Cultural Evolution

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Abstract

What gave rise to the mosaic of cultural expressions across the globe? Why are some societies more culturally diverse than others? This study develops a unified theory of cultural evolution, characterizing the forces that have governed this process over the course of human existence. The research advances the hypothesis that population movements and socioeconomic transformations generated a mismatch between inherited cultural traits and prevailing ecological and societal conditions, setting in motion an evolutionary process governed by adaptation-based vertical transmission, horizontal diffusion, and fitness-based evolutionary selection. The theory generates novel testable predictions concerning the origins of the global cultural mosaic and the cross-societal variation in cultural diversity. First, greater ecological distance between ancestral environments generated greater cultural distance across societies. Second, prehistoric differences in ancestral diversity contributed to divergent adaptive capacity and greater cultural distance. Third, societies descended from more diverse prehistoric populations exhibit greater cultural diversity despite convergence induced by adaptation to a common environment and societal norms. Drawing on measures of cultural distance and diversity derived from folkloric and musical traditions among ethnic groups, visual representations of common concepts, and the dispersion of norms, values, and attitudes, the empirical analysis lends credence to the predictions of the theory.

Keywords: Cultural Diversity, Adaptation, Fitness, Cultural Evolution, Vertical Transmission, Social Norms

JEL Classifications: O10, Z10

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1. Introduction

Cultural traits have left a profound imprint on the wealth of nations. Norms, values, and behavioral predispositions, notably a future-oriented mindset, investment in child quality, and cooperation, have shaped human capital formation, innovative activity, and market efficiency, fostering the growth process. Moreover, cultural diversity, reflected in the coexistence of distinct perspectives and values, has influenced the development process, fostering the cross-fertilization of ideas while undermining social cohesion.

Why have distinct cultural traits emerged and persisted across world regions? Why do societies differ in their degree of cultural diversity? This research develops a unified theory of cultural evolution that characterizes the fundamental forces that have governed this process over the course of human existence, shedding light on the emergence of the cultural mosaic across the globe and the origins of societal variation in cultural diversity.

The central hypothesis advanced in this research posits that cultural evolution during the formative stages of human history was set in motion by recurrent mismatches between prevailing cultural traits and those compatible with emerging environments. As populations encountered novel and diverse ecological niches during the Out-of-Africa dispersal and the diffusion of Neolithic farmers, and as urbanization transformed prevailing societal conditions, inherited cultural traits became misaligned with the new environment. Socioeconomic transformations, notably the Neolithic and Industrial Revolutions, generated analogous mismatches by diminishing the compatibility of previously adaptive traits with the emerging environment.

The emerging mismatch triggered a process of cultural adaptation in which poorly suited traits gradually receded, whereas those better aligned with prevailing conditions became increasingly prevalent across generations. Cultural evolution consequently induced gradual convergence toward traits better suited to the new environment. Yet as this adaptive process unfolded across distinct ecological environments, differences in local ecology, including climate, disease exposure, and resource constraints, favored distinct cultural adaptations across regions, giving rise to the mosaic of cultural expressions across the globe. Moreover, societies descended from more diverse prehistoric populations experienced a greater degree of cultural adaptation while exhibiting greater cultural diversity despite convergence in cultural expressions induced by adaptation to a common environment and prevailing societal norms.

The proposed theory rests on three pillars: adaptation-based vertical transmission, horizontal diffusion among contemporaneous individuals, and fitness-based evolutionary selection. Nesting these forces within a unified analytical framework, the theory provides microeconomic foundations for the evolutionary process that governed cultural adaptation during the formative stages of human history. Vertical transmission directs cultural traits toward those better suited to the prevailing environmental conditions, horizontal diffusion fosters cultural convergence among individuals within society, and fitness-based evolutionary selection, arising from culturally induced variation in reproductive success, shapes the propagation of traits across generations, shifting their distribution

toward those more compatible with the prevailing environment.[1] Yet while all dynasties are drawn toward the trait compatible with the prevailing environment, intergenerational transmission remains anchored in their inherited cultural predispositions, leading each dynasty to converge to its own steady state and giving rise to persistent cultural dispersion in the long run.

The theory generates several novel testable predictions concerning the origins of the mosaic of cultural traits across societies and cultural diversity within them. First, greater ecological distance between ancestral environments tended to generate greater cultural distance across societies as populations adapted to their respective environments. Yet, since ancestral diversity governed the extent of cultural adaptation, this effect diminished as differences in ancestral diversity widened. Second, prehistoric cross-societal differences in ancestral diversity contributed to divergent adaptive capacity and greater cultural distance. Third, societies descended from more ancestrally diverse populations have exhibited greater cultural diversity, despite convergence in cultural expressions induced by adaptation to a common environment and prevailing societal norms, provided that fitness differences conferred limited reproductive advantages during the formative stages of human history and did not induce a drastic compression of the distribution of cultural traits.

Consistent with the prediction that greater ecological distance across pairs of societies generated greater cultural distance, pairwise ecological distance is positively and significantly associated with cultural distance in folkloric and musical traditions, contemporary norms, values, and attitudes, and visual representations of common concepts. Moreover, consistent with the predicted interaction effect, this association weakens as differences in ancestral diversity across societies widen, since greater asymmetry in adaptation diminishes the extent to which ecological divergence was reflected in cultural distance. Furthermore, greater cross-societal differences in ancestral diversity are associated with greater cultural distance, consistent with divergent adaptive capacity. The findings therefore suggest that divergences in both ancestral ecology and prehistoric ancestral diversity were formative forces in the emergence of cultural variation across societies.

The empirical analysis provides support for the prediction that societies descended from populations characterized by greater predicted ancestral diversity in the distant past would exhibit greater cultural diversity across multiple domains, spanning historical settings and modern societies. Indigenous ethnic groups provide an especially informative setting because their cultural traditions largely reflect patterns that evolved prior to the potentially confounding effects of colonial rule and the major migration waves of recent centuries. The analysis therefore examines whether ethnic groups descended from more diverse ancestral populations exhibit greater diversity within their own folkloric and musical traditions. Consistent with the theory, the analysis reveals a pronounced and highly significant positive association between predicted ancestral population diversity in the distant past and folkloric and musical diversity.

Evidence from modern societies first draws on a novel measure of cultural diversity based on visual representations of common concepts across countries. The measure captures the extent to

[1] In the Malthusian epoch, fitness-based selection was one of the central forces governing cultural evolution, whereas in the post-demographic-transition era, as the link between resources and reproductive success eroded across most societies, it largely ceased to operate.

which contributors within each country depict the same concepts in heterogeneous ways. Consistent with the theory, the analysis reveals a pronounced and highly significant association between lower ancestral diversity in the distant past and lower diversity in these visual representations.

Greater prehistoric ancestral diversity is also associated with greater dispersion in values and attitudes within contemporary multiethnic societies. Evidence from the World Values Survey reveals a pronounced and highly significant association between lower prehistoric ancestral diversity and lower dispersion in contemporary cultural values. Evidence from the European Social Survey reveals a similarly pronounced and highly significant association between the predicted prehistoric diversity of parental homelands and the dispersion of cultural values among second-generation migrants who were born and reside in the same host country. Since these individuals share the contemporary economic and institutional environment of the host country, this setting alleviates concerns that the observed relationship reflects institutions and economic development that evolved endogenously in response to historical population diversity.

Fundamental Conceptual Departures Existing theories of cultural evolution can be broadly divided into three strands. The first develops general theories of cultural transmission and evolution that characterize the mechanisms governing cultural persistence and change without focusing on a particular cultural trait or ecological environment. The second examines the evolution of specific cultural traits and their implications for comparative development. The third analyzes deliberate parental investment in the intergenerational transmission of particular cultural traits. Yet none of these strands provides a unified framework that integrates adaptation-based vertical transmission, horizontal diffusion, and fitness-based evolutionary selection, whose interplay is critical for understanding cultural evolution during the formative stages of human history. The integration of these forces within a unified framework enables the theory to account for the adaptive evolution of cultural traits across heterogeneous environments, the emergence of the global cultural mosaic, and systematic cross-societal variation in cultural diversity.

The first strand of research emphasizes the role of imitation, social learning, and identity-preserving processes in cultural evolution (Boyd and Richerson (1988, 2005); Bisin and Verdier (2000, 2001)). Yet these foundational frameworks do not capture the formative stages of cultural evolution in human history. In particular, their abstraction from adaptation-based vertical transmission, which was central to the evolution of cultural traits during the dispersal of humanity across heterogeneous ecological niches, limits their capacity to shed light on this historical process and on the roots of cultural diversity within and across societies. They therefore do not characterize cultural change as a directed evolutionary process arising from adaptation-based vertical transmission and fitness-based evolutionary selection.

Boyd and Richerson (1988, 2005) develop non-dynastic models of intergenerational cultural transmission across successive generations, driven by social learning and imitation through payoff-biased or frequency-dependent mechanisms. In these models, deliberate vertical transmission is absent and, in particular, adaptation-based vertical transmission plays no role. Bisin and Verdier

(2000, 2001), in contrast, develop dynastic models of intergenerational cultural transmission in which parents deliberately transmit traits to preserve their identity across generations, rather than to adapt cultural traits to local environmental conditions.

The second strand, which is closer in spirit to the proposed unified theory, examines the evolution of specific cultural traits (Spolaore and Wacziarg, 2013; Ashraf et al., 2021; Galor, 2022). Research on long-term orientation (Galor and Özak, 2016) combines adaptation-based vertical transmission with fitness-based cultural evolution. Other contributions study the evolution of predispositions toward education (Galor and Moav, 2002), entrepreneurial spirit (Galor and Michalopoulos, 2012), and loss aversion (Galor and Savitskiy, 2018) through fitness-based cultural evolution with non-deliberate vertical transmission. While these contributions uncover the historical origins of economically consequential traits, they do not provide a general account of the joint evolution of cultural traits and cultural diversity across heterogeneous populations and environments.

The third strand focuses on deliberate parental intergenerational transmission, including the transmission of cooperative values (Tabellini, 2008), patience (Doepke and Zilibotti, 2008) and risk aversion (Klasing and Milionis, 2014), while abstracting from evolutionary selection and population-level cultural dynamics. The proposed theory departs from this literature by embedding deliberate adaptation-based transmission within a unified evolutionary framework in which horizontal diffusion and differential reproductive success jointly govern the long-run distribution of cultural traits. Rather than focusing on particular traits in specific historical or economic settings, the framework characterizes the joint evolution of cultural traits and cultural diversity during the formative stages of human history across heterogeneous ecological environments.

