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Swimming with the Current?

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Abstract

I embed a probabilistic choice model in a dynamic model of cultural transmission. The probability of adopting a certain variant of a cultural trait depends on its intrinsic values and on popularity. Enculturation takes place in two stages, first in the family and later in society. Families differ on how strongly they transmit their own culture. It is shown that both conformism and anti-conformism lead to stable plural societies.


Keywords: Cultural transmission, conformism, anti-conformism.

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On matters of style, swim with the current, 
on matters of principle, stand like a rock.
Thomas Jefferson

1 Introduction

Conformism is the tendency to behave in accordance with prevailing standards or customs. Anthropologists have argued (Boyd and Richerson, 1982) that a conformist bias could be adaptive in spatially varying environments if selective forces lead to an increase in the frequency of the locally favored variant. In those circumstances individuals following the simple rule "when in Rome, do as the Romans do" would be likely to acquire the "right" variant wherever they are and would have higher fitness than individuals following other more costly learning rules. On a long run perspective, the imitation of the ideas and behaviors expressed by the majority leads to within-group cultural homogeneity, is compatible with cultural diversity across groups, but cannot explain the initial spread of new views, customs and technologies. On this ground, conformism is often seen as a hindering factor in the creation and diffusion of novel ideas.

In this paper I define conformity in the framework of a probabilistic choice model of cultural transmission. The probabilistic model aims at capturing, in a simple and tractable manner, the idea that individuals may not have a clear ranking of the available alternatives or that the utility of each of them is subject to randomness. Think of choices among sets of alternatives which differ on several dimensions all of which are relevant to the choice, the superiority (or the perception of it) of a particular alternative depending on the decision maker’s mood and whims, on current fashions and attitudes, on the particular circumstances in which the choice is made, on the choice protocol used by the decision maker...

Consider for instance a decision maker deciding, on a particular day, whether to dress in white or in black. The choice may well depend on the activities one has to attend to, on own’s mood, on the weather, on current fashions and norms... so that some days he will dress in white, some other days in black. The individual’s behavior can then be modeled as being probabilistic.\footnote{The appropriateness of the random choice model is also substantiated by frequent violations of transitivity (Tversky, 1969).} This is the starting point of this paper,
namely that decision makers are endowed with random preferences or probabilistic decisions rules so that the different available alternatives (cultural traits) will be chosen with (possibly different) positive probabilities. Moreover the choice probabilities may depend on the distribution of traits in the population.

To fix the main idea consider the choice between dressing black ($b$) or white ($w$), and assume that when half of the population dresses white and half black the decision maker chooses white with probability

$$\frac{v_w}{v_b + v_w},$$

(1)

where $v_i > 0$ is a scale value assigned to colour $i$ (Luce (1950)).\(^2\) This probability reflects the effect of all the random factors which influence the individual’s behaviour. Unlike in the standard algebraic model of choice\(^3\) the observed diversity is not the result of the agent being indifferent between alternatives and choosing them in any random manner but of some randomness in the decision process itself or in the utilities derived from the different alternatives which leads to the choice probabilities given by (1). This probability corresponds to the individual’s independent-from-society preferences since the population distribution of colours, being even, does not, and cannot, favour one alternative over the other.

I shall refer to an individual who dresses always according to (1) and not only when both colours are evenly distributed in the population as an independent. I define a conformist as someone who is more likely than an independent to follow the majority. On the contrary, an anti-conformist is more likely than an independent to follow the minority. In particular when more than 50% of the population dresses white, a conformist will choose white with a probability larger than (1) and an anti-conformist with a probability which is smaller. When both colours are evenly distributed in the population, all three types of agents dress according to (1) since there is no clear fashion to follow or to be against to.

I propose a general and simple probabilistic choice function which has each of these three types of agents as a special case. I assume that the probability of choosing option $i$ from a set $K$ depends not only on the scale values assigned to the different alternatives

\(^2\)Random choice functions like (1) can be derived from random utility models (Thurstone (1929)) with extreme value distributions (McFadden, 1980).

