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Computational Methods: Final project

Random change on conformity bias in cultural transmission

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Link to the Colab notebook

https://colab.research.google.com/drive/1_83UfWxwsBIH0sOiODJNC5a9mDU9bfDc?usp=sharing

I. Background literature

The evolution of a cultural trait within a society eventuates through different mechanisms. The cultural evolutionary theory identifies these mechanisms as either transmission biases (Boyd and Richerson 1985; Mesoudi 2011) or social learning strategies (Laland 2004; Rendell et al. 2011). Namely, such biases affect the rate by which a trait is adopted within a society and across generations. Researchers categorized these biases into two or more categories (Joseph Henrich and McElreath 2003; Kendal et al. 2018). Specifically, the context-based category relates to choosing a trait based on characteristics derived from the social context. Frequency-dependent biases, such as conformity and anticonformity, are its derivatives.

Conformity and anticonformity translate into the disproportionate adoption of the most common trait (Boyd and Richerson 1985; Morgan et al. 2012). The previous theoretical research (Boyd and Richerson 1985; Joe Henrich and Boyd 1998) indicates that conformity evolves under several conditions, such as environmental variables varying by time and space.

A. Temporal variation

Empirical research proved that the degree to which humans conform to a trait or behavior varies through time, sometimes moving from conformity to anticonformity and vice versa. In Acerbi & Bentley's study (Acerbi and Alexander Bentley 2014), the US baby names popularity function displayed a concave trend between 1960 and 2010, exhibiting anticonformity. On the contrary, earlier trends of male baby names, from 1880 to 1930, showed a convex turnover function indicating a conformity bias. Thus, modeling such behaviors requires implementing time-dependent conformity coefficients.

While most prior models implemented a fixed conformity coefficient along the temporal variations, some studies allowed it to toggle between conformity and anticonformity (Jędrzejewski and Sznajd-Weron 2017; Nyczka and Sznajd-Weron 2013; Nyczka, Sznajd-Weron, and Cisko 2012). Yet, none had randomized such variations of the coefficient. Hence, Denton & Liberman filled the gap. They generalized Boyd and Richerson's deterministic model (Boyd and Richerson 1985). Namely, they allowed the conformity coefficient random variation through each generation besides other modifications.

B. Spatial variation

Transmission biases such as conformity prevent migration from eliminating between-group variation. In evolutionary theory, migrants can acculturate to other groups' local behaviors through such social learning strategies. Thus, modeling the combined effect of migration and acculturation between the subgroups of a population became of interest to many researchers. One of the recent models addressing such phenomena, showed that migrating without acculturating to local behaviors eliminates between-group

variation, while conformist acculturation can maintain between-group cultural variation (Mesoudi 2018). The ability of conformity to preserve between-group variations, however, is not always true, according to a 2020 study (Kaleda Krebs Denton et al. 2020). Up to now, as stated by Denton & Liberman (Kaleda K. Denton, Liberman, and Feldman 2021), all similar models had included a non stochastic conformity coefficient.

C. Motivation, hypothesis and questions

In this study, our aim is to investigate the combined effect of migration and temporally varying conformity behavior on population dynamics. Since empirical research suggest that Denton & Liberman stochastic model (Kaleda K. Denton, Liberman, and Feldman 2021) captures reality better than nonstochastic ones, we will follow the same approach and build upon their model to capture more realistic effects of migration. We intend to compare within group trait variation, and between groups trait variation using a stochastic conformity coefficient. We hypothesize that migration hinders the acculturation rate within a subpopulation. Thus, we predict that the probability of the adoption of a trait will converge to the equilibrium faster in the absence of migration. In the following we will try to answer the following question:

- What is the combined effect of migration and temporally varying conformity behavior on population dynamics?
- In the presence of migration, does the different subgroups converge to similar or different equilibria?

II. Model description

As previously mentioned, we will follow Denton & Liberman's approach in building our model. Denton & Liberman generalization of the deterministic model of Boyd & Richerson (Boyd et Richerson 1985) comprehended mainly the random variation of the conformity coefficient, as well as increasing the number of demonstrators (role models) within a population. In our case, we will build a simplified version of their model by only implementing a stochastic conformity coefficient in the Boyd and Richersons' model where we will add the migration component and fix the number of role models to 3.

