Supporting Information for ‘Migration, acculturation, and the maintenance of between-group cultural variation’

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S1 Results

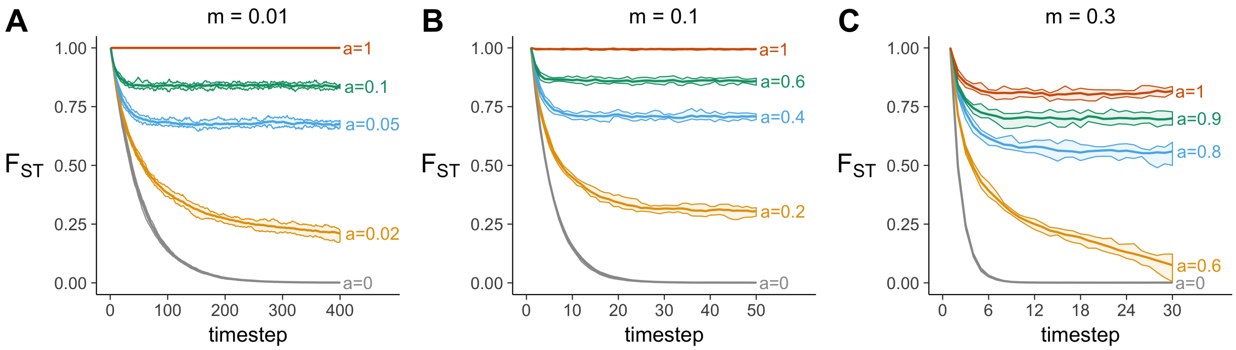
Individual-based version of Model 1

In order to verify the recursion-based models that track trait frequencies, I created analogous individual-based models in which individuals and their traits are explicitly simulated. These individual-based models have the same assumption of s sub-populations and s traits. Now, however, we specify the number of individuals in each sub-population, N. This is different to n, which is the number of demonstrators sampled during conformist acculturation. n is also implemented in the individual-based models, so individuals pick n demonstrators from the N members of their sub-population (so $n \leq N$). The individual-based simulations start with the same complete between-group structure as the recursion models, i.e. all N individuals in sub-population 1 have trait 1, all N individuals in sub-population 2 have trait 2, etc. F_{ST} is calculated in the same way as for the recursion-based model after calculating overall trait frequencies from individuals' traits. Migration occurs in the same way as the island model. Every time-step, each individual moves to a common migrant pool with probability m, and then randomly disperses across the newly vacant spots ignoring sub-population structure. Conformist acculturation is implemented slightly differently. Following all migration, each individual chooses n demonstrators from within their sub-population, and with probability a adopts the most common trait among those n demonstrators. Otherwise they retain their existing trait. This is conceptually the same as the recursion-based conformity described above, but without the multinomial theorem implementation, thus providing a conceptual replication of conformity as implemented in the main text. For each of the n chosen demonstrators, with probability $1 - r$ that demonstrator is chosen randomly from the focal individual's sub-population. With probability r that demonstrator has the same trait as the focal individual. Consequently, when assortation parameter $r = 1$, then individuals only ever learn from demonstrators with the same trait as themselves. Parameter definitions for the individual-based model are given in S3 Table. Full code of all models is available in https://github.com/amesoudi/migrationmodels.

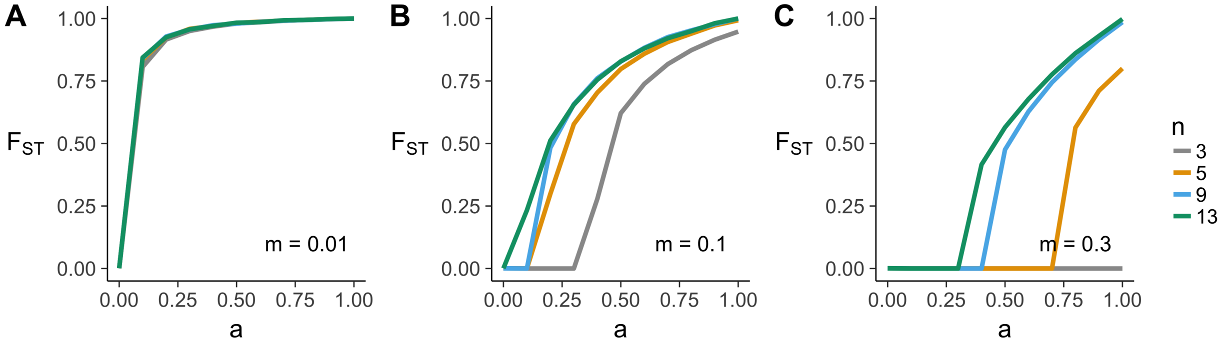
S3 Table: Parameter definitions for Model 1 individual-based simulations