\(^3\)An individual would either prefer white to black, black to white or be indifferent between the two colours. Only in case of indifference would we observe someone who does not always dress the same way.
when traits are evenly distributed (see (1)), but also on the actual proportion of agents choosing each of the alternatives. In the two colour example, the probability of choosing white will be written as

\[
\frac{v_w x_w^\alpha}{v_b x_b^\alpha + v_w x_w^\alpha}
\]

(2)

where \(x_i > 0\) is the share of population choosing \(i\) \((i \in \{b, w\})\). It is easy to see that (2) delivers conformism when \(\alpha > 0\), anti-conformism when \(\alpha < 0\) and independence when \(\alpha = 0\). Moreover, (2) is equal to (1) for any \(\alpha\) when \(x_b = x_w = 1/2\). Deviations from independence are larger the larger is \(|\alpha|\).

The main objective of this paper is to study the effect that independence, conformism and anti-conformism have on the long run distribution of cultural traits. To do so I propose a two stage model of cultural transmission in which children are first educated in the family, where they acquire (provisionally) the family culture, and later, in society, where they revise their culture according to a \(n\)-variant version of (2). The family sets the default culture and only occasionally are children allowed to change it. One can think of some groups being less subject to outside influences than others so that their children are more likely to be like the parents, or that some parents push their culture more strongly or are less willing to accept diversity and more willing to punish defectors. I model this by assuming that traits differ not only by the probability that they can be copied but also by the probability with which they can be revised. I characterise the long-run distribution of variants in the population for all values of \(\alpha\) and show that conformism (swimming with the current) leads to cultural homogeneity only if the current is strong enough \((\alpha \geq 1)\), otherwise societies will be characterized by cultural pluralism i.e., co-existence of different cultural variants. Moreover, initial conditions only matter when \(\alpha > 1\). Homogeneity will also be the long run outcome if \(\alpha = 1\), in this case, unlike when \(\alpha > 1\), initial conditions do not matter and the only surviving variant is the one on the highest ratio between the scale value \(v\) and the probability that the variant is revised. If all variants are equally changeable the surviving variant will be the one with the highest value \(v\).

Independence (standing like a rock) results in long run shares which reflect the independent preferences only if all variants can be revised with the same probability, otherwise those variants which are more difficult to change will have disproportionate large shares. When \(\alpha < 1\) the long run shares depend not only on the level of conformism but also on the ratios between the attractiveness of the variant and the probability that the variant can be changed. Those variants which are more attractive
or/and less susceptible to change will have larger shares. Unattractive variants may survive if the children of those having those variants are very likely to be like their parents. These are variants which are unlikely to be copied by outsiders but whose carriers have it difficult to change.

Weak conformism leads to the co-existence of several variants in equilibrium. Differences across groups are not due to differences in initial conditions (as would happen with strong conformism) but to differences in the evaluation of the variants and/or in the probabilities of revision or to differences in the sets of variants the agents are aware of.

Copying the majority generates diffusion curves which are similar to those documented in the empirical literature (Heinrich, 2006), with one caveat: in order to observe diffusion of novel ideas or technologies a large enough proportion of agents must initially adopt the new variant. Weak conformism can generate S-shaped diffusion curves with long tails, so that adoption is slow at the beginning, picks up in the middle and slow down as the innovation becomes dominant, without relying on unreasonably high proportion of initial adopters. In fact, it does not impose any constraint. If individuals differ in their degree of conformity, new ideas would initially spread through weak-conformist or/and independent agents who respond more to objective advantages than to popularity. Once a large enough share has adopted the new variant the strong conformists would follow suit and the new variant would invade the population. Since the advantages of the new variant also matter for adoption, a new superior variant could be adopted by almost everybody even if agents are not strong conformists.

Figure 1: Heterogeneous vs. homogeneous populations.
In order to see this consider Figure 1 which shows how a new superior variant spreads in a homogeneous population of strong conformists (empty circles) and in a heterogeneous population with 20% of weak conformists and 80% of strong conformists (black circles). More than a 10% of the population would need to adopt the new variant in the homogeneous population for the variant to diffuse while no such a threshold is needed in the heterogeneous case.

Figure 2 shows the ”true” diffusion curve for the hybrid corn seed in Iowa.

![Figure 2: Diffusion of hybrid corn seed in Iowa.](image)

The paper is organized as follows. In Section 2 I describe the model and define independence, conformism and anti-conformism. Section 3 characterizes the dynamics and its steady states. Section 4 discusses the implications of the model concerning the diffusion of new cultural variants. Section 5 concludes.