A. Model description: conformist model

Deterministic model: $p' = p + D * p * (1-p) * (2p-1)$ [1]

In Eq. 1, the D coefficient specifies the disproportionate adoption degree of the most common trait within a subpopulation; it covers both conformist and anticonformist biases, where $D > 0$ implies conformity, $D < 0$ implies anticonformity, $D = 0$ implies random copying, and $-2 < D < 1$. As the equation specifies, the same D is maintained regardless of

the generation. The probability of adopting a trait A is p while it is $1-p$ for the trait B. Then, the probability of adopting the trait A in the next generation is denoted by p' (Kaleda K. Denton, Liberman, et Feldman 2021).

Generalized model: $p_{t+1} = p_t + D_t * p_t * (1-p_t) * (2p_t-1)$ [2]

In Eq. 2, Denton & Liberman generalized Boyd & Richerson's deterministic model by allowing the D coefficient to vary randomly at each generation. The t indicates the generation number where $t = (0, 1, \dots, t_{max})$. Also, each D_t is independent of p_t in each generation t . They made the assumption that the D_t coefficient is identically distributed between -2 and 1 . While p_t is the probability of adopting the trait A in the generation t , p_{t+1} is for the next generation, $t+1$. In their model, the p_t converges to one of the three following equilibria $p^* = 0$, $p^* = 1$, or $p^* = \frac{1}{2}$, as $t \rightarrow \infty$ (Kaleda K. Denton, Liberman, et Feldman 2021).