2. A Unified Theory of Cultural Evolution

This section develops a unified theory of cultural evolution that captures the central forces that have shaped cultural adaptation over the course of human existence. In view of the central hypothesis advanced in this research, cultural evolution is set in motion by a mismatch between prevailing cultural traits, formed in preceding environments, and those compatible with the novel ecological or socioeconomic environments that humans have encountered in the process of development. Cultural evolution therefore constitutes a directional process of cultural adaptation that progressively aligns cultural traits with local conditions and thereby enhances individual fitness in new environments, as indeed transpired during the formative stages of humanity.

Cultural evolution within an ecological niche is governed by a law of motion that reflects the interplay between three universal forces: adaptation-based vertical transmission within lineages, horizontal diffusion across individuals within society, and fitness-based differential reproductive success. The path of cultural evolution is determined by the cultural predispositions of its founder population, the extent of ancestral diversity within that population, and the cultural trait most compatible with the new environment. Central to this process is the dependence of adaptation-based intergenerational transmission on the proximity of founders' cultural predispositions to the environment-specific fitness-maximizing cultural trait.

2.1. Cultural Predispositions of the Founder Population

Consider the settlement of a novel ecological niche by a heterogeneous founder population characterized by ancestral diversity, ω. This heterogeneity reflects ancestral variation in behavioral predispositions, cultural backgrounds, and formative environments, giving rise to differences in cultural predispositions among members of the founder population. It constitutes the foundation for diversity in individuals' beliefs, norms, values, preferences, decision-making, and social interactions, shaping cultural expressions and the capacity for adaptation and forming the basis from which cultural evolution proceeds within the newly settled ecological niche.

Upon the arrival of the founder population, consisting of L_0 individuals, the environment's carrying capacity greatly exceeds this initial population size. The resulting resource abundance generates rapid population growth toward the steady-state level $\bar{L}$, determined by the carrying capacity of the environment.

Individuals in the founder population belong to a continuum of cultural types indexed by $j \in J$, which differ only in their cultural predispositions, $\theta^j \in (0,1)$. These predispositions are given by

$$\theta^j = \hat{\theta} + \sigma(\omega) z^j, \tag{1}$$

where $\sigma'(\omega) > 0$, and z^j follows a standardized truncated normal distribution with mean zero, variance one, and bounded support $[\underline{z}, \tilde{z}]$, where $\underline{z} < 0 < \tilde{z}$. The distribution of cultural predispositions is therefore truncated normal with mean $\hat{\theta}$ and variance $\mathrm{Var}(\theta^j) = \sigma^2(\omega)$, which increases with ancestral diversity, ω. Moreover, the support of the distribution is $[\hat{\theta} + \sigma(\omega)\underline{z},\ \hat{\theta} + \sigma(\omega)\tilde{z}] \equiv [\underline{\theta}(\omega), \tilde{\theta}(\omega)] \in (0.1)$, where $\underline{\theta}'(\omega) < 0 < \tilde{\theta}'(\omega)$, $\underline{\theta}(\omega) > 0$, and $\tilde{\theta}(\omega) < \theta^* < 1$, where θ^* is the environment-specific fitness-maximizing cultural trait. Hence, greater ancestral diversity expands both the variance and the support of the distribution of cultural predispositions.

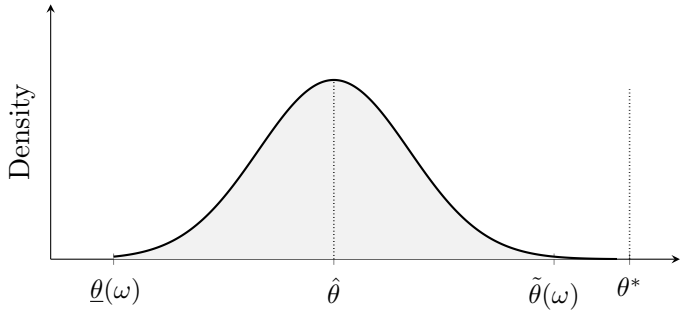


Figure 1: The Distribution of Cultural Predispositions

Thus, the distribution of cultural predispositions within the founder population is not aligned with prevailing environmental conditions. In particular, $\theta^j < \theta^*$ for all $j \in J$. [2] This misalignment created the impetus for cultural adaptation toward the environment-specific fitness-maximizing

[2]For expositional convenience, cultural evolution is modeled as unidirectional. Since the direction of the trait scale is immaterial, θ^* could instead lie below the initial support without altering the qualitative implications.

cultural trait, θ^*, defined as the trait that maximizes reproductive fitness in the prevailing environment, E, i.e., $\theta^* = \arg\max_\theta G(\theta, E)$, where $G(\theta, E)$ is the reproductive fitness associated with cultural trait θ in environment E.

Yet, upon settling in this novel environment, members of the founder population, unfamiliar with its ecological conditions, lacked the accumulated knowledge needed to infer the value of θ^*. Repeated and prolonged observation of the mapping from the range of cultural predispositions within the founder population to their comparative reproductive fitness enabled them, however, over decades, to infer the value of θ^* (Appendix D). Adaptation-based vertical transmission was therefore set in motion as this learning process unfolded and the value of θ^* became evident. Since the knowledge required to identify θ^* emerged from experience accumulated after settlement, systematic sorting across ecological environments on the basis of preexisting traits better aligned with local conditions was not feasible at the time of settlement.

2.2. Dynastic Behavior, Fitness, and Resources

The overlapping-generations economy in the newly settled ecological niche is populated by individuals who live for two periods. During the first period, childhood, individuals are passive economic agents who consume a fraction of their parents' resources. During the second period, adulthood, they work, raise children, and devote effort to the cultural adaptation of their offspring.

In each period $t = 0, 1, 2, \ldots$, the population, L_t, in the ecological niche consists of a continuum of dynasties indexed by $j \in J$, where the adult population of dynasty j in period t is L_t^j, and $L_t = \int_{j \in J} L_t^j \, dj$. Dynasties differ in their cultural predispositions θ^j, inherited from their ancestral environment, and in their cultural expressions, θ_t^j, which evolve in the course of adaptation.

Preferences: Adult members of dynasty $j \in J$ at time t derive utility from their own consumption, the number of their children, and their contribution to the fitness of their children. However, they incur disutility from the effort devoted to enhancing their children's fitness. Their preferences are represented by the utility function

$$u_t^j \;=\; (1-\gamma)\,\ln c_t^j \;+\; \gamma\Big[\ln n_t^j \;+\; \ln h(e_t^j) \;-\; g(e_t^j)\Big], \tag{2}$$

where c_t^j is their consumption, n_t^j is the number of their children, $h(e_t^j)$ captures the impact of effort, e_t^j, directed toward enhancing the fitness of all their offspring, and $g(e_t^j)$ represents the disutility associated with this effort.

In particular, parental effort, $e_t^j \in (0, 1)$, has a positive but diminishing effect on parental cultural transmission to each child, $h(e_t^j) \in (0, 1)$, where $h'(e) > 0$ and $h''(e) < 0$, whereas effort is associated with an increasing and convex utility cost, $g(e_t^j)$, where $g(0) = g'(0) = 0$, $\lim_{e \to 1} g'(e) = \infty$, and, for all $e > 0$, $g'(e) > 0$ and $g''(e) > 0$.[3]

[3] Appendix E establishes that allowing parents to account for their impact on their offspring's realized cultural trait preserves convergence, ordering, and persistent cross-dynasty cultural dispersion.

Fitness and Income: Given the size of the adult population, the effective resource constraint, and the technological environment, the mean income per adult at time t is y_t. Yet, income is distributed unequally across dynasties, reflecting relative fitness. Fitness affects access to resources and the distribution of income across individuals.

At each date t, adults of dynasty $j \in J$ generate income y_t^j that exceeds y_t if the dynasty's fitness lies above the population-weighted mean fitness and falls below it otherwise. Accordingly, $y_t = \int_{j \in J} y_t^j s_t^j \, dj$, where $s_t^j \equiv L_t^j / L_t$ is the population share of dynasty j.[4]

The income of an adult of dynasty j at time t, y_t^j, is

$$y_t^j = \Big[1 + \kappa_t \big(f_t^j - \bar{f}_t\big)\Big] y_t, \tag{3}$$

where $f_t^j - \bar{f}_t$ is the fitness of dynasty j relative to the population-weighted mean fitness, $\bar{f}_t \equiv \int_{j \in J} f_t^j s_t^j \, dj$, and $\kappa_t \in [0, 1)$ reflects the extent to which the socioeconomic environment permits variation in fitness to be translated into differences in income and, in a Malthusian environment, differences in reproductive success.

As long as $\theta_t^j < \theta^*$, a condition that is satisfied along the equilibrium path, the fitness of dynasty j, f_t^j, increases as the gap narrows between the dynasty's cultural trait in period t, θ_t^j, and the environment-specific fitness-maximizing cultural trait, θ^* :

$$f_t^j = 1 - \nu \left(\theta^* - \theta_t^j\right), \qquad \nu \in (0, 1). \tag{4}$$

Yet, as the population L_t approaches the carrying capacity $\bar{L}$, the selection-intensity parameter κ_t fades, i.e.,[5]

$$\kappa_t = b(1 - L_t / \bar{L}), \qquad b \in (0, 1), \tag{5}$$

where b governs the intensity of evolutionary selection.[6] The carrying capacity $\bar{L}$ represents the population-supporting capacity attained by the end of the Malthusian epoch. The model thus characterizes cultural evolution during the period in which income differences translated into differential reproductive success. Following the demographic transition, such differences no longer systematically affect reproductive success; fitness-based selection therefore recedes, while cultural evolution continues through adaptation-based vertical transmission and horizontal diffusion.

Budget Constraint: Adults of dynasty j in period t allocate their income, y_t^j, between consumption, c_t^j, and children, n_t^j:

$$c_t^j + \rho n_t^j \leq y_t^j, \tag{6}$$

where $\rho > 0$ is the resource cost per child.

[4] Fitness affects the distribution of income and reproductive success across dynasties without altering aggregate resources, capturing the relative nature of evolutionary selection. Allowing aggregate productivity to depend on fitness leaves the qualitative results unchanged (Appendix F).