## 2 The model

I consider an overlapping generation model with a large population which comprises adults and children. Each adult is characterized by a fixed variant of a cultural trait. The set of existing variants is finite and denoted by $K = \{1, 2, \ldots, k\}$, with $k \geq 2$. Time is discrete and each period is subdivided in two. At the beginning of the first sub-period each adult has a child with probability $\lambda > 0$. During the first sub-period the new born is educated in the family (i.e, by the parent) and acquires provisionally the parent’s variant. Families differ in the strength with which they transmit their variant so that some children are later more susceptible to outside influences than others. I
capture this by assuming that the probability that a child with variant $i$ keeps the family culture differs across variants (or equivalently across families). Let $p_i \in [0, 1)$ denote this probability, and let $p$ denote the vector of $p$’s.

A child who revises his trait is assumed to copy trait $i \in K$ with a probability equal to $P(i; v, x)$, where $x$ is the vector of population shares of the different traits and $v$ is the vector of scale values assigns to the variants, with $v_i \geq 0$ for all $i$.

After this second stage of societal influence, culture is definitively fixed and children become adults. In order to keep the population constant I assume that at the end of the period "old" adults die with probability $\lambda$. This leads to a system of differential equations describing the dynamics of the adult population:

$$x_i(t+1) = (1-\lambda)x_i(t) + \lambda(p_ix_i(t) + P(i; v, x(t))) \sum_{s=1}^{k} (1-p_s)x_s(t), \quad i = 1, 2, ..., k. \quad (3)$$

The first term on the RHS are the surviving adults while the first term in the bracket are the new born who have acquired trait $i$ and do not change, and the second term are those who revise their trait and acquire trait $i$. Subtracting $x_i(t)$ from both sides of (3) and eliminating the time indexes I obtain the following system

$$\Delta x_i = \lambda(P(i; v, x) \sum_{j=1}^{k} (1-p_j)x_j - x_i(1-p_i)), \quad i = 1, 2, ...k. \quad (4)$$

This dynamics describe also the evolution of a fixed population of agents, a proportion $\lambda$ of which is allowed every period to revise their trait, they do so with a probability that depends on their current trait, and, when they change, follow $P(i; v, x(t-1))$.

### 2.1 Conformity, anti-conformity and independence

I consider a $n$-variant version of (2). In particular, I assume that $P(i; v, x)$ has the following functional form

$$P(i; v, x) = \frac{v_i x_i^\alpha}{\sum_{j \in K} v_j x_j^\alpha}, \quad i = 1, 2, ..., k. \quad (5)$$

Note that when $\alpha \leq 0$, (5) is not well defined unless $x_i > 0$ for all $i$.

The parameter $\alpha$ is a measure of how individuals evaluate popularity of variants in the population and the scale values $v_i \geq 0$ ($i \in K$) capture the variants’ intrinsic values,
i.e., those that govern choice when popularity does not matter. \( P(i; v, x) \) captures some important aspects of cultural transmission which have been widely documented (see Boyd and Richerson (1985)). In particular i) agents are influenced by the frequency of the different variants in the population they interact with, and ii) variants may also differ in attractiveness due to some intrinsic value of the variant (direct bias) or to the fact that children use some other feature (like wealth, success, leadership) to evaluate the value of a different variant (indirect bias). The latter makes some variants more likely to be copied than others.

The probability \( P(i; v, x) \) is monotonically increasing (decreasing) in \( x \) when \( \alpha > 0 \) (\( \alpha < 0 \)), it is constant and equal to

\[
\frac{v_i}{\sum_{j \in K} v_j}
\]  

(6) when \( \alpha = 0 \) or when all variants are equally distributed, irrespective of \( \alpha \). I shall then refer to \( \alpha > 0 \) as conformist transmission, \( \alpha < 0 \) as anti-conformist transmission and to \( \alpha = 0 \) as independent transmission. If all variants are equally attractive (i.e. \( v_j = v \) for all \( j \)), then i) the probability to copy a variant is equal to its frequency when \( \alpha = 1 \), ii) all existing traits are copied with the same probability when \( \alpha = 0 \), iii) only the most frequent variant is copied when \( \alpha = \infty \) and, iv) only the least frequent variant is copied when \( \alpha = -\infty \).

When the \( v \)'s differ, there is a positive (negative) merit-bias towards those variants which have higher (lower) than average merit. In particular when all variants are evenly distributed, so that popularity is irrelevant, those variants with a higher (lower) than average merit are copied with a probability which is larger than their population shares. I say that transmission is positively (negatively) biased towards those variants. Figure 3 illustrates these cases.

