf{v} - \mathbf{B}\mathbf{r}).$$
(17)

Note that the asymptotic value of **r** is **1**, the vector with all components unity. Thus we put $\mathbf{R} = \mathbf{1} - \mathbf{r}$. Note that $\mathbf{B}^{-1}\mathbf{v} = \mathbf{1}$, so that we can write:

$$\dot{\mathbf{R}} = -\frac{2}{\mathcal{N}} \mathbf{B} \mathbf{R}.$$
(18)

Denote by λ_i the eigenvalues and ν_i eigenvectors of *B*. Then the solution to (18) can be written:

$$\mathbf{r}(t) = \mathbf{1} - \sum_{i} \left(\mathbf{R}(0) \cdot v_i \right) e^{-2\lambda_i t / \mathcal{N}} v_i.$$
(19)

This can be used to make an estimate of the extinction time T for the system [14], namely as the rate of approach of **r** to its asymptotic value. At long times the term which survives in (19) is the one with the smallest eigenvalue. Provided the eigenvalues are well separated, we have the approximation:

$$T \approx \mathcal{N} / \lambda_{\min},$$
 (20)

up to a factor of order unity.

Consider first the case $q \ll 1$. We can write $\mathbf{B} = \mathbf{B}_o + q \mathbf{B}_1$. We have:

$$\mathbf{B}_{o} = \begin{pmatrix} 1 & 0 & -1 \\ 0 & \frac{1}{N-1} & 0 \\ -\frac{1}{N-1} & 0 & \frac{1}{N-1} \end{pmatrix},$$
(21)

$$\mathbf{B}_{1} = \begin{pmatrix} -\frac{M-2}{M-1} & 0 & 1\\ 0 & \frac{N-2}{N-1} & -1\\ \frac{1}{N-1} & -\frac{1}{M-1} & \frac{1}{M-1} - \frac{1}{N-1} \end{pmatrix}.$$
 (22)

The smallest eigenvalue of \mathbf{B}_o is 0 and the corresponding eigenvector is $v_o = (1, 0, 1)^T$. Rayleigh-Schroedinger perturbation theory tells us that, to first order in q, the smallest eigenvalue is:

$$q\frac{\nu_o \cdot \mathbf{B}_1 \nu_o}{\nu_o \cdot \nu_o} = q/(M-1).$$
⁽²³⁾

Thus our estimate of T in this regime is NM(M-1)/q, in agreement with (5) and Fig. 4. Numerical solution of the minimum eigenvalue accounts well for the higher order differences observed in exit time for distinct pairs of N and M with fixed product NM^2 .

A comparison between the scaling results and the smallest eigenvector are shown in Fig. 5. From the Figure we see that the estimate gives the exit times correctly up to a factor ≈ 0.7 .

A solution for the exit times in the Wright island model was recently found using coalescent theory. It agrees with the scaling with system size and migration rate that we found here using simpler techniques [4].



4 Discussion

In this paper, we have considered a generalization of the standard voter model that includes forces for dissonance avoidance as well as conformity. Such an assumption applies to a variety of social settings including cultural formation, political party platform creation, and organizational goal setting. Members of these collectives desire conformity, but they also desire consistency across issues or domains. For example, members of a political party want to cohere on common stands on issues but they also want a consistent underlying set of principles that relates positions across issues. The same forces also apply in some biological systems. Genetic drift creates conformity but epistatic interactions across genes create pressures for consistency, albeit in a more complex form than our generalized model captures.

At its core, this paper considers the effects of adding these two forces. It is an exercise in showing the strengths and limitations of science as decomposition. We ask: does a model that includes both conformity and consistency perform like the product of the two individual models? We find that if the two forces apply at the same scale, if the probability of a voter conforming is of the same order as the probability of a voter ridding itself of an inconsistency, then the answer is a qualified yes. The exit time is of order N^2M^2 , which is the product of the exit times of the individual models: a conformity model and an consistency model. However, when one force far outweighs the other, the answer is an unequivocal no. In this case, the exit time rises at a rate 1/r, where r is the probability that the less likely force is applied. Thus, in a model in which the voters care much more about conforming than being consistent, the exit time can be substantial. And, even in models with small numbers of agents and few dimensions, as $r \rightarrow 0$, the exit time goes to infinity.

This last result is of mathematical interest because it shows how exit times can have a nonlinear relationship to the relative weights of forces. Empirically, the result tells us something about the persistence of heterogeneity. Models of cultural convergence and genetic drift show a quick dampening of diversity as do simple models of dissonance reduction. Adding the two forces, as we have shown, reveals much longer exit times, particularly when one force is stronger than the other. Thus, a society (resp. political party or species) may take a long time converge to a consistent culture (platform, or genetic sequence) even though the forces are in place for that to happen. If one force is very weak, the exit time may be so long that we would expect the system to not attain it in any practical time frame. As a result, heterogeneity would persist. Moreover, voter model dynamics are extremely sensitive to the addition of noisy dynamics, for instance becoming unstable with any amount of extra noise on 2D lattices [7, 8]. If we add a small amount of a noisy process to this generalized model, we find stable levels of heterogeneity that far outstrip those produced by the standard voter model [2].

Social interactions rarely take place on a regular topology. Neither are they so random as to be captured by a fully mixed model. Accordingly, our results are not meant to accurately represent the social world. That said, our main findings, that the two dynamics occur much more slowly than either dynamic on its own, and that near the boundaries the behavior differs, would also hold for other interaction structures.

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