[5] As population approaches its carrying capacity and mean income converges to subsistence, persistent inequality becomes unsustainable, pushing some dynasties below the survival threshold and triggering conflict and redistribution. These forces counteract evolutionary selection in the steady state, preventing the elimination of less-fit dynasties and preserving a non-degenerate distribution of cultural predispositions. Cultural expressions may nevertheless converge, inducing cultural homogeneity through adaptation-based vertical transmission and horizontal diffusion.

[6] Appendix G establishes that the results remain valid when dynastic fitness also depends on aggregate cultural dispersion, provided that its effect on the intensity of selection is bounded.

Optimization: Adults of dynasty j at time t choose consumption, c_t^j, the number of children, n_t^j, and the effort devoted to increasing their children's fitness, e_t^j, to maximize utility subject to the budget constraint. Given the utility function, a fraction $1-\gamma$ of income is allocated to consumption and a fraction γ to child-rearing. Accordingly, optimal consumption and fertility are given by

$$c_t^j = (1-\gamma)y_t^j \quad \text{and} \quad n_t^j = (\gamma/\rho)y_t^j. \tag{7}$$

Parental optimization with respect to effort, e_t^j, implies that $h'(e_t^j)/h(e_t^j) = g'(e_t^j)$. Given the concavity of $h(e)$, the convexity of $g(e)$, and the boundary conditions, the optimal level of effort is unique and independent of time, income, and cultural predisposition: $e_t^j = e \ \ \forall(t,j)$.

2.3. Dynastic Cultural Dynamics

This section examines the evolution of each dynasty's cultural expression from its inherited cultural predisposition to its dynasty-specific steady state. In particular, it explores how the forces of vertical and horizontal transmission induce the cultural expression of each dynasty to converge toward the environment-specific fitness-maximizing cultural trait.

This process begins with the founding members of dynasty j, who are endowed with an inherited cultural predisposition, θ^j, which constitutes the dynasty's initial cultural expression, i.e., $\theta_0^j = \theta^j$. The mismatch between this inherited predisposition and the environment-specific fitness-maximizing cultural trait, θ^*, sets in motion a directional process of cultural adaptation. Across successive generations, the cultural expression of dynasty j, θ_t^j, evolves, progressively narrowing the gap between the dynasty's ancestral predisposition and the cultural trait most compatible with the prevailing environment.

This process is governed by the interplay between two channels of cultural transmission. Vertical transmission reflects adaptation-based parent-to-child transmission within the dynasty, through which parents seek to align their children's cultural traits more closely with the prevailing environment. Horizontal transmission captures the contemporaneous diffusion of cultural traits across dynasties within society. These two transmission channels shape the evolution of each dynasty's cultural expression from its inherited predisposition toward the environment-specific fitness-maximizing trait.

Vertical Transmission

The process of vertical transmission and the associated adaptation depend on four factors: (i) the dynastic cultural predisposition, θ^j, (ii) the parental cultural trait, θ_t^j, (iii) the environment-specific fitness-maximizing cultural trait, θ^*, and (iv) the effectiveness of parental effort, $h(e) \in (0,1)$, in inducing the child's cultural trait to approach θ^*.

The dynastic cultural predisposition, θ^j, is transmitted from parent to child without alteration, providing an inherited cultural baseline that persists across generations and constrains the extent to which parents can adapt their children's cultural traits toward the environment-specific fitness-

maximizing trait, θ^*.[7] Building upon the inherited dynastic predisposition, parents seek to adapt their children's cultural traits toward θ^*. They augment the dynastic cultural predisposition, θ^j, by transmitting to their children the cultural experience embodied in their own cultural trait, θ_t^j, and by directing them toward θ^*.

In particular, parents transmit to their offspring a fraction $(1-\delta) \in (0,1)$ of the extent to which their own realized cultural trait exceeds the inherited dynastic predisposition. Thus, the cultural experience transmitted from parent to child is given by $(1-\delta)(\theta_t^j - \theta^j)$, where $(1-\delta) < 1$ captures the extent of its intergenerational transmission. Lastly, the effectiveness of parental effort, $h(e) \in (0,1)$, increases the weight placed in the transmission process on the environment-specific fitness-maximizing cultural trait, θ^*.

Vertical transmission from generation t to generation $t+1$ within dynasty j, V_{t+1}^j, is therefore

$$V_{t+1}^j = \theta^j + [1-h(e)](1-\delta)(\theta_t^j - \theta^j) + h(e)(\theta^* - \theta^j) \equiv V(\theta_t^j; \theta^j), \tag{8}$$

where $V(\theta_t^j; \theta^j)$ is a strictly increasing affine transformation, $V(\theta_0^j; \theta^j) > \theta^j$, and $V'(\theta_t^j, \theta^j) < 1$.

Horizontal Transmission

Horizontal cultural transmission captures the diffusion of cultural characteristics across contemporaneous individuals within the same social environment. It encompasses the blending of traits through education and social interaction and operates through imitation and learning, contributing to partial assimilation toward the prevailing local cultural benchmark. These processes are reinforced by socially articulated norms that are codified and taught and that find expression in folklore, musical traditions, cuisine, and other cultural forms.

For a member of dynasty j in generation $t+1$, horizontal transmission, H_{t+1}^j, captures the cultural influence arising from society-wide forces. Accordingly, horizontal transmission is represented by a society-wide cultural influence, $H(\hat{\theta})$, derived from the mean underlying cultural predisposition, $\hat{\theta}$.[8]

$$H_{t+1}^j = \lambda\hat{\theta} \equiv H(\hat{\theta}), \tag{9}$$

where $\lambda > 1$ measures the intensity of horizontal diffusion and $\tilde{\theta} < \lambda\hat{\theta} < \theta^*$.

Cultural Evolution Within a Dynasty

Cultural evolution within dynasty $j \in J$ reflects both vertical transmission, $V(\theta_t^j; \theta^j)$, and horizontal transmission, $H(\hat{\theta})$, where $\mu \in (0,1)$ is the relative weight of horizontal transmission in this process. The evolution of the cultural trait within dynasty j, $\{\theta_t^j\}_{t=0}^{\infty}$, is therefore governed by the first-order affine dynamical system

[7] As is customary, reproduction is modeled as asexual, preserving dynastic cultural predispositions across generations. Under sexual reproduction, an analogous transmission structure could arise as the equilibrium outcome of assortative mating. Since individuals would prefer partners whose inherited predispositions are closer to the fitness-maximizing trait, mutual partner choice would generate perfectly assortative matching. Individuals would mate with partners of their own type, and their offspring would inherit the corresponding dynastic predisposition.

[8] Alternatively, horizontal transmission could be represented by the diffusion of the contemporaneous population-weighted mean cultural expression, $\bar{\Theta}_t$, significantly complicating the analysis. Yet, as established in Appendix H, this specification does not alter the qualitative results.

$$\theta^j_{t+1} = (1-\mu)V(\theta^j_t;\theta^j) \;+\; \mu\, H(\hat{\theta}) \equiv \psi(\theta^j_t;\theta^j), \tag{10}$$

where $\psi(\theta^j_t;\theta^j)$ is a strictly increasing affine transformation, $\psi(\theta^j_0;\theta^j) > \theta^j_0$, $\psi(\theta^*;\theta^j) < \theta^*$, and $\psi'(\theta^j_0;\theta^j) < 1$. Hence, ψ maps $[\theta^j_0, \theta^*]$ into itself and ψ is a contraction mapping on this interval.

As depicted in Figure 2, for any initial cultural trait $\theta^j_0 < \bar{\theta}^j$, cultural adaptation induces the cultural trait of dynasty j to converge monotonically to its unique and globally stable dynasty-specific steady state, $\bar{\theta}^j = \psi(\bar{\theta}^j;\theta^j) < \theta^*$.

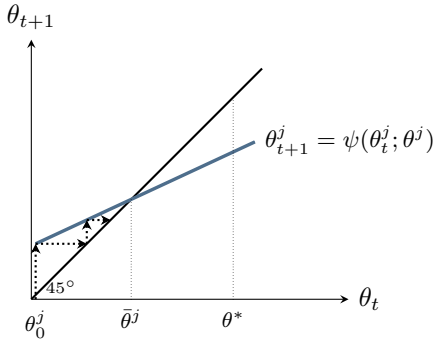


Figure 2: Cultural evolution within dynasty j.

2.4. Societal Cultural Dynamics

This section examines the evolution of the societal distribution of cultural traits from its initial truncated normal distribution to its steady-state distribution. In particular, it explores whether the forces that induce all dynasties to converge toward the same environment-specific optimal trait ultimately generate cultural homogeneity within each ecological niche in the steady state.

At any time $t = 0, 1, 2, \ldots$, the dynamical system maps the cross-dynasty distribution of cultural expressions into the distribution prevailing at time $t+1$, conditional on the environment-specific fitness-maximizing cultural trait, θ^*, and the parameters governing vertical transmission and horizontal diffusion. While vertical and horizontal transmission draw all dynasties toward the same environment-specific fitness-maximizing cultural trait, they do not eliminate cross-dynasty cultural differences in the long run. Inherited predispositions shape parental transmission in every generation, anchoring the cultural traits transmitted to children despite parental efforts to move them toward θ^*. Each dynasty therefore converges toward its own steady state. Accordingly, greater ancestral diversity generates greater persistent cross-dynasty cultural dispersion.

As depicted in Figure 3, the degree of ancestral diversity in this ecological niche determines the range of initial cultural predispositions, $(\underline{\theta}, \tilde{\theta})$, and thereby the range of cultural expressions in the steady state, $(\bar{\theta}_{\min}, \bar{\theta}_{\max})$, where $\bar{\theta}_{\max} < \theta^*$.

For any dynasty j with inherited cultural predisposition $\theta^j = \theta^j_0$, its long-run cultural trait is given by the strictly increasing affine mapping $\bar{\theta}^j = \xi(\theta^j)$, where ξ is determined by the cultural adaptation dynamics $\theta^j_{t+1} = \psi(\theta^j_t;\theta^j)$. Since each dynasty's inherited cultural predisposition, θ^j,

anchors its cultural evolution, complete convergence across dynasties does not occur. Although all dynasties are drawn toward the same environment-specific fitness-maximizing trait, their distinct inherited predispositions lead them to converge to distinct steady states.