On the horizontal axes I have plotted the proportion of agents with variant 1 and on the vertical the probability that someone who revises his culture copies that variant. The thick lines in each panel correspond to \( v_1 = v_2 \) and the thin ones to \( v_1 > v_2 \). The horizontal lines in all four panels correspond to \( \alpha = 0 \), our benchmark case. Note that in all panels the two lines of the same thickness cross at \( x_1 = 1/2 \). In panels ii)-iv) the transmission is conformist since the lines are increasing and above (below) the horizontal lines of the same thickness when \( x_1 > 1/2 \) (\( x_1 < 1/2 \)). The reverse happens in panel i) which corresponds to anti-conformism (\( \alpha < 0 \)). Given \( \alpha \), the positive bias
towards variant 1 moves all the functions upwards so that the increase in $v_1$ makes the acquisition of variant 1 more likely for all values of $x$. Only when $v_1 = v_2$ and $\alpha = 1$ is the transmission linear (panel iii)).

I shall refer to $\alpha \geq 1$ as ”strong” conformism” and to $0 < \alpha < 1$ as ”weak” conformism. Similarly I will refer to ”weak” and ”strong” anti-conformism to cases with $-1 < \alpha < 0$ and $\alpha \leq -1$, respectively.

3 Dynamics

In this section I characterize the rest points of the dynamic system (3) and analyze the long run implications of the different types of conformism/anti-conformism.

The system (3) can be written, after subtracting $x_i(t)$ from both sides, substituting
(5) in and eliminating the time indexes, as

$$
\Delta x_i = \lambda \left( \frac{v_i x_i^\alpha}{\sum_{j \in K} v_j x_j^\alpha} \sum_{j=1}^k (1 - p_j) x_j - x_i (1 - p_i) \right), \quad i = 1, 2, \ldots, k.
$$

(7)

The ratio between a variant’s scale value and the probability that it can be changed,

$$
f_i = \frac{v_i}{1 - p_i} \geq 0
$$

will play an important role. I shall refer to (8) as variant $i$’s fitness. Note that a variant can be ”fit” either because it is attractive, i.e has a high value $v$ or because it is difficult to change, i.e, has a high $p$. As we will see in the next results, only when the popularity weights are linear ($\alpha = 1$) will the variant(s) with the highest fitness take over the whole population.

The following proposition shows that there is a unique steady states in which all existing variants have positive shares. Its corollary shows that when $\alpha \in \mathbb{R}^{++} \setminus \{1\}$ the system has $\sum_i \binom{k}{i}$ rest points.

**Proposition 1.** Assume $p_i \in [0, 1)$ for all $i$ and $\alpha \neq 1$. The interior state $x^*$

$$
x_i^* = \frac{f_i^{1/\alpha}}{\sum_{j \in K} f_j^{1/\alpha}} \quad \forall i \in K
$$

(9)
is the unique rest point with full support in $K$.

**Proof.** Assume that $x^*$ is an interior rest point with full support. It follows from (7) that in a rest point

$$
x_i^* = \left( \frac{\sum_{j \in K} (1 - p_j) x_j^*}{\sum_{j \in K} x_j^{*\alpha} v_k} \right)^{1/\alpha} f_i^{1/\alpha}, \quad \forall i \in K
$$

(10)

summing over $K$ and rearranging I get,

$$
\left( \frac{\sum_{j \in K} (1 - p_j) x_j^*}{\sum_{j \in K} x_j^{*\alpha} v_j} \right)^{1/\alpha} = \frac{1}{\sum_{j \in K} f_j^{1/\alpha}}.
$$

(11)

Substituting (11) in (10) yields (9). Q.E.D.
Corollary 1. Assume that $\alpha \in \mathbb{R}^{++} \setminus \{1\}$, and consider any non empty subset $\bar{K} \subseteq K$,

$$x_i^* = \frac{f_i^{\frac{1}{1-\alpha}}}{\sum_{j \in K} f_j^{\frac{1}{1-\alpha}}}, \forall i \in \bar{K} \text{ and }$$  \hspace{1cm} (12) \\

$$x_i^* = 0, \forall i \notin \bar{K}$$  \hspace{1cm} (13)

is the unique rest point with full support in $\bar{K}$. There are $\sum_{i=1}^{k} \binom{k}{i}$ non empty subsets of $K$.

