

## Electronic Enhancements

### Full expression for $\Delta q_1$

In the text, we gave an expression for the change in  $q_1$  due to imitation, when  $D$ , the covariance between marker and behavior, is close to zero. When the absolute value of  $D$  is large, the full expression is:

$$\Delta q_1 = 2\delta D(p_1 - p_0) \left\{ \left(1 - \frac{e}{2}\right) - (1-e) \frac{D}{q_1 q_0} \left( \frac{q_1 - q_0}{p_1 - p_0} \right) \right\} \quad (4)$$

Thus as the absolute covariance between marker and behavior increases, the correlated response on markers decreases for a given difference in behavior frequencies.

### Expression for $\Delta D$

In the text, we showed expressions for the changes in behavior and marker frequencies due to imitation. Here, we derive a similar expression for the change in  $D$ , the covariance between marker and behavior in a particular population. The expression for  $\Delta D$  is more complex than the previous recursions, but by deriving the expression for small (near-zero) values of  $D$ , the expression can provide some insight.

$\Delta D$  is defined as,

$$\Delta D = x_{11} \left( \frac{W_{11}}{\bar{W}} \right) x_{00} \left( \frac{W_{00}}{\bar{W}} \right) - x_{10} \left( \frac{W_{10}}{\bar{W}} \right) x_{01} \left( \frac{W_{01}}{\bar{W}} \right) - D \quad (5)$$

Where  $x_{ij}$  is the frequency of maker  $i$  and maker  $j$  in the population of interest. By substituting fitnesses and expressing all  $x_{ij}$ 's in terms of  $p$ ,  $q$  and  $D$ , then canceling all terms of order  $D^3$  and assuming selection is weak such that  $\bar{W} \approx 1$  and terms of order  $\delta^2 \approx 0$  results in

$$\Delta D \approx \delta \left\{ D(2p_1 p_0 (1-e) + 1) + (1-e) \frac{D^2}{q_1 q_0} (p_1 - p_0)(q_1 - q_0) \right\} \quad (6)$$

Finally, ignoring terms of order  $D^2$  yields

$$\Delta D \approx \delta D(2p_1 p_0 (1-e) + 1) \quad (7)$$

Thus when  $D$  is small in absolute value and selection is weak, the covariance increases essentially exponentially.

## A general coordination game structure leads to similar results

In the text, we presented a general version of the coordination game as Table 2. This payoff structure leads to an unstable equilibrium (Figure 7) at

$$\tilde{p} = \frac{\delta + h}{2\delta + g + h} \quad (8)$$

We ran a number of simulations varying the values of  $h$  and  $g$ . In sum, even large deviations from the perfect coordination structure allow the system to evolve ethnic-like groups much of the time (see Figures 8 and 9). Thus our results do not depend in a sensitive way on the perfect nature of the game structure we have chosen.

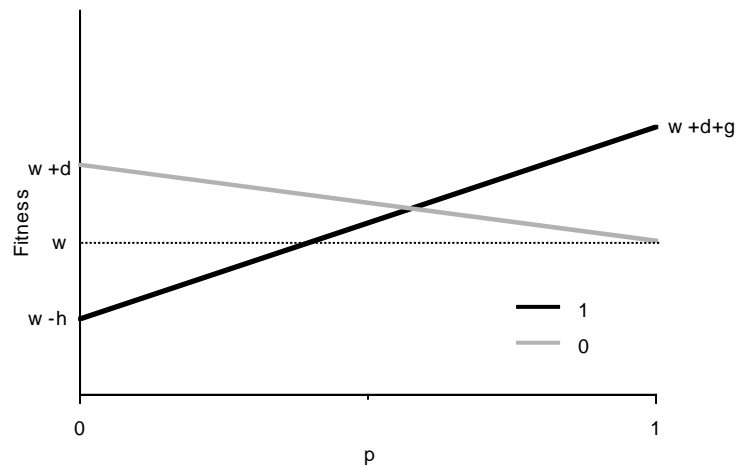


Figure 7. Fitnesses based on general coordination game structure in Table 2. The black line corresponds to behavior 1, the gray line to behavior 0.  $p$  is the frequency of behavior 1 ( $p_1$ ). Adjusting the values of  $g$  and  $h$  allows us to change the domains of attraction of the two behaviors, as well as make one behavioral equilibrium more fit.

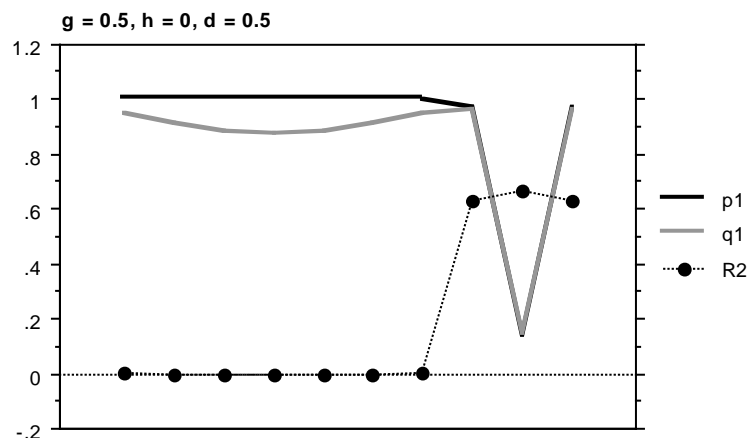


Figure 8. Spatial plot of the equilibrium state of a simulation of a circular ring of groups. The horizontal axis is space, with the far right group connecting back to the far left group. R2 (the dotted line) is the squared correlation between marker and behavior. In settings where  $g = 0.0$ , we normally see a more equal distribution of groups practicing behaviors 1 and 0. With  $g = 0.5$  here, the domain of attraction for the first behavior is larger, and more groups arrive at that equilibrium.