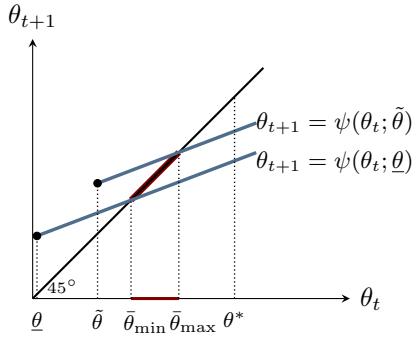


Figure 3: Societal cultural evolution. The interval $(\bar{\theta}_{\min}, \bar{\theta}_{\max})$ is the range of societal cultural traits in the steady state.

Proposition 1 (Declining Cultural Dispersion and Long-Run Persistence)**.**

(i) For any two dynasties $j, k \in J$ such that $\theta_0^k > \theta_0^j$, the cultural gap at time t, $\Delta_t^{jk} \equiv \theta_t^k - \theta_t^j$, declines monotonically over time but persists in the long run, i.e.,

$$0 < \Delta_{t+1}^{jk} < \Delta_t^{jk} \quad \textit{for all } t \geq 0 \quad \textit{and} \quad \lim_{t\to\infty} \Delta_t^{jk} \in (0, \Delta_0^{jk});$$

(ii) The variance of cultural traits across dynasties $j \in J$ at any time t, $\mathrm{Var}_J(\theta_t^j)$, declines monotonically over time but persists in the long run, i.e.,

$$0 < \mathrm{Var}_J(\theta_{t+1}^j) < \mathrm{Var}_J(\theta_t^j) \quad \textit{for all } t \geq 0 \quad \textit{and} \quad \lim_{t\to\infty} \mathrm{Var}_J(\theta_t^j) \in \big(0, \mathrm{Var}_J(\theta_0^j)\big);$$

(iii) The steady-state variance of cultural traits across dynasties is strictly increasing in ancestral diversity, ω, i.e.,

$$\frac{\partial \,\mathrm{Var}_J(\bar{\theta}^j)}{\partial \omega} > 0.$$

Proof: See Appendix C.1.

Proposition 1 implies that societies characterized by greater ancestral diversity in cultural predispositions retain a broader range of cultural traits in the steady state.

2.5. Societal Population and Income Dynamics

At time t, given the prevailing technological level, A, the land endowment, X, and the working population, L_t, output in the ecological niche, Y_t, is given by

$$Y_t = (AX)^{\alpha} L_t^{1-\alpha}, \qquad 0 < \alpha < 1. \tag{11}$$

Output per worker in period t, $y_t = (AX/L_t)^\alpha$, is therefore strictly increasing and strictly concave in effective resources per worker in the ecological niche.

While fitness affects access to resources and the distribution of income across individuals, it is assumed, for simplicity, to have no direct effect on labor productivity. [9] Individuals therefore supply homogeneous units of labor.

2.5.1. Population Dynamics

The evolution of the working population of each dynasty is determined by the size of the dynasty's working population in the previous period and the number of children per adult in that dynasty. The working population of dynasty j in period $t+1$, L^j_{t+1}, is therefore

$$L^j_{t+1} = n^j_t L^j_t. \tag{12}$$

The aggregate population at time $t+1$ is therefore

$$L_{t+1} = \int_J L^j_{t+1} dj = \int_J n^j_t L^j_t dj = L_t \int_J s^j_t n^j_t dj, \tag{13}$$

where $s^j_t = L^j_t/L_t$ is the population share of dynasty j. Hence, the aggregate population law of motion is $L_{t+1} = n_t L_t$, where $n_t \equiv \int_J s^j_t n^j_t dj$ is the mean number of children per adult. As derived in (7), the number of children per adult belonging to dynasty j is $n^j_t = (\gamma/\rho) y^j_t$, implying that $n_t = (\gamma/\rho) y_t$, where $y_t = \int_J s^j_t y^j_t dj$.

The time path of the working population is therefore governed by

$$L_{t+1} = (\gamma/\rho)(AX)^\alpha L_t^{1-\alpha} \equiv \Phi(L_t). \tag{14}$$

As depicted in Figure 4, $\Phi(L_t)$ is strictly increasing and strictly concave in L_t, where $\Phi(0) = 0$, $\lim_{L_t \to 0} \Phi'(L_t) = \infty$, and $\lim_{L_t \to \infty} \Phi'(L_t) = 0$. Hence, given $L_0 > 0$, there exists a unique and positive level of the working population, $\bar{L} = (\gamma/\rho)^{1/\alpha} AX$, which is globally stable on the positive domain.

Culturally induced heterogeneity in income and fertility governs the evolution of dynasty shares but does not independently affect aggregate population growth, which depends only on societal income per worker. In particular, the population share of dynasty j evolves according to $s^j_{t+1} \equiv L^j_{t+1}/L_{t+1} = s^j_t (n^j_t/n_t)$. Dynasties with above-average reproductive success increase their population shares, whereas those with below-average reproductive success experience declining shares.

[9] Appendix I allows individual labor productivity to depend on fitness. Cultural adaptation raises the productivity of each dynasty as its cultural trait moves toward the fitness-maximizing trait, while evolutionary selection further raises aggregate productivity by increasing the population share of more productive dynasties. Nevertheless, the main implications for cultural evolution remain unchanged. Steady-state income per worker is unaffected, while the steady-state population is larger because higher productivity enables the ecological niche to support a larger population.

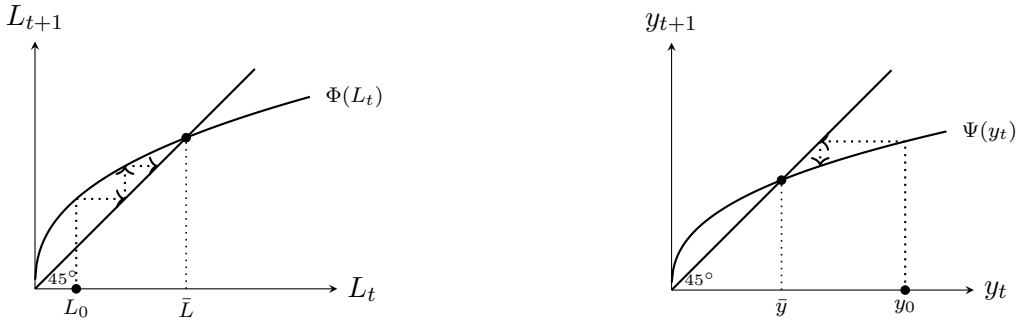
2.5.2. The Time Path of Income per Worker

The evolution of income per worker is governed by

$$y_{t+1} = (AX/L_{t+1})^{\alpha} = (AX/(n_t L_t))^{\alpha} = (\rho/\gamma)^{\alpha} y_t^{1-\alpha} \equiv \Psi(y_t). \tag{15}$$

As depicted in Figure 4, $\Psi(y_t)$ is strictly increasing and strictly concave, where $\lim_{y_t \to 0} \Psi'(y_t) = \infty$, $\lim_{y_t \to \infty} \Psi'(y_t) = 0$, and $\Psi(0) = 0$. Thus, there exists a unique positive steady-state level of income per worker, $\bar{y} = \rho/\gamma$, which is globally stable on the positive domain.

As depicted in Figure 4, upon the arrival of the founder population, the population in the ecological niche grows from its initial level, $L_0 < \bar{L}$, to its steady-state level, $\bar{L}$, while income per worker converges to its unique positive steady-state value, $\bar{y}$.



(a) Founder population dynamics.

(b) Income per worker dynamics.

Figure 4: Malthusian adjustment dynamics.

2.6. Population-Weighted Cultural Diversity

Differential fitness alters the demographic composition of the population, increasing the representation of dynasties whose cultural traits lie closer to the fitness-maximizing one. Accordingly, cultural diversity is captured by the population-weighted variance of cultural traits, $Var_p(\theta_t^j)$, rather than the unweighted variance of cultural traits across dynasties, $Var_J(\theta_t^j)$.

2.6.1. Dynamics of Dynastic Population Shares

The evolution of the population of dynasty j is given by $L_{t+1}^j = n_t^j \, L_t^j$, where, as follows from individual optimization, $n_t^j = (\gamma/\rho)\, y_t^j$. Hence, the size of dynasty j at time $t+1$ is

$$L_{t+1}^j = (\gamma/\rho)\big[1 + \kappa_t\big(f_t^j - \bar{f}_t\big)\big] y_t \, L_t^j. \tag{16}$$

The share of dynasty j in the overall population, $s_t^j = L_t^j/L_t$, therefore evolves according to

$$s_{t+1}^j = \big[1 + \kappa_t\big(f_t^j - \bar{f}_t\big)\big] s_t^j. \tag{17}$$

The reproductive advantage of each dynasty depends on the alignment of its cultural trait with the fitness-maximizing norm. Parental effort raises the fitness of each child and accelerates cultural convergence, but since effort is uniform across dynasties, it does not affect their relative ranking.

As L_t approaches the carrying capacity of the ecological niche, $\bar{L}$, fertility converges to 1, income per worker converges to $\bar{y} = \rho/\gamma$, selection intensity vanishes, and the population share of each dynasty stabilizes.[10] Consequently, cultural diversity persists as aggregate population converges to the carrying capacity $\bar{L}$. Although dynasties closer to the environment-specific fitness-maximizing cultural trait expand more rapidly at first, the fading of selection intensity as population approaches $\bar{L}$ preserves the representation of all dynasties and their heterogeneous cultural predispositions. The steady-state size of dynasty j is therefore constant at $\bar{L}^j = \bar{s}^j \bar{L}$.

2.6.2. Ancestral Diversity and Population-Weighted Cultural Diversity

Cultural transmission alters the cultural expression of each dynasty and therefore the range and the dispersion of cultural characteristics prevalent in the population, whereas fitness and the resulting differential reproductive success change the weight of each trait in population-wide cultural diversity. Dynasties whose cultural traits lie closer to the environment-specific fitness-maximizing trait represent larger population shares over time. Yet these shares stabilize as the economy reaches a steady state. Consequently, the corresponding population-weighted mean cultural trait, $\bar{\Theta} \equiv \int_J \bar{s}^j \bar{\theta}^j \, dj$ and the population-weighted variance of cultural traits, $\mathrm{Var}_p(\bar{\theta}^j)$ reflect both the long-run dispersion of cultural traits across dynasties and the demographic composition generated during the transition. In particular, the population-weighted variance of cultural traits is

$$\mathrm{Var}_p(\bar{\theta}^j) = \int_J \bar{s}^j \left(\bar{\theta}^j - \bar{\Theta}\right)^2 dj. \tag{18}$$

The initial distribution of cultural predispositions is truncated normal. Since the mapping from inherited cultural predispositions to long-run cultural traits is affine, the unweighted long-run distribution of cultural traits across dynasties remains a truncated normal distribution, with a compressed support and variance. Differential reproductive success, however, alters the population weights assigned to these traits, skewing the population-weighted distribution toward the environment-specific fitness-maximizing cultural trait, θ^*.