Proof. For $\alpha > 0$ $\Delta x_i = 0$ whenever $x_i = 0$. Proposition 1 applies to any non empty subset $\bar{K} \subseteq K$, provided $\alpha > 0$. Q.E.D.

When $\alpha = 1$, interior rest points will exist if there are at least two variants with the same ratio $(1-p)/v$ as the following proposition shows.

Proposition 2. Assume $\alpha = 1$ and that $x^*$ is an interior rest point, then

$$f_i = f_j$$

for all $i$ and $j$ in the support of $x^*$.

Proof. Assume that $\alpha = 1$ and let $x^*$ be a rest point with support $\bar{K} \subseteq K$. It follows from (7) that in a rest point

$$f_i = \frac{\sum_{j \in K} v_j x_j^*}{\sum_{j \in K} (1-p_j) x_j^*} \text{ for all } i \in \bar{K},$$

Q.E.D.

The reminder of the section is devoted to characterizing the long run behaviour. As it will become clear the qualitative results depend mainly on the values of $\alpha$. Only when $\alpha \leq -1$ do the actual values of $\lambda$ and $p$ play a role, so that for the same values of $\alpha$ both convergence to $x^*$ or divergence can be observed, depending on the values of $\lambda$ and $p$.

It is useful to define the ratio,

$$y_i(t) = \frac{x_i(t)}{x_i^*}.$$  \hspace{1cm} (14)
which is a measure of the deviation from the equilibrium value (9). Note that when $x = x^*$, $y_i = 1$ for all $i$ but if $x \neq x^*$ then $y_i > 1$ for at least one $i$ and $y_j < 1$ for at least one $j$.

The following two sets will prove useful for our results:

$$\bar{M}(x; x^*) = \{i \in K / y_i \geq y_j \forall j \in K\} \quad (15)$$

and

$$\underline{M}(x; x^*) = \{i \in K / y_i \leq y_j \forall j \in K\}. \quad (16)$$

Only when $x = x^*$ do the two sets coincide and are equal to $K$. Moreover $y_i \geq 1$ for all $i \in \bar{M}$ and $y_i \leq 1$ for all $i \in \underline{M}$.

As a preliminary step I analyze the extreme case with $p_i = 0$ for all $i$ and $\lambda = 1$. Values of $\lambda$ smaller than unity introduce inertia in the system (see eq. (7)) without changing the equilibrium values. Increases in $p_i \in (0, 1)$ not only introduce inertia but may also change the equilibrium values (9).

Assuming $p_i = 0$ for all $i$ and $\lambda = 1$ renders our dynamics equivalent to those of a given population of adults who change their traits responding to the popularity of the traits in the previous period, namely

$$x_i(t+1) = \frac{v_ix_i(t)^\alpha}{\sum_{j \in K} v_jx_j(t)^\alpha}, i = 1, 2, \ldots, k. \quad (17)$$

Dividing both sides by $x_i^*$ and multiplying and dividing the denominator by $x_j^*$ gives

$$y_i(t+1) = \frac{y_i(t)^\alpha}{\sum_{j=1}^{k} y_j(t)^\alpha v_j^{1-\alpha}}. \quad (18)$$

It is now easy to show the following lemma.

**Lemma 1.** Assume $p_i = 0$ for all $i$, $\lambda = 1$ and $x(0) \neq x^*$. Then,

a) $$\bar{M}(x(t+1); x^*) = \underline{M}(x(t); x^*) \quad \text{and} \quad \underline{M}(x(t+1); x^*) = \bar{M}(x(t); x^*)$$

$\forall \alpha < 0$.

b) $$\bar{M}(x(t+1); x^*) = \bar{M}(x(t); x^*) \quad \text{and} \quad \underline{M}(x(t+1); x^*) = \underline{M}(x(t); x^*)$$
∀\alpha \in \mathbb{R}^+ \setminus \{1\}.

c) 
\[ y_i(t+2) > y_i(t) \text{ and } y_j(t+2) < y_j(t) \]
∀|\alpha| > 1, all \( i \in \bar{M}(x(t); x^*) \) and all \( j \in M(x(t); x^*) \)

d) 
\[ y_i(t+2) < y_i(t) \text{ and } y_j(t+2) > y_j(t), \forall t \]
∀|\alpha| < 1, all \( i \in \bar{M}(x(t); x^*) \) and all \( j \in M(x(t); x^*) \)

d) 
\[ y_i(t+2) = y_i(t) \]
when \( \alpha = -1 \)

