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Electronic appendices are refereed with the text. However, no attempt has been made to impose a uniform editorial style on the electronic appendices.

## **Electronic Appendix A – Model Development**

The phenomenological model developed below tracks how cultural identity and group membership change through time following the onset of exposure to novel cultural markers. The model does not explicitly incorporate the psychological conditions leading to particular social behaviours, but rather assumes that these mechanisms have evolved in the past to protect group integrity and maintain cooperation. Within-group cooperation is the basis of selection in the model, whereby novel cultural markers are counter-selected, thereby increasing within-group marker similarity and promoting cultural ideals.

Theory suggests that markers may serve as honest signals, employed in making decisions of whether or not to cooperate in social interactions (e.g., Sherratt & Roberts 1998; Hochberg et al. 2003). As such, a culture is an ensemble of individual members with aligned common interests and when faced with defectors, competing individuals or competing groups, the establishment, integration and protection of markers and their specificity will tend to be positively selected to maintain cooperation. In the large social groups envisaged in the model presented below, such cooperation could be maintained by prosocial punishment (Boyd & Richerson 1992). The general problem can be regarded as a manifestation of Hamilton's rule (Frank 1998), whereby "relatedness" is signalled by honest group-specific markers buttressed by aligned interests between similarly signalling individuals (see e.g., van Baalen & Jansen 2003). Developing formal models from first principles based on these considerations will be an important step towards a more general and robust theory of cultural change.

In the model presented here, members of a culture each are characterized by a large, unspecified number of markers. Each marker is analogous to a locus in formal population genetics. Population genetic concepts can be usefully applied to human cultures insofar as cultures are manifestations guided by laws similar to quantitative genetics, whereby cultural markers combine in some fashion to determine the “fitness” of the cultural phenogotype (Cavalli-Sforza & Feldman 1981; Gintis 2003). Quantitative genetic models, developed notably by Lande (1976) (see also Turelli & Barton 1994) assume that a phenotypic trait is influenced by a set of genes, each of minor effect. Each genetic locus controlling the trait is under weak selection, and this selection tends to push the trait towards the fitness optimum. Thus, in adopting this formalism, we do not explicitly track specific markers, but rather model their population-level changes from their ideal states. Deviations in the cultural model are analogous to mutations in genetic models.

Cultural integrity is eroded when markers change attribute from the ideal, for example following prestige-based copying, the copying individual is said to have increased his/her deviation load,  $d$ , by one unit. More generally, any individual  $i$  at time  $t$  has  $d_{it}$  markers that deviate from the cultural ideal. We denote  $d_t$  as the mean deviation load over the whole population at time  $t$ . It is assumed that individual cultural states in the population follow a normal distribution about  $d_t$ , with constant variance, normalized here to unity.

Cultural integrity is influenced by three basic processes: deviation input, selection and regeneration. First, integrity is disrupted by the constant broadcasting ( $U$ ) of unspecified alternatives to cultural markers. Alternative states to these markers correspond to specific markers from other source groups, but  $U$  could also be interpreted to include the simple probabilistic loss of specific attributes without replacement.  $U$  is the maximum increase in the mean deviation load per unit time and is assumed to be Poisson distributed. If for example  $U=0.1$ , then over a fixed time step 90.5% of individuals will remain unchanged, 9% will

increase by one deviation, 0.5% by two deviations and so forth. A constant  $U$  for the population is a reasonable assumption when large segments of a culture are exposed to external input, but would be an oversimplification for markers that spread principally by diffusion (Boyd & Richerson 2002).  $U$  may be a function of a number of processes, but given current evidence, the most likely to explain rapid evolution is prestige-based copying of other cultures (Henrich & Gil-White 2001).

Second, mean-level membership integrity is increased following selection, which acts differentially on the most deviation-loaded classes. A general function for membership loss following selection is  $W_i\{d_i\}=\exp\{-(sd_i)^x\}$  (Peck et al. 1999), where  $s$  is a constant reflecting the selective effect per marker, and the parameter  $x$  ( $x \geq 1$ ) represents the level of synergism in selection on  $d$ . Synergism means that the probability of selection occurring is an increasing function of the mean deviation load. If cultural markers are numerous, then changes in a small proportion will have negligible impacts on cultural recognition compared to the costs of recognition, selection and regeneration. Behaviourally speaking therefore, the costs of these will mean that individuals are expected to tolerate small deviation loads more than large ones. Put another way, behaviours may be selected not to react five different times to five different deviations, but rather to react once to the accumulation of five deviations. This will be expressed as lower selection to low deviation loads and higher selection to high loads, leading to selection being an increasing (linear or non-linear) function of deviation load (i.e.,  $x > 1$ ).

Third, the culture may be regenerated ( $r$ ) through dominance and prestige-based reintegration and recruitment, and vertical transmission of cultural markers from older to younger individuals. Members (re-)integrating into the culture following regeneration are assumed to have deviation loads that follow the current probability distribution in the population.

The model has two equations, one that follows the mean state of deviations from the cultural ideal and the other the population density of the culture. Deviation and population levels are assessed every  $b$  time units. An assessment begins with a regeneration phase, which is in reaction to population changes occurring  $b$  time units previously. This regeneration event is then followed rapidly by selection. For more proactive cultures,  $b$  should be very small, on the scale of days or weeks, whereas for retroactive tendencies or cultures making more seasonal or event-related assessments, the scale would be months to years.

With these assumptions in mind, the basic equation for cultural change from time step  $t$  to  $t+b$  is

$$d_{t+b} - d_t = U + D_t \{N_t\} [\partial \ln W_t / \partial d]. \quad [A1]$$

Deviations, although each having a slightly negative effect expressed through the quantity  $\partial \ln W_t / \partial d$ , may propagate simply because selection does not act fast enough to curb input,  $U$ . A second force included in equation [1] that may limit the efficiency of selection is drift,  $D_t$ , which is approximated by  $D_t \{N_t\} = \rho N_t / (1 + \rho N_t)$  (Lynch et al. 1993). The constant parameter  $\rho$  scales population density  $N_t$  into population numbers meaning  $\rho N_t \geq 0$ . Note that as  $\rho$  and/or  $N_t$  decreases, selection still operates on the highest deviation classes, but in addition, some of the lowest deviation classes go stochastically extinct, resulting in less effective selection.

The population equation makes no explicit assumptions regarding the exact fate of individuals, but rather tracks only the density of the reference culture ( $N$ ). I employ a modification of the Ricker model (Ricker 1954) to describe the effects of selection and regeneration, whereby density changes from time step  $t$  to  $t+b$  as

$$\ln \{N_{t+b}/N_t\} = r (1 - N_t) - W_t. \quad [A2]$$

The full model therefore has five parameters ( $\rho, r, x, s, U$ ).  $\rho$  is population numbers,  $r$  is the natural logarithm of the maximum fractional increase in population density,  $x$  is a

dimensionless constant, and  $s$  and  $U$  are in units of mean deviations.  $r$ ,  $s$  and  $U$  are scaled to the length of the assessment period,  $b$ .

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