Proposition 1 establishes that greater ancestral diversity increases long-run cultural dispersion across dynasties when dynasties retain their founder-population weights. Fitness-based selection alters these weights by increasing the representation of dynasties whose cultural traits lie closer to the environment-specific fitness-maximizing trait. If cumulative selection were unbounded, this process would ultimately concentrate the population among the fittest dynasties and eliminate population-weighted cultural dispersion. Since, however, selection intensity vanishes as population approaches the carrying capacity, cumulative selection is finite, preserving a non-degenerate limiting distribution of dynasty shares (Appendix J). Although finite cumulative selection prevents fitness-based selection from eliminating cultural dispersion by preserving a non-degenerate distribution of dynasty shares, it does not determine whether demographic reweighting attenuates or amplifies the effect of ancestral diversity on population-weighted cultural dispersion. Proposition 2 establishes

[10] A sufficient condition for non-degenerate long-run population shares is finite cumulative selection, as ensured by the population law of motion (Appendix J).

that, when the reproductive advantage generated by fitness differences is limited, as captured by $b \in (0, \bar{b})$, the association between ancestral diversity and long-run population-weighted cultural dispersion is necessarily positive.

Proposition 2 (Ancestral Diversity and Long-Run Population-Weighted Cultural Dispersion)**.** *Given $b \in (0, \bar{b})$, the steady-state population-weighted variance of cultural traits, $\mathrm{Var}_p(\bar{\theta}^j)$, is strictly increasing in ancestral diversity, ω, i.e.,*

$$\frac{\partial \mathrm{Var}_p(\bar{\theta}^j)}{\partial \omega} > 0.$$

Proof: See Appendix C.2.

Testable Prediction: Proposition 2 generates a testable prediction concerning the relationship between ancestral diversity and contemporary cultural diversity. When the reproductive advantage generated by fitness differences remained limited, societies descended from more diverse founder populations should exhibit greater cultural diversity, despite the forces operating toward cultural convergence. For measurable cultural traits, this would be reflected in greater within-society dispersion in norms, values, and attitudes. For non-measurable expressive traits, it would be reflected in a richer repertoire of distinct folkloric motifs, musical forms, visual representations, and other cultural expressions. Thus, the relationship between ancestral diversity and contemporary cultural diversity is nuanced and does not simply reflect the persistence of ancestral cultural dispersion. If fitness differences generated sufficiently pronounced reproductive advantages, greater ancestral diversity could instead have led to lower contemporary cultural diversity.

Beyond its effect on long-run cultural dispersion, ancestral population diversity would have fostered adaptation toward θ^*. Greater ancestral diversity would have expanded the dispersion of steady-state cultural traits without affecting their unweighted mean (reflecting a mean-preserving spread of dynastic predispositions preserved by the affine transmission mapping), while fitness-based selection would have increased the shares of dynasties whose traits lay closer to θ^*. Consequently, greater ancestral diversity would have shifted the population-weighted cultural mean toward θ^*.

Proposition 3 (Ancestral Diversity and Cultural Adaptation)**.** *The population-weighted steady-state mean cultural trait, $\bar{\Theta}$, is strictly increasing in ancestral diversity, ω, and therefore lies closer to the environment-specific fitness-maximizing cultural trait, θ^*, i.e.,*

$$\frac{\partial \bar{\Theta}}{\partial \omega} > 0 \qquad \textit{and} \qquad \frac{\partial(\theta^* - \bar{\Theta})}{\partial \omega} < 0.$$

Proof: See Appendix C.3.

2.7. Ecological Distance and Cultural Distance

The adaptive nature of cultural evolution implies that ecological distance, which captures the extent of divergence between societies' environment-specific fitness-maximizing cultural traits, generated persistent cultural differences across societies. As cultural evolution in each society was directed toward its environment-specific fitness-maximizing trait, ecological divergence gave rise

to distinct trajectories of cultural evolution and, ultimately, to the emergence of distinct cultural traits across societies.

Yet, ancestral diversity is associated with greater adaptability and thus with greater proximity to the environment-specific fitness-maximizing cultural trait (Proposition 3). Greater ecological distance between societies would therefore be expected to increase their cultural distance. Moreover, the impact of ecological distance would be expected to diminish as the difference in ancestral diversity increases, since it depends on how far both societies have advanced along their respective adaptation paths; greater asymmetry in adaptation would weaken this impact.

Proposition 4 (Ecological Distance, Differences in Ancestral Diversity, and Cultural Distance)**.** *Consider two societies $i, \ell \in I$ governed by common parameters of cultural transmission and evolutionary selection. Let $d^c_{i\ell}$ be their cultural distance, $d^e_{i\ell}$ their ecological distance, and $d^\omega_{i\ell} \equiv |\omega_i - \omega_\ell| > 0$ the absolute difference in their ancestral diversity. For a given average degree of adaptation across the two societies and for ecological distance in the interior of its feasible range:*
(i) Cultural distance is increasing in ecological distance:

$$\partial d^c_{i\ell}/\partial d^e_{i\ell} > 0;$$

(ii) Cultural distance is increasing in the difference in ancestral diversity:

$$\partial d^c_{i\ell}/\partial d^\omega_{i\ell} > 0;$$

(iii) The effect of ecological distance on cultural distance is decreasing in ancestral diversity distance:

$$\partial^2 d^c_{i\ell}/\partial d^e_{i\ell}\partial d^\omega_{i\ell} < 0.$$

Proof: See Appendix C.4.[11]

Testable Predictions: Proposition 4 generates three testable predictions concerning the origins of cross-societal cultural differences. Cultural distance should be positively associated with ecological distance and with the absolute difference in ancestral diversity between societies, whereas the interaction between ecological distance and ancestral-diversity distance should be negative.

2.8. Neutral Cultural Dynamics and Expressive Diversity

In the core framework, cultural evolution was directional, drawing cultural traits toward the environment-specific fitness-maximizing cultural trait. Yet many cultural characteristics possess no intrinsic hierarchy under which one expression is more adaptive or culturally superior to another. This section demonstrates that the central implications of the model extend to such neutral cultural domains.

Neutral cultural traits may take two distinct forms. Some can be measured along a continuous scale despite the absence of an intrinsic hierarchy. Others, including many expressive traditions, are

[11] An increase in the distance in ancestral diversity is modeled as a widening of the difference between the two societies' levels of ancestral diversity, for a given average degree of cultural adaptation. This isolates the effect of greater asymmetry in adaptation across the pair from that of a change in their average degree of adaptation.

not naturally represented by directly observable cardinal values. In the latter case, the underlying cultural predisposition is latent, and its observable manifestation is the range or richness of distinct expressive forms.

2.8.1. Measurable Neutral Cultural Traits

Consider a founder population consisting of dynasties $j \in J$ endowed with inherited cultural predispositions $\theta^j = \hat{\theta} + \sigma(\omega)z^j$, as specified in Section 2.1. In the neutral setting, these cultural traits do not affect reproductive fitness and are therefore not subject to fitness-based evolutionary selection. The population share of each dynasty consequently remains equal to its initial share.

A measurable neutral cultural predisposition may capture, for example, a preference for faster rather than slower musical tempo or for more rather than less ornamentation in visual culture. Both characteristics can be ordered and measured along a continuous scale, although neither faster tempo nor greater ornamentation is inherently more adaptive or viewed as culturally superior.

Neutral cultural evolution remains governed by vertical transmission within dynasties and horizontal diffusion across dynasties. Vertical transmission preserves the inherited dynastic predisposition and carries forward a fraction $(1-\delta) \in [0,1)$ of the parental cultural expression in excess of that predisposition: $V^j_{t+1} = \theta^j + (1-\delta)(\theta^j_t - \theta^j)$. As in the core framework, horizontal transmission operates through the mean inherited cultural predisposition, $\hat{\theta}$, and is given by $H(\hat{\theta}) = \lambda\hat{\theta}$. The evolution of the cultural expression of dynasty j is therefore

$$\theta^j_{t+1} = (1-\mu)\left[\theta^j + (1-\delta)\left(\theta^j_t - \theta^j\right)\right] + \mu\lambda\hat{\theta}, \qquad \mu \in (0,1), \tag{19}$$

where $(1-\mu)(1-\delta) < 1$. Hence, the cultural expression of each dynasty converges to a unique and globally stable steady state:

$$\bar{\theta}^j = \eta\theta^j + \varsigma\hat{\theta}, \tag{20}$$

where $\eta \equiv \frac{(1-\mu)\delta}{1-(1-\mu)(1-\delta)} \in (0,1)$, $\varsigma \equiv \frac{\mu\lambda}{1-(1-\mu)(1-\delta)} > 0$, and $\mathrm{Var}_p\left(\bar{\theta}^j\right) = \eta^2 \mathrm{Var}_p\left(\theta^j\right) = \eta^2\sigma^2(\omega)$.

Thus, as was the case in the baseline model:
(i) Neutral cultural transmission compresses initial cultural differences but does not eliminate them:

$$\left|\bar{\theta}^k - \bar{\theta}^j\right| = \eta\left|\theta^k - \theta^j\right| > 0 \qquad \text{for all } \theta^k \neq \theta^j.$$

(ii) Greater ancestral diversity generates greater long-run dispersion in measurable neutral traits:

$$\frac{\partial \mathrm{Var}_p(\bar{\theta}^j)}{\partial\omega} = \eta^2\frac{\partial\sigma^2(\omega)}{\partial\omega} > 0.$$

2.8.2. Non-Measurable Expressive Traits

In expressive domains such as folklore, oral traditions, musical forms, and the arts, cultural characteristics are not naturally represented by directly observable cardinal values. For example, societies may differ in the folkloric motifs through which they represent salient animals and environmental challenges, or in the musical forms through which they organize rhythm and melody.