Proof. \( x(t+2) \), can be written as
\[ x_i(t + 2) = \frac{x_i(t+1)\alpha v_i}{\sum_{j=1}^{k} x_j(t+1)\alpha v_j} = \frac{x_i(t)\alpha^2 v_i^{1+\alpha}}{\sum_{j=1}^{k} x_j(t)\alpha^2 v_j^{1+\alpha}} \tag{19} \]
or equivalently as,
\[ y_i(t + 2) = \frac{y_i(t)\alpha^2}{\sum_{j=1}^{k} x_j^* y_j(t)\alpha^2}. \tag{20} \]
a) and b) follow from (18), c) and d) from (20) and d) from (19). Q.E.D.

Lemma 1 shows: i) when \( \alpha < -1 \) the long run dynamics exhibits oscillations which tend to the boundaries, ii) when \( \alpha = -1 \) the system oscillates between \( x(0) \) and \( x(1) \), iii) initial conditions matter when \( \alpha > 1 \) and the variant with the highest \( y_i(0) \) will take over the whole population and iv) only when \( \alpha \in (-1, 1) \) is the long run distribution independent of the initial conditions.

Using the results of lemma 1 we can now characterize the long runs distribution of traits for all values of \( \alpha, \lambda \) and \( p \).

**Proposition 3.** Assume that agents adopt cultural traits according to (5) and that \( x(0) \neq x^* \). Then,

a) Conformism in its strong form \( (\alpha \geq 1) \) always leads to cultural homogeneity. The variant which is actually selected depends on the initial conditions when \( \alpha > 1 \) and it is the one with the highest fitness when \( \alpha = 1 \).
b) Conformism and anti-conformism in their weak form ($|\alpha| < 1$) lead always to plural societies, the share of each trait in the long run is given by (9).

c) Strong anti-conformism $\alpha \leq -1$ is compatible with plural stable societies given by (9) as well as with frequent cultural changes.

Proof. See Appendix.

Proposition 3 states that strong conformism is incompatible with cultural pluralism and that weak conformism and weak anti-conformism always lead to coexistence of cultural variants, the shares in equilibrium being larger for those variants with the highest fitness ratio (8), that is, variants which are more attractive (high $v$) and/or more difficult to change (high $p$). Higher $p$’s lead to stronger inertia in the system and to convergence to the interior equilibrium (9) when agents are strongly anti-conformist. The same is true if there is little turn over in the population, i.e. when $\lambda$ is small. When neither of these conditions applies, strong anti-conformism will result in drastic changes, with a new variant coming along every six months just to die six months later.

Figure 4 shows, in a 2 variant case, how changing $p$ and/or $\lambda$ modifies the dynamic behaviour when anti-conformism is strong (result c)). The black circles correspond to $\lambda = 1$, $p_1 = p_2 = 0$ and $v_1 = v_2$, in this case Lemma 1 applies and the system oscillates between the state in which all have variant 1 and the state in which all have variant 2. The triangles and squares correspond to increases in both $p$’s such that $p_1 = p_2$ (this is equivalent to a decrease in $\lambda$). These changes lead to convergence to the equilibrium $(x^*_i = 1/2, i = 1, 2)$, the triangles corresponds to smaller increases in the $p$’s. Finally, the white circles correspond to a larger increase in $p_1$ than in $p_2 > 0$ so that there is not only convergence but also a change in the equilibrium value, with variant 1 having a larger share, not because it is more attractive but because it is more permanent. Making the revision of traits more difficult facilitates convergence to a plural society when agents are strongly anti-conformist.

4 Diffusion

The model has clear-cut predictions concerning the diffusion of new variants. It follows from Proposition 3 that variants with higher fitness $f$ will spread in a world which is not too conformist, and this is true irrespective of the initial conditions. When agents are strong conformists initial conditions matter and new variants may need large initial
shares in order to grow in the population. In order to see this, assume that $\alpha > 1$ and that there are only two possible variants, $i$ and $j$ and that initially the population is homogeneous with all agents having variant $j$. Variant $i$ will spread if its share $x_i$ is larger than

$$x_i^* = \frac{f_i^{\frac{1}{1-\alpha}}}{f_i^{\frac{1}{1-\alpha}} + f_j^{\frac{1}{1-\alpha}}} = \frac{1}{1 + R_{ji}^{\frac{1}{1-\alpha}}}$$  \hspace{1cm} (21)$$

where $R_{ji}$ is the ratio $f_j/f_i$.