1

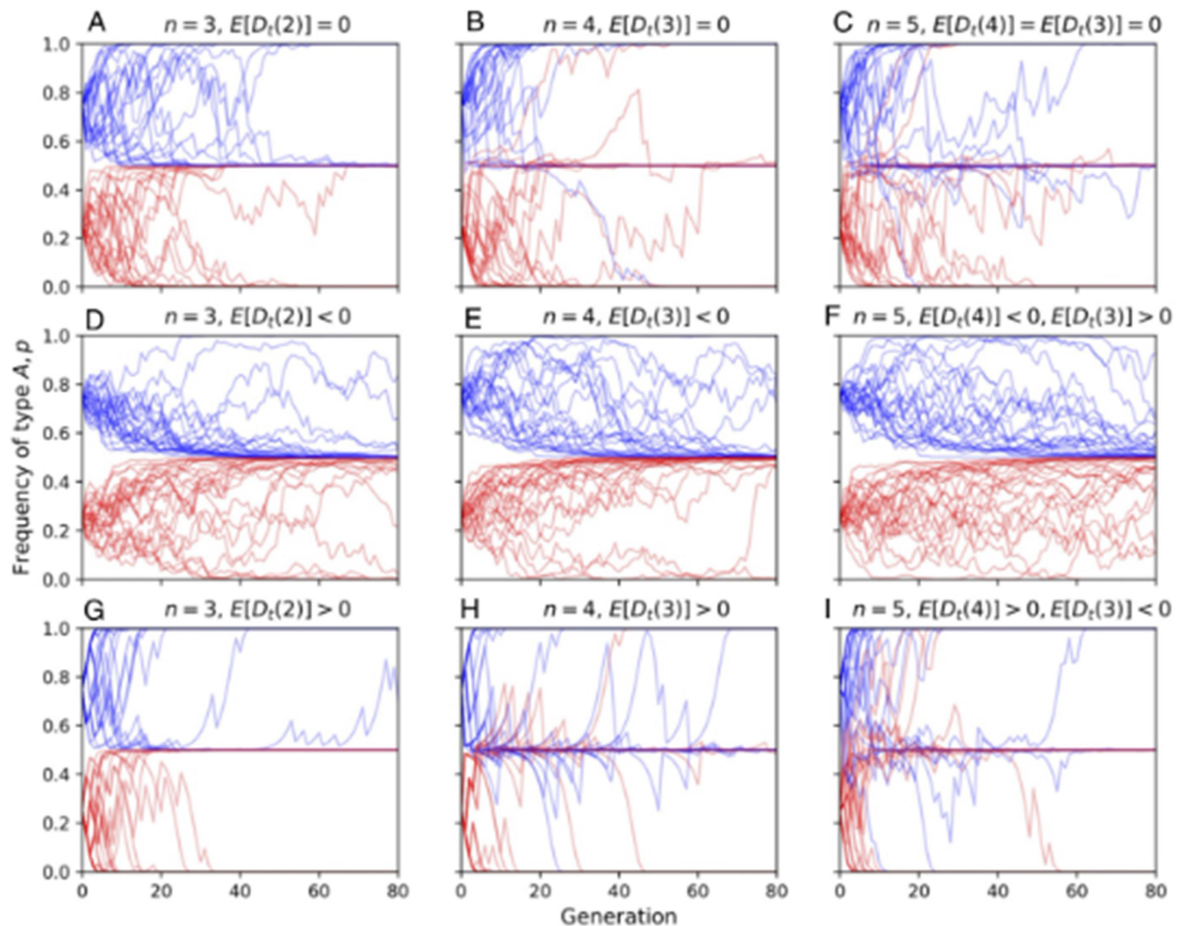


Fig. 1. Stochastic local stability of $p^* = 0, \frac{1}{2}, 1$. Each plot shows 25 runs with initial $p_0 = 0.25$ (red) and 25 runs with $p_0 = 0.75$ (blue). Eighty generations are shown, although equilibria $p^* = 0, \frac{1}{2}, 1$ may take longer to be reached; how often each equilibrium was reached is in *SI Appendix, section A* along with $E[D_t(i)]$, the mean of $\log[1 - D_t(n-1)]$, and the mean of $\log[1 + \frac{D_t(2)}{2}]$ for $n=3$. (A) $n=3$, $D_t(2) \sim U[0, 1]$ with probability $\frac{2}{3}$ and $D_t(2) \sim U[-2, 0]$ with probability $\frac{1}{3}$. (B) $n=4$, $D_t(3) \sim U[0, 1]$ with probability $\frac{2}{3}$ and $D_t(3) \sim U[-3, 0]$ with probability $\frac{1}{3}$. (C) $n=5$, $D_t(4) \sim U[0, 1]$ with probability $\frac{4}{5}$ and $D_t(4) \sim U[-4, 0]$ with probability $\frac{1}{5}$. $D_t(3) \sim U[0, 2]$ with probability $\frac{2}{5}$ and $D_t(3) \sim U[-3, 0]$ with probability $\frac{3}{5}$. (D) $n=3$, $D_t(2)$ is sampled from a truncated normal distribution on $(-2, 1)$ with mean (before truncation) -0.05 and SD 0.5 . (E) $n=4$, $D_t(3)$ is sampled from a truncated normal distribution on $(-3, 1)$ with mean (before truncation) -0.05 and SD 0.5 . (F) $n=5$, $D_t(4)$ is sampled from a truncated normal distribution on $(-4, 1)$ with mean (before truncation) -0.05 and SD 0.5 . $D_t(3)$ is sampled from a truncated normal distribution on $(-3, 2)$ with mean (before truncation) 0.05 and SD 0.5 . (G) $n=3$, $D_t(2) = 0.99$ with probability $\frac{2}{3}$ and $D_t(2) = -1.5$ with probability $\frac{1}{3}$. (H) $n=4$, $D_t(3) = 0.99$ with probability $\frac{2}{3}$ and $D_t(3) = -2.5$ with probability $\frac{1}{3}$. (I) $n=5$, $D_t(4) = 0.9$ with probability $\frac{4}{5}$ and $D_t(4) = -3$ with probability $\frac{1}{5}$. $D_t(3) = 1.5$ with probability $\frac{2}{5}$ and $D_t(3) = -2.85$ with probability $\frac{3}{5}$.