Such expressions can be classified as distinct cultural forms, but they cannot generally be placed on a meaningful numerical scale. A motif centered on snow and seals and one centered on drought and lions therefore represent qualitatively distinct, rather than quantitatively ordered, cultural forms. In these domains, θ^j should therefore be interpreted as an underlying cultural predisposition rather than as a directly measurable expressive trait.

The latent cultural anchors underlying these expressions evolve according to the same neutral cultural dynamics described for measurable neutral traits. In particular, their steady-state cultural anchors satisfy $\bar{\theta}^j = \eta\theta^j + \varsigma\hat{\theta}$. The mean $\hat{\theta}$ is therefore the mean of the underlying predispositions, not an arithmetic mean of the observed motifs, musical forms, or artistic expressions. The observable implication of the distribution of these cultural anchors is not its numerical variance per se, but the range of distinct expressive features that it can generate, where the variance of these steady-state cultural anchors is $\bar{\sigma}^2 \equiv \mathrm{Var}_p\left(\bar{\theta}^j\right)$.

Let $\{\tau_k\}_{k=1}^K$ denote the positions associated with K potential expressive features, such as musical categories, folkloric motifs, or narrative structures. These positions locate the underlying cultural anchors associated with the expressive features; they do not assign numerical magnitudes to the observed features themselves. A dynasty j generates feature k if its steady-state cultural anchor lies within an interval $r > 0$ of τ_k, i.e., $\left|\bar{\theta}^j - \tau_k\right| \leq r$.

Let $f_{\bar{\sigma}}$ denote the population-weighted density of steady-state cultural anchors, $\bar{\theta}^j$. The probability that feature k is generated by a randomly drawn dynasty is therefore

$$p_k(\bar{\sigma}) = \Pr\left(\left|\bar{\theta}^j - \tau_k\right| \leq r\right) = \int_{\tau_k - r}^{\tau_k + r} f_{\bar{\sigma}}(x)\, dx. \tag{21}$$

The analysis therefore focuses on the long-run repertoire generated by dynasties' steady-state cultural anchors. Accordingly, consider a sample of $N \geq 2$ dynasties drawn independently from $f_{\bar{\sigma}}$. The probability that feature k appears at least once in the sample is $1 - [1 - p_k(\bar{\sigma})]^N$. Hence, the expected number of distinct expressive features represented in the sample is

$$\mathbb{E}[S_N(\bar{\sigma})] = \sum_{k=1}^{K} \left\{1 - [1 - p_k(\bar{\sigma})]^N\right\}.^{12} \tag{22}$$

Suppose that the potential expressive features span the relevant range of cultural anchors and that an increase in $\bar{\sigma}$ strictly redistributes probability from more frequently represented features toward less frequently represented ones, while preserving the sum of the feature probabilities.[13] Consequently, for any $\bar{\sigma}' > \bar{\sigma}$, $\mathbb{E}[S_N(\bar{\sigma}')] > \mathbb{E}[S_N(\bar{\sigma})]$. Thus, greater dispersion in steady-state cultural anchors generates a broader expected range of expressive features across dynasties.

Since the steady-state cultural trait of dynasty j, $\bar{\theta}^j = \eta\theta^j + \varsigma\hat{\theta}$, is an affine transformation of its inherited predisposition, $\bar{\sigma}^2 = \mathrm{Var}_p(\bar{\theta}^j) = \eta^2\,\mathrm{Var}_p(\theta^j) = \eta^2\sigma^2(\omega)$. Thus, since $\sigma^2(\omega)$ is strictly

[12] If N is interpreted as a continuous sampling intensity, the expectation takes the Poisson form $\mathbb{E}[S_N(\bar{\sigma})] = \sum_{k=1}^K \left[1 - e^{-Np_k(\bar{\sigma})}\right]$, without affecting the qualitative comparative static.

[13] Formally, for any $\bar{\sigma}' > \bar{\sigma}$, assume that the vector of feature probabilities $\{p_k(\bar{\sigma}')\}_{k=1}^K$ is strictly less concentrated in the majorization order than $\{p_k(\bar{\sigma})\}_{k=1}^K$. Since $1 - (1-p)^N$ is strictly concave in p for $N > 1$, this redistribution strictly increases the expected number of distinct features represented in the sample.

increasing in ancestral diversity, for any $\omega' > \omega$, $\mathbb{E}[S_N(\bar{\sigma}(\omega'))] > \mathbb{E}[S_N(\bar{\sigma}(\omega))]$. Greater ancestral diversity therefore generates a richer expected repertoire of observable expressive features.

3. Data and Measurement

To assess the testable predictions of the theory, the empirical analysis combines five sources of cultural data spanning indigenous ethnic groups and contemporary national populations. Berezkin's Folklore and Mythology Catalogue (Berezkin, 2015; Michalopoulos and Xue, 2021), Lomax's Cantometrics (Lomax, 1962; Wainstock, 2026), the World Values Survey (WVS), and visual representations from *Quick, Draw!* (Google Creative Lab, 2017) support the construction of measures of both cultural distance across societies and cultural diversity within them. In addition, the European Social Survey (ESS) (ESS ERIC, 2023) provides a complementary setting for examining cultural diversity within groups of second-generation migrants who share a common host-country environment.[14]

3.1. Cultural Measures

Folklore. The folklore data are drawn from Berezkin's Folklore and Mythology Catalogue, which compiles traditional narratives from indigenous ethnic groups worldwide and classifies them according to recurrent motifs (Berezkin, 2015; Michalopoulos and Xue, 2021). The resulting sample covers 958 indigenous ethnic groups and 2,564 motifs (Figure 5). Each group is represented by a binary vector recording the presence or absence of every motif. Cultural distance between two groups is measured by the Jaccard distance between their motif vectors, while folkloric diversity within a group is measured by the number of distinct motifs recorded in its narrative tradition.

Figure 5: Global Distribution of Indigenous Ethnic Groups in the Folklore Sample

Notes: Locations of the 958 indigenous ethnic groups surveyed in Berezkin's Folklore and Mythology Catalogue.

Music. The music data are drawn from Lomax's Cantometrics, which compiles traditional songs from indigenous ethnic groups worldwide and classifies them according to vocal, rhythmic, melodic,

[14]The ESS is not used for the analysis of cultural distance since cultural differences across migrant groups may reflect differential convergence toward the culture of the host country rather than differences at their ancestral homelands.

and structural characteristics (Lomax, 1962; Wainstock, 2026). The sample covers 825 ethnic groups and represents each musical tradition using 216 features (Figure 6). Cultural distance between two groups is measured by the Jaccard distance between their musical-feature vectors, while musical diversity within a group is measured by the number of distinct musical features recorded in its tradition.

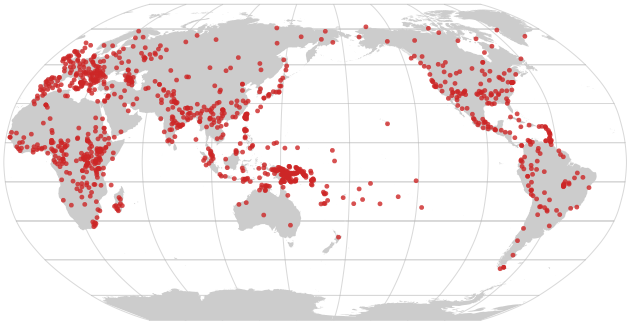


Figure 6: Global Distribution of Indigenous Ethnic Groups in the Music Sample

Notes: Locations of the 825 indigenous ethnic groups surveyed in Lomax's Cantometrics.

Norms, Values, and Attitudes in National Populations. The World Values Survey (WVS) dataset covers the period from 1981 to 2021 and contains more than six hundred thousand individual survey responses from 112 countries worldwide (Figure B.5). Cultural distance between countries is measured using the fixation index, F_{ST}, which captures between-country differences in the distributions of responses across norms, values, and attitudes relative to total variation (Muthukrishna et al., 2020). Cultural diversity within each country is measured by the coefficient of variation of individual responses to each survey question.[15]

Norms, Values, and Attitudes Among Second-Generation Migrants. The European Social Survey (ESS), covering the period 2002–2022, provides data on social norms, values, and attitudes among European second-generation migrants from the same ancestral homeland. The dataset consists of more than twenty thousand second-generation migrants from 133 ancestral origins (Figure B.6).[16] Cultural diversity is measured by the coefficient of variation of survey responses among individuals from the same ancestral homeland residing in the same host country.[17]

[15]Survey questions that are nominal categorical or permit only binary responses do not naturally map to a measure of variation and are therefore excluded from the analysis.

[16]Since cultural transmission tends to be stronger along maternal lineages, the baseline analysis uses the mother's country of birth to define ancestry. Yet, the association between ancestral diversity and contemporary cultural diversity remains qualitatively intact when ancestry is defined by the father's country of birth (Figure B.4).

[17]In both the WVS and ESS, the coefficient of variation normalizes within-group dispersion in each survey item by the corresponding group mean. To verify that the results are not driven by this normalization, we reconstruct cultural diversity using the within-group standard deviation of each item, both alone and while controlling for the corresponding group–item mean. Under both alternatives, the estimated relationship remains statistically significant and qualitatively unchanged.

Visual Representations. The data on visual representations are derived from *Quick, Draw!* (Google Creative Lab, 2017), an online game in which contributors receive an English-word prompt and have 20 seconds to depict the corresponding concept. The public corpus contains more than 50 million drawings of 345 concepts, together with their vector strokes, recognition status, creation time, and an IP-based country code. The country code identifies the inferred location of each contribution rather than the contributor's nationality. Contributors are self-selected, and the public data do not report stable user identifiers, contributor demographics, or device characteristics. The observations therefore do not constitute representative national samples.

Each recognized drawing is uniformly scaled and centered and then converted into a 384-dimensional embedding using the fixed, pretrained DINOv2 computer-vision model (Oquab et al., 2024). An embedding is a numerical representation of visual content that places drawings with similar features close to one another. Cosine distance between embeddings therefore provides a common measure of dissimilarity between drawings. For the within-country analysis, visual conceptual diversity (VCD) for each country and prompted concept is the mean cosine distance across all pairs of 100 recognized drawings. The country-level index averages this measure across the 245 concepts observed in all 65 countries, assigning equal weight to each concept, and is multiplied by 100 to express it in VCD points.