Parameter	Definition
s	The number of sub-populations, and also the number of alternative cultural trait values
m	Migration rate: the probability in one time-step that an individual moves to a randomly chosen sub-population (equivalently, the proportion of the population that moves in one time-step)
n	The number of demonstrators from whom individuals learn during acculturation
a	Acculturation rate: the probability that an individual adopts the most-common trait among n demonstrators chosen from their sub-population, as opposed to retaining their existing trait. When $a = 1$, there is 100% chance of copying the most-common trait (if there is one).
N	The number of individuals in each sub-population (giving Ns individuals in the entire population)
r	The probability that a demonstrator is chosen who has the same trait as the focal individual, rather than chosen at random.

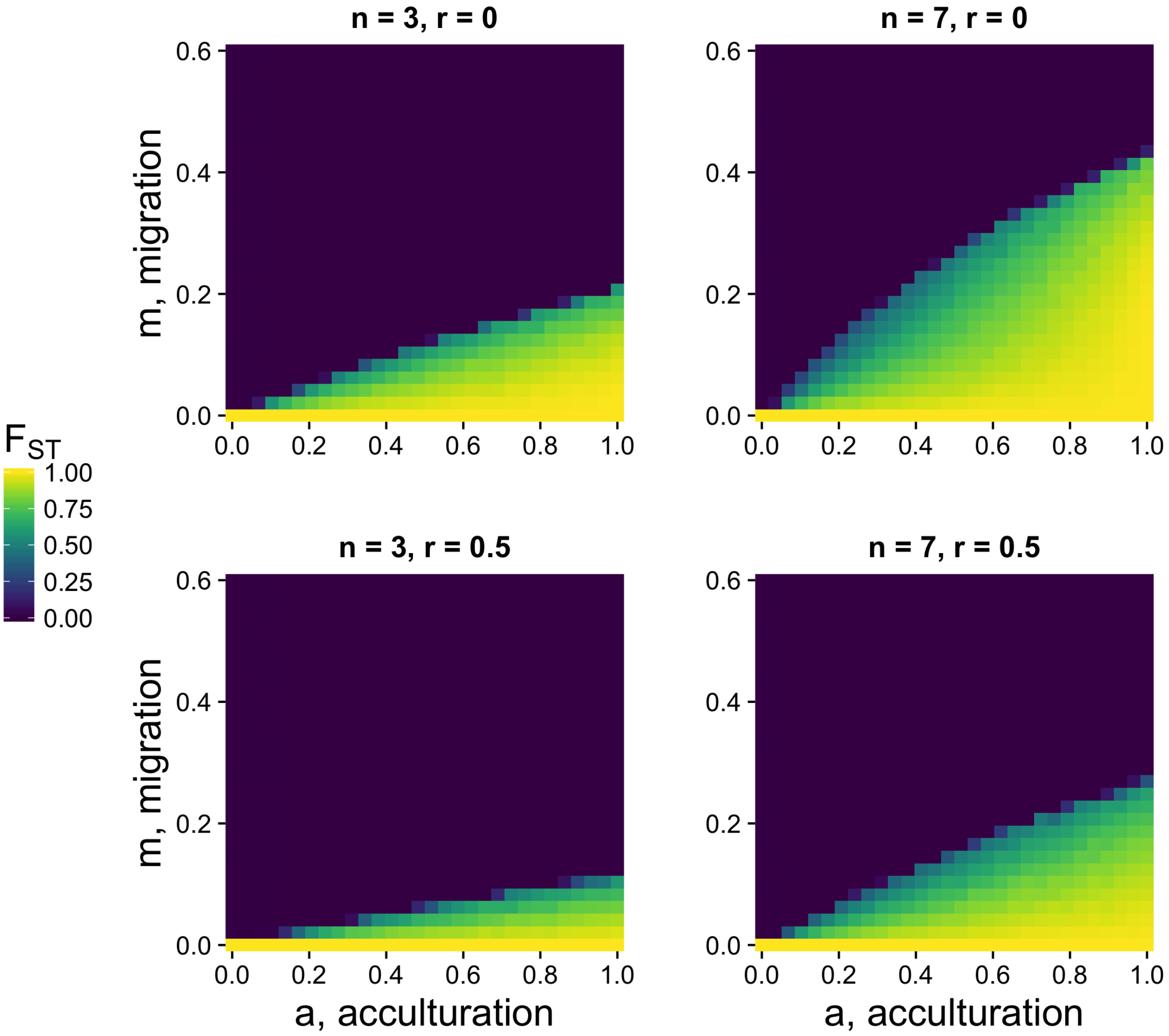
S8, S9 and S10 Figs show the individual-based model results equivalent to the recursion-based model results shown in Figs 1, 2 and 3 respectively. There is very little difference between the two models, despite their different implementation, increasing our confidence in the robustness of the conclusions. There is a slight tendency for F_{ST} to be lower in the individual-based model than the recursion-based model, especially when diversity is low (e.g. $a = 0.6$ in S8 Fig C). This may be due to drift which operates only in the finite populations of the individual-based models. If a trait is lost due to drift, then diversity will be reduced. S11 Fig repeats Fig 2 and S10 Fig but with larger n than is computationally feasible with the recursion-based model. Here we can see that increasing n above 13 does not change the dynamics, except at very low values of a when migration is very high (S11 Fig C).