Figure 1: Denton & Liberman's stochastic model results

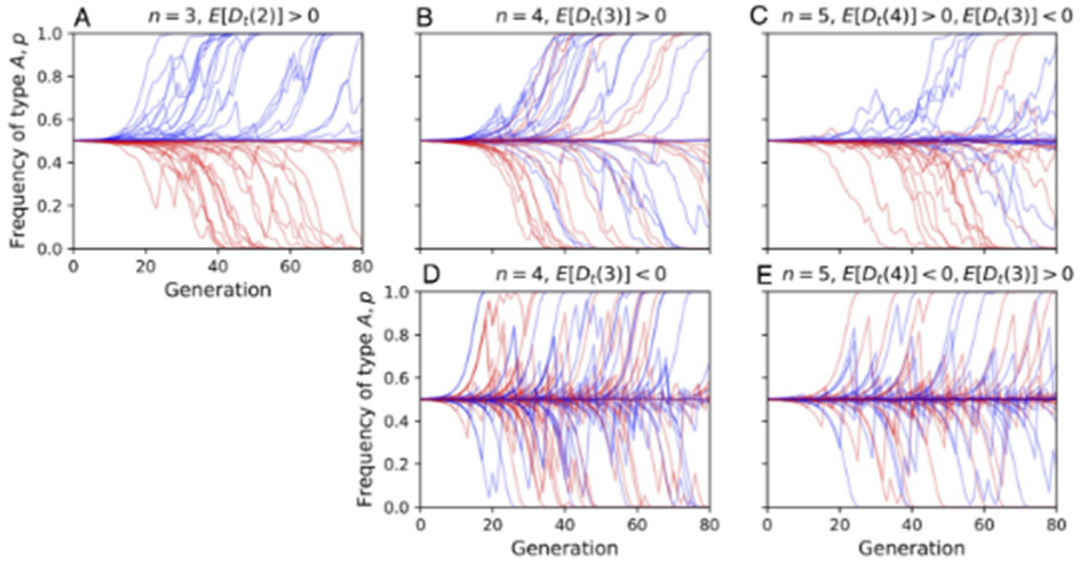


Fig. 2. Stochastic local stability of $p^* = 0, 1$ and instability of $p^* = \frac{1}{2}$. Each plot shows 25 runs with initial $p_0 = 0.499$ (red) and 25 runs with $p_0 = 0.501$ (blue). The first 80 generations are shown, although equilibria may take longer to be reached; how often each equilibrium was reached is in *SI Appendix, section A*, along with $E[D_t(j)]$, the mean of $\log[1 - D_t(n-1)]$, and the mean of $\log[1 + \frac{D_t(2)}{D_t(3)}]$ for $n=3$. (A) $n=3$, $D_t(2) \sim U[0, 1]$ with probability 0.9 and $D_t(2) \sim U[-2, 0]$ with probability 0.1. (B) $n=4$, $D_t(3) \sim U[0, 1]$ with probability 0.925 and $D_t(3) \sim U[-3, 0]$ with probability 0.075. (C) $n=5$, $D_t(4) \sim U[0, 1]$ with probability 0.98 and $D_t(4) \sim U[-4, 0]$ with probability 0.02. $D_t(3) \sim U[0, 2]$ with probability 0.55 and $D_t(3) \sim U[-3, 0]$ with probability 0.45. (D) $n=4$, $D_t(3) = 0.99$ with probability $\frac{3}{4}$ and $D_t(3) = -2.99$ with probability $\frac{1}{4}$. (E) $n=5$, $D_t(4) = 0.99$ with probability $\frac{3}{4}$ and $D_t(4) = -3.99$ with probability $\frac{1}{4}$. $D_t(3) = 0.1$ with probability $\frac{3}{4}$ and $D_t(3) = -0.1$ with probability $\frac{1}{4}$.