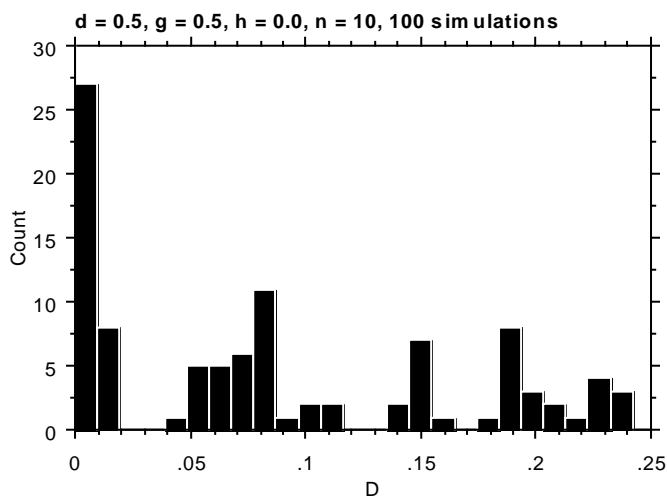


Figure 9. Histogram results of 100 simulations with parameter values found in Figure 8. Even under such extreme advantage for behavior 1, almost a quarter of all simulations evolve informative ethnic markers at equilibrium, showing that the model is not delicately sensitive to the perfect symmetry of our original coordination game.

### Natural selection favors smaller values of $e$

We have already assumed that cultural transmission is not vertical—people acquire their behavior and marker by imitating successful people, not their parents. When cultural transmission is not vertical, there is a high degree of recombination between culture and genes, and therefore “gene-culture covariation” (Cavalli-Sforza and Feldman, 1981) can be ignored. This means that we can calculate the fitness of genes that affect social interaction and cultural transmission by assuming that they are randomly associated with the cultural variants in the population.

Suppose that an individual’s propensity to interact with others who have the same marker,  $e$ , is affected by heritable genetic variation. The fitness of an individual in group  $k$  with a particular value of  $e$ , say  $e'$ , is:

$$W(e') = 1 + \delta \left( p_1^2 + p_0^2 + (1 - e') \frac{D^2}{U} \right) \quad (9)$$

Thus individuals with smaller values of  $e$  will have higher fitness as long as the covariance between marker and behavior is not exactly zero. As we saw before, migration will generate covariance between behavior and marker, and any random variation in the frequency of the marker in space will tend to generate non-zero values of  $D$ . Thus it seems in coordination games a preference for individuals with a marker similar to one’s own is quite easy to evolve genetically.

### Natural selection favors smaller values of $r$

Since the strength of other learning processes,  $r$ , has such a strong effect on the system’s outcome, it would be useful to know how selection would affect a gene that increases or decreases the rate of recombination between marker and behavior loci.

Events here occur in the following sequence. Again ignoring gene-culture covariation, imagine first that, in each time period, recombination occurs before individuals interact. This change does not alter the characteristic behavior of the model, and it allows us to easily calculate how accumulated recombination affects fitness. That is, individuals imitate to acquire markers and behaviors, other learning processes may then break up those associations, and finally individuals pair-up and interact. If different individuals operate on different rates of recombination, then markers will be more informative in some classes of individuals than in others, once all actors reach the interaction phase.

Now imagine an allele that causes individuals on average to recombine marker and behavior traits at a rate  $r$ . The fitness of this allele is

$$W(r) = rD[(W_{10} + W_{01}) - (W_{11} + W_{00})] + \bar{W} \quad (10)$$

Genes that decrease  $r$  by an amount  $s$  will be favored by selection as long as

$$sD \left[ \underbrace{(W_{10} + W_{01})}_A - \underbrace{(W_{11} + W_{00})}_B \right] < 0 \quad (11)$$

Suppose  $D$  is positive. Then term  $B$  in expression (11),  $(W_{11} + W_{00})$ , is greater than term  $A$ ,  $(W_{10} + W_{01})$ , and so the contents of the brackets are negative and (11) is satisfied. The reason term  $B$  is greater when  $D$  is positive is because matched behavior and marker combinations do well when there is positive covariance between behavior and marker. This means the fitnesses in term  $B$  are greater than those in term  $A$ , because individuals receiving term  $B$  payoffs are avoiding costly errors in interaction, while those receiving term  $A$  payoffs are not.

Similarly, when  $D$  is negative,  $(W_{11} + W_{00})$  is less than  $(W_{10} + W_{01})$ , and so the terms in brackets are positive, resulting in the same reversed inequality and result. Smaller values of  $r$  lead to higher average payoffs, higher values lead to lower payoffs. This is not a surprising result, as the covariance of behavior and marker traits establishes a coadaptation, and any allele that reduces that covariation is therefore less fit. This analysis suggests that, to the extent that it is not constrained to higher values, selection will reduce  $r$  zero.