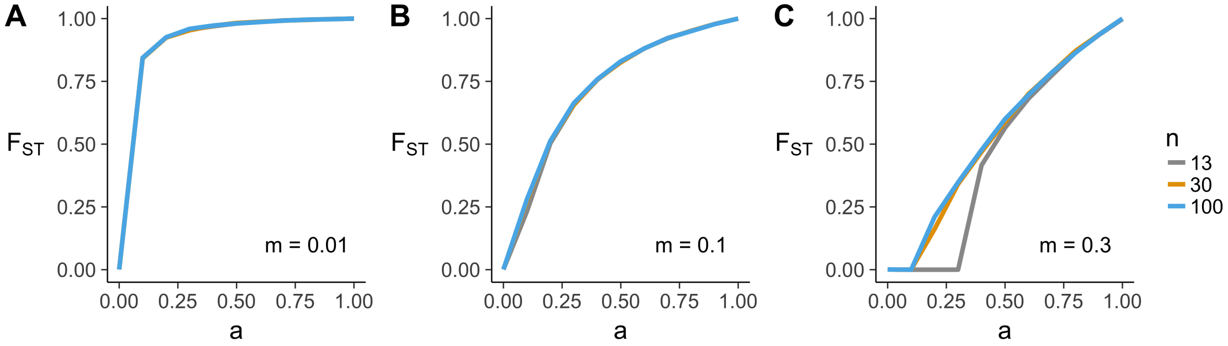
S8 Fig: Time series showing changes in F_{ST} over time for (A) a low migration rate m=0.01, (B) a moderate migration rate m=0.1, and (C) a high migration rate m=0.3, at varying strengths of acculturation, a, in the individual-based model. Other parameters: s=5, n=5, N=1000; results are the average of 10 independent simulation runs.



S9 Fig: The relationship between a and F_{ST} at three different migration rates, and different values of n, for the individual-based model. Other parameters: s=5, 500 timesteps, N=1000; results are the average of 10 independent simulation runs.



S10 Fig: Heatmap showing F_{ST} for varying acculturation rates, a, and migration rates, m, separately for three different values of n, the number of demonstrators, for the individual-based model. Other parameters: s=5, N=1000, 500 timesteps; results are the average of 10 independent simulation runs.



S11 Fig: The relationship between a and F_{ST} at three different migration rates, for three large values of n, for the individual-based model. Other parameters: s=5, 500 timesteps, N=1000; results are the average of 10 independent simulation runs.