Figure 2: Denton & Liberman stochastic model results 2

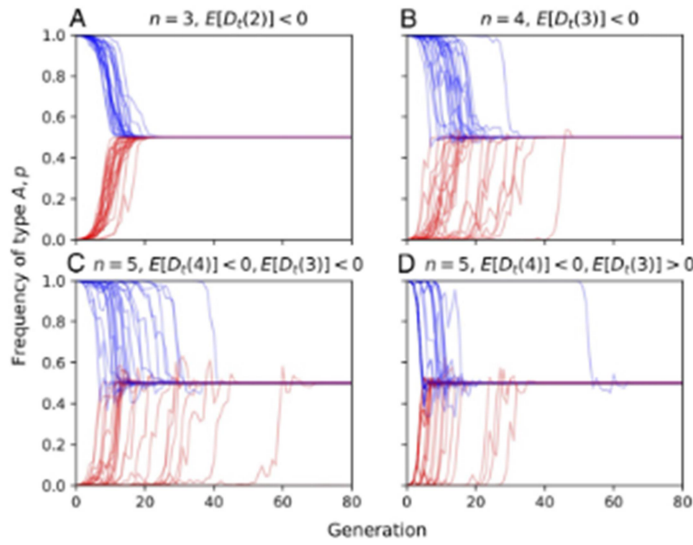


Fig. 3. Stochastic local stability of $p^* = \frac{1}{2}$ and instability of $p^* = 0, 1$. Each plot shows 25 runs with initial $p_0 = 0.001$ (red) and 25 runs with $p_0 = 0.999$ (blue). The equilibrium $p^* = \frac{1}{2}$ is reached in every case, although only the first 80 generations are shown and this equilibrium may take longer to be reached. *SI Appendix, section A* reports $E[D_t(j)]$, the mean of $\log[1 - D_t(n-1)]$, and the mean of $\log[1 + \frac{D_t(2)}{D_t(3)}]$ for $n=3$. (A) $n=3$, $D_t(2) \sim U[0, 1]$ with probability 0.05 and $D_t(2) \sim U[-2, 0]$ with probability 0.95. (B) $n=4$, $D_t(3) \sim U[0, 1]$ with probability 0.25 and $D_t(3) \sim U[-3, 0]$ with probability 0.75. (C) $n=5$, $D_t(4) \sim U[0, 1]$ with probability 0.4 and $D_t(4) \sim U[-4, 0]$ with probability 0.6. $D_t(3) \sim U[0, 2]$ with probability 0.1 and $D_t(3) \sim U[-3, 0]$ with probability 0.9. (D) $n=5$, $D_t(4) = -3.9$ with probability $\frac{3}{4}$, $D_t(4) = 0.9$ with probability $\frac{1}{4}$, $D_t(3) = 0.9$ with probability $\frac{3}{4}$, and $D_t(3) = -1.9$ with probability $\frac{1}{4}$.

Figure 3: Denton & Liberman stochastic model results 3

B. Model description: migration model

Description of Wright's island model (Hartl and Clark 1997; Wright 1931) as stated in Alex Mesoudi's paper (Mesoudi 2018):

“Assume a large population divided into equally sized and partially isolated sub-populations. Consider a trait that has mean frequency across the entire population of \bar{p} . Every timestep, each individual migrates with probability m . Migration is random and simultaneous, such that a proportion m of individuals is randomly removed, and this pool of migrants is randomly allocated across all newly-vacant spots in the entire population. Hence a proportion m of individuals in each sub-population will be immigrants, taken from a pool with trait frequency \bar{p} . Consider a particular sub-population in which the frequency of the trait before and after migration is p and p' respectively. For a randomly chosen trait in this sub-population, the trait either came from a non-migrant with probability $1-m$, with the frequency among those non-migrants p , or from a migrant with probability m , with the frequency among those migrants being \bar{p} . The overall frequency after migration is therefore (Hartl and Clark 1997; Wright 1931):

$$p' = p(1 - m) + \bar{p} * m$$

We are interested in how migration breaks down, and acculturation prevents the break down, of between-group cultural variation. Assume therefore that initially there is complete between-group cultural variation, and no within-group variation. Consequently, assume s cultural traits, and at time $t = 0$ all individuals in sub-population 1 have trait 1, all individuals in sub-population 2 have trait 2, and so on.”

C. Model description: combined model

In our model we implement the migration component to the conformist model and specify three locations where the members of the population migrate.