For the between-country analysis, visual conceptual distance for each pair of countries and prompted concept is the mean cosine distance between a drawing from each country net of the average within-country distance in the two countries. This adjustment isolates differences between the countries' average visual representations from their internal visual dispersion. For countries a and b and concept k, the construction satisfies

$$C_{abk} = (Q_{ak} + Q_{bk})/2 + B_{abk}, \tag{23}$$

where C_{abk} is expected cross-country drawing distance, Q_{ak} and Q_{bk} are the two within-country diversity measures, and B_{abk} is visual conceptual distance. The country-pair index gives equal weight to the same 245 concepts and is multiplied by 100. Thus, the within-country and between-country measures are components of a common Rao-diversity decomposition.[18,19]

3.2. Ecology

For each society, ancestral ecological conditions are represented by a vector of 40 geographical endowments capturing agricultural suitability, terrain, and climatic conditions. These include overall and crop-specific caloric suitability, elevation, irrigation potential, and bioclimatic indicators summarizing temperature and precipitation levels, seasonality, and extremes. Ancestral ecological distance between two societies is measured as the cosine distance between their vectors of geograph-

[18]Related studies use sketches to characterize variation in shared meaning (Lewis et al., 2021) and cross-cultural conceptual structure (Pera et al., 2026).

[19]Appendix B.2 presents the preprocessing and model details, the construction of the common support, and the formal within–between decomposition.

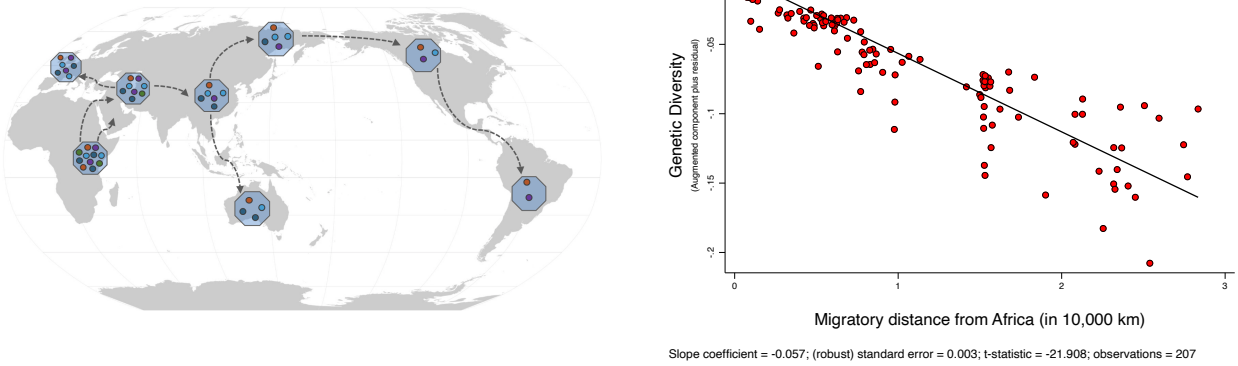
ical endowments. This measure captures differences in the composition of ancestral environments independently of their scale.

3.3. Population Diversity

Ancestral population diversity captures the dispersion of inherited predispositions within the founder population that settled each ecological niche and initiated the process of cultural evolution. Its global distribution was shaped by humanity's dispersal across the globe during the prehistoric Out-of-Africa migration and the associated serial founder effect, which generated systematic variation in inherited diversity across ancestral homelands.

Prehistoric Human Dispersal and the Serial Founder Effect. The long-run imprint of ancestral diversity on cultural heterogeneity is examined by leveraging the prehistoric exodus of humankind from Africa tens of thousands of years ago and the subsequent dispersal of humanity across the planet as a quasi-natural experiment in the formation of population diversity worldwide.

This dispersal generated systematic cross-societal variation in ancestral diversity that predates recorded history and is exogenous to subsequent institutional, economic, and cultural developments. As successive waves of migrants departed from earlier settlements to populate new territories, the sequential nature of this dispersal produced the well-documented serial founder effect, in which subsampling and population bottlenecks generated a progressive decline in inherited diversity among founder populations located at greater migratory distances from the cradle of humanity in Africa (Figure 7).[20]



(a) The Serial Founder Effect

(b) Distance from Cradle & Declining Diversity

Figure 7: The Serial Founder Effect and the Decline in Inherited Diversity

Notes: Panel (a) illustrates the progressive decline in population diversity along prehistoric migratory routes from East Africa. Panel (b) presents the unconditional association between inherited diversity within indigenous ethnic groups and their migratory distance from East Africa (Table A.4, Column (1)).

[20] Appendix A.3 presents an extensive analysis of the serial founder effect and its robust empirical foundations. In particular, it establishes that the relationship is robust to the inclusion of a wide array of geographical controls and continent fixed effects, as well as to the exclusion of Africa.

Beyond providing a quasi-natural experiment in the formation of ancestral diversity, the prehistoric Out-of-Africa migration constituted a fundamental force shaping its global distribution. By generating systematic differences in inherited heterogeneity across human populations, it established the deep historical foundation for contemporary cross-societal variation in cultural diversity.[21]

Measuring Population Diversity Across Empirical Settings. The measure of ancestral population diversity is adapted to the population structure of each empirical setting. For indigenous ethnic groups, whose ancestral populations are associated with a specific ethnic homeland, ancestral population diversity is captured by the migratory distance from East Africa to that homeland along prehistoric migration routes. The serial founder effect implies that ethnic groups located at greater migratory distances descended from less diverse founder populations.

Contemporary national populations, by contrast, often descend from multiple ancestral homelands as a result of post-1500 population movements. Their ancestral population diversity is therefore captured by ancestry-adjusted migratory distance, constructed as the weighted average of the migratory distances from East Africa to the ancestral homelands represented in the contemporary population, with weights reflecting their proportional representation.[22] The same adjustment is applied to the ancestral homelands of second-generation migrant groups, since these homelands may themselves comprise populations of multiple deeper ancestral origins.

4. Roots of the Cultural Mosaic Across Societies

Differences in ancestral ecological conditions shaped the global mosaic of cultural expressions. As populations adapted to their respective environments, cultural evolution induced convergence toward traits better suited to local conditions. Yet ecological distance between ancestral environments generated cultural distance across societies, giving rise to the mosaic of cultural traits across the globe. The theory predicts that greater ecological distance between the ancestral environments of founder populations tended to generate greater cultural distance between their descendant societies. This relationship is predicted to be less pronounced the larger is the difference in ancestral diversity between the two populations, reflecting differential adaptive capacity.

4.1 Empirical Strategy

The empirical strategy exploits the predetermined nature of ancestral ecological conditions, ruling out reverse causality. Nevertheless, ecological distance may be correlated with other historical forces that contributed to cultural divergence.

[21] As is customary, we associate the cradle of humanity with East Africa and estimate the impact of migratory distance from East Africa on population diversity. Although there is some uncertainty regarding the specific regions within Africa where humans originated (e.g., Ragsdale et al. (2023)), since humans appear to have dispersed to the rest of the globe via East Africa, different points of origin within the continent would only result in augmenting the distances to ancestral homelands outside Africa by a similar constant, sustaining the qualitative relationship between migratory distance and inherited diversity. However, given the uncertainty about humanity's dispersal patterns within Africa, the estimated effect would be expected to be more precise when African populations are excluded.

[22] The ancestry weights are derived from the post-1500 migration matrix of Putterman and Weil (2010).

The pairwise structure of the analysis permits the inclusion of society fixed effects, absorbing all characteristics associated with either society in a pair, including its geography, history, institutions, economic development, and ancestral composition. Identification therefore derives from whether a given society is culturally more distant from societies whose ancestral environments were more dissimilar, relative to its average cultural distance from all other societies. Consequently, only factors that vary at the pair level can confound the estimated relationship.

The principal pair-level concern is geographical separation. Spatially distant societies may have developed more distinct cultural traits because limited interaction constrained cultural diffusion and may also have been characterized by more dissimilar ancestral environments. The analysis therefore accounts for the geodesic distance between each pair of societies.

Lastly, selection into environments based on preexisting cultural traits would have been largely infeasible, since populations entering novel ecological niches tens of thousands of years ago would have lacked the knowledge needed to identify the environment-specific fitness-maximizing cultural trait before settlement. Post-settlement experimentation and observation over decades were required to infer the trait best suited to the prevailing environment (Appendix D).

4.2 Empirical Model

The prediction is examined using pairwise regressions with society fixed effects of the form

$$d^c_{ij} = \alpha + \beta_1 d^e_{ij} + \beta_2 d^\omega_{ij} + \beta_3 \left(d^e_{ij} \times d^\omega_{ij}\right) + X'_{ij}\Gamma + z_i + z_j + \varepsilon_{ij}, \tag{24}$$

where d^c_{ij} is the cultural distance between societies i and j, d^e_{ij} is the ecological distance between their ancestral environments, and $d^\omega_{ij} \equiv |\omega_i - \omega_j|$ is the absolute difference in ancestral diversity between societies i and j. The vector X_{ij} includes the geodesic distance between the two societies, while z_i and z_j are fixed effects for societies i and j, respectively. Both focal distance variables are standardized before estimation, and the interaction is formed from their standardized values. The theory predicts that $\beta_1 > 0$, $\beta_2 > 0$, and $\beta_3 < 0$.[23] Standard errors are two-way clustered at the society level.

4.3 Findings

The ethnic-pair results, reported in Table I and Figure 8, are consistent with the predicted signs of the main effects and interaction. Ancestral ecological distance exhibits a positive and highly significant association with cultural distance in both folkloric and musical traditions. The association remains positive and highly significant after accounting for differences in ancestral diversity and geodesic distance. Moreover, the interaction between ancestral ecological distance and the absolute difference in ancestral diversity is negative and highly significant across both

[23] The linear interaction provides an approximation to the nonlinear comparative statics derived in Proposition 4. The Proposition implies that the ecological-distance gradient remains positive but diminishes as ancestral-diversity distance increases. Yet, the linear interaction imposes a constant rate of decline in this gradient and therefore does not permit it to flatten toward zero. Consequently, at sufficiently high levels of ancestral-diversity distance, a negative interaction may mechanically generate a negative fitted gradient.

cultural domains, providing evidence that the ecological-distance gradient declines as the difference in ancestral diversity increases.