The value (21) defines the invasion barrier or the minimum threshold needed for
the variant $i$ to invade a population in which everybody has variant $j$. For any given $R_{ji} < 1$, the invasion barrier is larger the larger is $\alpha$, and given $\alpha$ it is larger the larger $R_{ji}$. This is illustrated in Figure 5. On the horizontal axes I have plotted the ratio $R_{ji}$, ranging from 0 to 1. Each curve corresponds to a different degree of conformism $\alpha$. I have taken values equal to $\frac{3}{2}$ (dashed line), 2 (thin line) and 3 (thick line). All three lines coincide when the two variants are equally fit ($R_{ji} = 1$), in this case the invasion threshold is $\frac{1}{2}$: in order to be invaded by a variant which is as fit as the existing one, at least $50\%$ of the population must adopt the new variant. A variant which is twice as good as the existing one ($R_{ji} = \frac{1}{2}$) has thresholds of $20\%$, $34\%$ and $42\%$ for $\alpha$ equal to $\frac{3}{2}$, 2 and 3, respectively.

Weak conformism does not impose any barrier to the invasion of new variants and is compatible with the S-shaped diffusion curves (stars in Figure 6). Independence does not impose any invasion barrier but does not generate the empirically obtained diffusion curves (squares in Figure 6), nor does anti-conformism (see Figure 4).

Figure 6: Diffusion curves: weak conformism (stars) and independence (squares)

5 Conclusion

I have presented a model of cultural evolution that introduces conformism in a random choice model. Cultural pluralism will be the long run outcome unless agents are strong conformists. The long run shares depend not only on the conformist parameter $\alpha$ but also on the agents ”independent” preferences and on the probability that they can be
changed. The last two parameters determine the fitness ratio of a variant, the larger the ratio the larger the long run share. Under weak conformism variants vanish not because of the strength of conformism but because they are unattractive or difficult to keep. Variants which render existing ones less desirable will, under weak conformism, spread at expenses of the worse one the way the computer has done with the typewriter, the latter being at the verge of extinction only used by old agents who have it difficult to adapt to the new technologies.

References


A Appendix

Proposition 3

Proof. a) when $\alpha = 1,$

$$\Delta x_i = \lambda v_i x_i \left( \frac{\sum_{j \in K} \frac{(1 - p_j)x_j}{v_j x_j}}{\sum_{j \in K} v_j x_j} - \frac{1 - p_i}{v_i} \right) \text{ for } i = 1, 2, ..k.$$ 

Note that the first term in the bracket is the same for all variant and only the variant with the smallest $r_i$ can have positive shares in the long run.
Assume now that \( \alpha > 1 \)

\[
\Delta x_i = \lambda \left( \frac{x_i^{\alpha} v_i}{\sum_{j=1}^{k} x_j^{\alpha} v_j} \sum_{j=1}^{k} (1 - p_j) x_j - x_i(1 - p_i) \right) =
\]

\[
\lambda \frac{x_i^{\alpha} v_i}{\sum_{j=1}^{k} x_j^{\alpha} v_j} \left( \sum_{j=1}^{k} (1 - p_j) x_j - \frac{x_i(1 - p_i) \sum_{j=1}^{k} x_j^{\alpha} v_j}{x_i^{\alpha} v_i} \right)
\]

\[
= \lambda \frac{x_i^{\alpha} v_i}{\sum_{j=1}^{k} x_j^{\alpha} v_j} \sum_{j=1}^{k} (1 - p_j) x_j \left( 1 - \frac{f_i x_i^{1-\alpha}}{f_j x_i^{1-\alpha}} \right)
\]

where \( f_i = (1 - p_i)/v_i \). Since \( x_j \leq 1 - x_i \) for all \( j \), and \( f_j \geq f_{\min} = \min_i(1 - p_i)/v_i \), I can set an upper limit to the term in the last bracket,

\[
\frac{f_i x_i^{1-\alpha}}{f_j x_i^{1-\alpha}} \leq \frac{f_i (1 - x_i)^{\alpha-1}}{f_j x_i^{\alpha-1}} \leq \frac{f_i}{f_{\min}} (1 - x_i)^{\alpha-1}.
\]