Parameter	Description
N	Number of population agents
p_a	Probability of adopting the trait A
m	Proportion of agents migrating from one subpopulation to another
t_{max}	Number of generations
r_{max}	Number of model simultaneous runs
D	The conformity coefficient

Before $t = 0$, we assume that there are two traits, A and B, and each population agent initially exists in one of the three locations: AA, BB, and CC. At $t = 0$, a randomly and simultaneously selected proportion of m of agents migrates from their location to another one. After migrating, each immigrant is exposed to a different set of three demonstrators randomly picked from their new site. When all demonstrators have the trait A, we set it to A with $p_a = 1$. When all demonstrators are B, we set to B with $1 - p_a$ where $p_a = 0$. When $2/3$ of the demonstrators have A or B, we set it to A with $p_a = (2/3) + (D/3)$ or B with $1 - p_a$ where $p_a = 1 - (2/3) + (D/3)$ respectively, with $-2 < D < 1$. If $1/3$ of the demonstrators have A or B, we set to A with $p_a = (1/3) - (D/3)$ or B with $1 -$

p_a where $p_a = 1 - (1/3) - (D/3)$ respectively. When the $0.5 < D \leq 1$, the new trait will be more likely the majority trait in the different combinations of demonstrators, and the minority trait otherwise.

III. Results

A. Without migration: Within-group variation

When $m = 0$ & $p_a = 0.75$ & $N = 1000$:

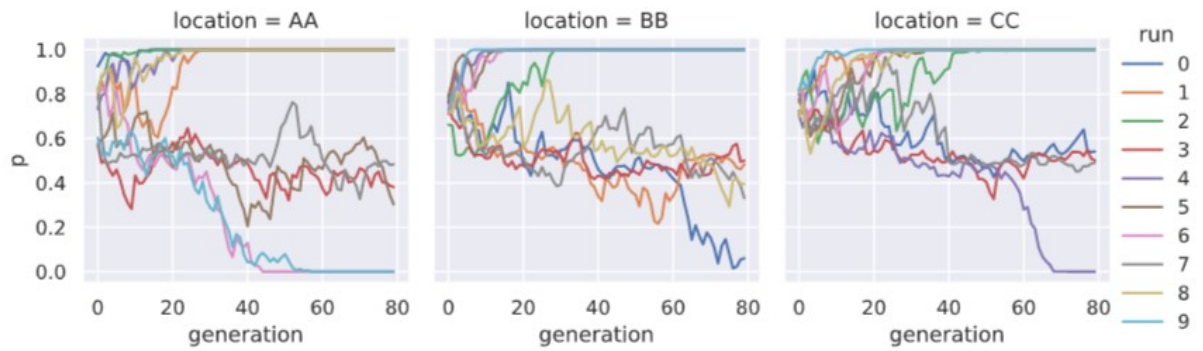


Figure 4: Conformist copying without migration

B. With migration: Between-group variation

- When $m = 0.5$ & $p_a = 0.75$ & $N = 1000$:

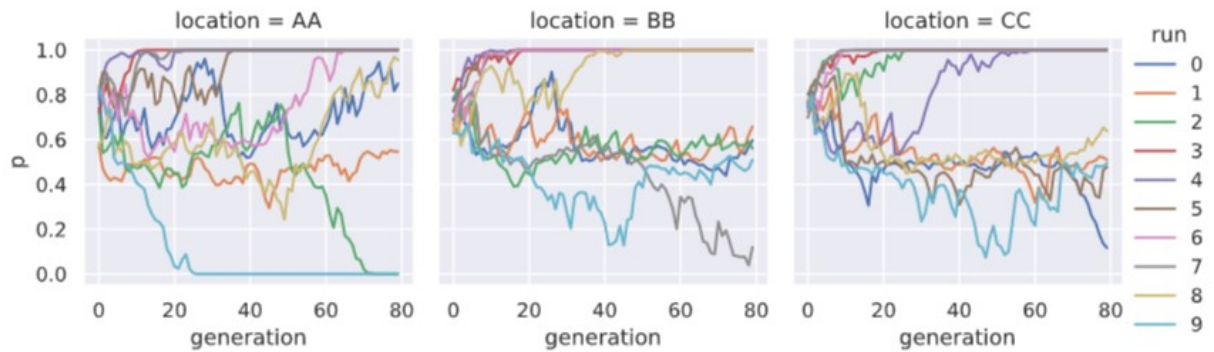


Figure 5: Conformist copying with $m = 0.5$

- When $m = 1$ & $p_a = 0.75$ & $N = 1000$:

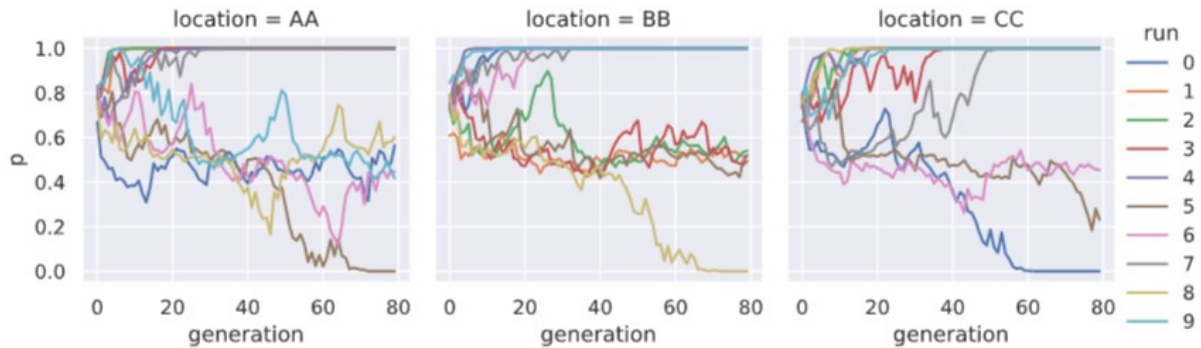


Figure 6: Conformist copying with $m = 1$

C. General comment

- The equilibriums in all three models were mainly 0, 0.5, or 1.
- There is one or more stable equilibrium.
- No significant differences between within-group and between-group variations.

IV. Discussion

So far, we have replicated Denton & Liberman's generalized model results (Kaleda K. Denton, Liberman, et Feldman 2021). The model converged around the three equilibria $p^* = 0$, $p^* = 0.5$, and $p^* = 1$. However, adding the migration component didn't seem to produce significant differences from the stochastic conformist model. It was still converging to the three equilibria, and neither fixation nor convergence was detected delayed. Hence, our prediction that migration hinders the process of reaching stability didn't hold. Subsequently, there was not a significant difference between within-group and between-group variations. Namely, all the subpopulations nearly converge to the same equilibrium. A potential cause for such a result could be the fixed probability of adoption of trait A through all subpopulations, let alone the initial state of the subpopulations where they all had both traits.

In Mesoudi's model (Mesoudi 2018), the effect of migration and conformist acculturation were better captured. The initial state of subpopulations was that each one contains only one trait. At generation zero, agents start migrating. They contrasted the results of migration without acculturation model to the one with conformist

acculturation. In the first scenario, migration eliminated the between-group variation, while acculturation maintained it in the second one. Namely, the results revealed that the migration rate, though small, eliminates the between-group cultural variations. On the other hand, acculturation breaks the migration effect as its conformity coefficient increases as well as the number of role models.

The major criticism of our model might be the number of traits limited to A and B, and the number of role models, in that they don't allow the model to capture more realistic trends. Moreover, some might argue that it is preferable to use a very large or an infinite population size as done in previous studies (Kaleda K. Denton, Liberman, et Feldman 2021; Kaleda Krebs Denton et al. 2020). Otherwise, the stochastic conformity coefficient and the embedding of the migration model within Boyd & Richerson's model (Boyd et Richerson 1985) provided added realism to the results.

Other than increasing the number of traits, role models, and population size, future possible extensions to our model could be studying the effect of migration between subpopulations of unequal population sizes with different or more than one acculturation strategy. When migrating from a subpopulation where a trait is acquired through a specific transmission bias to another location where it is going to be transmitted using another social strategy, it could be worthwhile to understand under which conditions both strategies of adopting the same trait are going to co-exist or when one dominates the other.

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