Then \( \Delta x_i > 0 \) whenever

\[
x_i(t) \geq \frac{f_i^{1/\alpha}}{f_i^{1/\alpha} + f_{\min}^{1/\alpha}}
\]

if it hold for \( t \), it also holds for \( t + 1 \), and \( \lim_{t \to \infty} x_i(t) = 1 \).

b) 

\[
x_i(t + 1) = (1 - \lambda) x_i(t) + \lambda p_i x_i(t) + \lambda \frac{x_i(t)^{\alpha} v_i}{\sum_{j=1}^{k} x_j(t)^{\alpha} v_j} \sum_{j=1}^{k} x_j(t)(1 - p_j)
\]

dividing by \( x_i^{*} \) and multiplying and dividing by \( x_j^{*} \)

\[
y_i(t + 1) = (1 - \lambda(1 - p_i)) y_i(t) + \lambda \frac{y_i(t)^{\alpha} v_i x_i^{*^{\alpha-1}}}{\sum_{j=1}^{k} x_j(t)^{\alpha} v_j} \sum_{j=1}^{k} x_j(t)(1 - p_j)
\]

\[
= (1 - \lambda(1 - p_i)) y_i(t) + \lambda \frac{y_i(t)^{\alpha} v_i x_i^{*^{\alpha-1}}}{\sum_{j=1}^{k} y_j(t)^{\alpha} x_j^{*^{\alpha-1}}} \sum_{j=1}^{k} y_j(t)(1 - p_j)^{\alpha} x_j^{*}
\]

\[
= (1 - \lambda(1 - p_i)) y_i(t) + \lambda \frac{y_i(t)^{\alpha} (1 - p_i)}{\sum_{j=1}^{k} y_j(t)^{\alpha} v_j^{1-\alpha} (1 - p_j)^{\alpha}} \sum_{j=1}^{k} y_j(t) v_j^{1-\alpha} (1 - p_j)^{\alpha-1}
\]
Assume that $x(t) \neq x^*$. And let $y_m = \max_j y_j(t)$. Substituting $y_m$ on both sides

$$y_i(t+1) - y_m = (1 - \lambda(1 - p_i))(y_i(t) - y_m) +$$

$$\lambda(1 - p_i)(y_i(t)^\alpha \sum_j y_j(t) v_j^{\frac{1}{\alpha}} (1 - p_j)^{\frac{1}{\alpha - 1}} - y_m)$$

$$= (1 - \lambda(1 - p_i))(y_i(t) - y_m) +$$

$$\lambda \sum_j (1 - p_j)^{\frac{\alpha}{\alpha - 1}} y_j(t) v_j^{\frac{1}{\alpha - 1}}$$

$$\times (y_i(t)^\alpha \sum_j v_j^{\frac{1}{\alpha}} (1 - p_j)^{\frac{\alpha}{\alpha - 1}} y_j(t)^\alpha y_j(t)^{1 - \alpha} - y_m)$$

$$= (1 - \lambda(1 - p_i))(y_i(t) - y_m) + \lambda \sum_j (1 - p_j)^{\frac{\alpha}{\alpha - 1}} y_j(t) v_j^{\frac{1}{\alpha - 1}}$$

$$\times \sum_k (1 - p_j)^{\frac{\alpha}{\alpha - 1}} v_j^{\frac{1}{\alpha - 1}} y_j(t)^\alpha \left( \frac{y_j(t)}{y_m} \right)^{1 - \alpha} - \left( \frac{y_i(t)}{y_m} \right)^\alpha - 1$$

For $\alpha \in [-1, 1)$ $y_i(t+1) - y_m < 0$ for all $i$. This proves convergence.

d) (7) can be written as

$$\Delta x_i = \lambda(1 - p_i) \left( \frac{v_i x_i^\alpha}{\sum_{j \in K} v_j x_j^\alpha} \sum_j (1 - p_j) x_j \right) - x_i, \ i = 1, 2, \ldots, k. \ \ (A.1)$$

Note that when $p_i = p$ for all $i$, these dynamics have the same sign, but smaller (absolute) values as those characterized in Lemma 1. For large enough $p$ or $\lambda$ the system converges for $\alpha \leq -1$.

Q.E.D.