Table I: Ancestral Ecological Distance and Cross-Ethnic Cultural Distance

	Folkloric distance			Musical distance		
	(1)	(2)	(3)	(4)	(5)	(6)
Ancestral ecological distance	0.010***	0.0075***	0.0076***	0.0075***	0.0052***	0.0050***
	(0.00041)	(0.00035)	(0.00035)	(0.00054)	(0.00055)	(0.00054)
Absolute difference in ancestral diversity			0.0097***			0.0047***
			(0.00063)			(0.00061)
Ancestral ecological distance × absolute difference in ancestral diversity			−0.0050***			−0.0035***
			(0.00032)			(0.00042)
Ethnicity FE	✓	✓	✓	✓	✓	✓
Geodesic distance		✓	✓		✓	✓
Dep. var. mean	0.96	0.96	0.96	0.67	0.67	0.67
Observations	457444	457405	457405	339074	339062	339062
Adjusted R^2	0.31	0.40	0.44	0.72	0.72	0.72

Notes: Each column reports estimates from pairwise regressions of cultural distance between societies on ancestral ecological distance, measured as the cosine distance between vectors of geographical endowments. Cultural distance is computed using the Jaccard distance for folkloric and musical traits. Ancestral ecological distance and the absolute difference in ancestral diversity are standardized before estimation. The interaction is formed from the standardized variables, while the outcomes remain in their natural units. Two-way standard errors are reported in parentheses. The unit of observation is an ethnic pair. *** Significant at the 1 percent level.

Thus, consistent with the predicted interaction effect, the association between ecological and cultural distance is weaker when the two populations differ more substantially in their ancestral diversity. The estimated magnitudes are meaningful. Based on the estimates in columns (1) and (4), a movement from the lowest to the highest level of ancestral ecological distance in the respective samples corresponds to a movement from the median to the upper bound of the pairwise folkloric-distance distribution and from the median to approximately the 58th percentile of the pairwise musical-distance distribution.

The country-pair results in Table II and Figure 8, reveal a similar pattern for contemporary norms, values, and attitudes and for visual representations of common concepts. Ancestral ecological distance is positively and highly significantly associated with both WVS distance and visual conceptual distance. The coefficients remain positive and highly significant after accounting for differences in ancestral diversity and geodesic distance. The interaction between ancestral ecological distance and the absolute difference in ancestral diversity is negative and highly significant, indicating that the association between ancestral ecological and cultural distance becomes weaker as the difference in ancestral diversity increases.[24] The magnitudes are substantial. Based on the estimates in Columns (1) and (4), a movement from the lowest to the highest level of ancestral ecological distance corresponds to a movement from the median to roughly the 86th percentile of the WVS-distance distribution and the 84th percentile of the visual-conceptual-distance distribution.

[24]Comparisons across second-generation migrants within a given host country do not provide an informative test in this setting, since cultural distance among them may reflect differences in rates of convergence toward the host-country cultural environment rather than the ecological distance between their parental homelands.

Table II: Ancestral Ecological Distance and Cross-Country Cultural Distance

	WVS distance			Visual conceptual distance		
	(1)	(2)	(3)	(4)	(5)	(6)
Ancestral ecological distance	0.027***	0.025***	0.023***	0.038***	0.024***	0.019***
	(0.0032)	(0.0033)	(0.0029)	(0.0036)	(0.0042)	(0.0042)
Absolute difference in ancestral diversity			0.013**			0.027***
			(0.0054)			(0.0062)
Ancestral ecological distance × absolute difference in ancestral diversity			−0.010***			−0.017***
			(0.0029)			(0.0038)
Country FE	✓	✓	✓	✓	✓	✓
Geodesic distance		✓	✓		✓	✓
Dep. var. mean	0.14	0.14	0.14	0.22	0.22	0.22
Observations	4751	4751	4751	2078	2078	2078
Adjusted R^2	0.49	0.50	0.51	0.75	0.82	0.84

Notes: Each column presents estimates from pairwise regressions of cultural distance between countries on ancestral ecological distance, measured as the cosine distance between vectors of geographical endowments. In Columns (1)–(3), cultural distance is computed using F_{ST} for norms, values, and attitudes from the World Values Survey. In Columns (4)–(6), visual conceptual distance is 100 times cross-country drawing distance net of average within-country drawing dissimilarity and averaged equally over the 245 concepts common to all 65 countries. Ancestral ecological distance and the absolute difference in ancestral diversity are standardized. The interaction is formed from the standardized variables, while the outcomes remain in their natural units. All columns include separate country fixed effects for the two endpoints. Two-way clustered standard errors at the country endpoints are reported in parentheses. The unit of observation is a country pair. *** Significant at the 1 percent level. ** Significant at the 5 percent level.

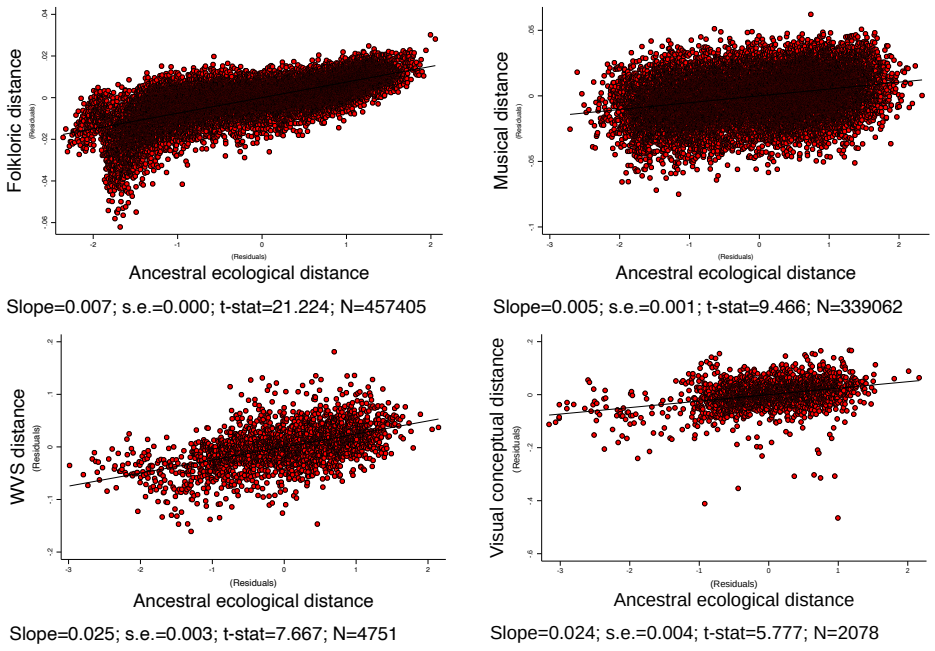


Figure 8: Ancestral Ecological Distance and Cultural Distance Across Societies

Notes: The figure presents partial-regression plots of the relationship between ancestral ecological distance and cultural distance across societies, accounting for geodesic distance and separate endpoint fixed effects. The upper panels report pairwise folkloric and musical distance across indigenous ethnic groups. The lower panels report pairwise distance in norms, values, and attitudes from the World Values Survey and visual conceptual distance across countries.

5. Roots of Cultural Diversity Within Societies

The theory predicts that founder populations characterized by greater population diversity give rise to greater cultural diversity in their descendant societies, despite convergence induced by adaptation to a common environment and prevailing societal norms.[25] This prediction is examined across four complementary empirical settings: (i) diversity in the folkloric and musical traditions of indigenous ethnic groups, (ii) dispersion in norms, values, and attitudes within contemporary nations, (iii) dispersion in norms, values, and attitudes among second-generation migrant groups, and (iv) diversity in visual representations of common concepts within contemporary societies. These settings permit the analysis to trace the imprint of ancestral population diversity across distinct cultural domains as well as historical and modern contexts, mitigating endogeneity concerns.

5.1. Empirical Strategy

The empirical strategy exploits the prehistoric Out-of-Africa migration and the associated serial founder effect as a source of variation in ancestral population diversity. The temporal sequence of events rules out reverse causality: cultural diversity observed in indigenous traditions or contemporary populations could not have influenced migratory distance from East Africa tens of thousands of years ago. The principal identification concern is therefore that migratory distance may be correlated with geographical and historical forces that independently shaped cultural diversity.

Across the different empirical settings, the analysis accounts for geographical characteristics that may be associated with both migratory distance and cultural diversity, including absolute latitude, ecological diversity, geographical isolation, and land suitability for agriculture. These factors may influence biodiversity, population density, community size, and opportunities for cultural creation and diffusion. In the contemporary-country analyses, the corresponding variables are adjusted for the ancestral composition of each population. The specifications also include continent fixed effects, thereby absorbing continent-specific geographical and historical forces. In the indigenous ethnic-group analyses, these fixed effects additionally mitigate concerns arising from regional differences in the documentation of folkloric and musical traditions.

More generally, differences in cultural diversity across both indigenous ethnic groups and contemporary national populations may partly reflect political and economic institutions that developed in response to historical population diversity.[26] To mitigate this concern, the analysis complements the cross-ethnic and cross-country evidence with evidence from second-generation migrants originating from different ancestral homelands but born and residing in the same host country. A host-country fixed effect absorbs differences in the contemporary institutional and economic environment, permitting the association to be examined across ancestral groups facing common contemporary conditions.

The contemporary national-population analyses raise two additional concerns. First, migratory distance from East Africa is associated with ethnolinguistic fragmentation (Ashraf and Galor,

[25] A substantial share of cultural diversity reflects variation *within* ethnic groups (Desmet et al., 2017).
[26] Arbatlı et al. (2020), Ashraf and Galor (2013b), and Galor and Klemp (2015).

2013a). The relationship between ancestral diversity and contemporary cultural diversity could therefore reflect variation between ethnic groups rather than cultural dispersion within them. The analysis consequently accounts for ethnic and ethnolinguistic fractionalization and examines whether the estimated relationship is primarily driven by within-group variation.

Second, post-1500 migration may have altered the ancestral composition of contemporary national populations. The analysis addresses this concern by constructing ancestry-adjusted measures of migratory distance and geographical characteristics and by examining alternative samples of countries that experienced more limited post-1500 population movements, including Old World countries and countries with substantial native populations.

5.2. Empirical Models

Folklore and Music. The proposed hypothesis is examined using linear regressions of cultural diversity on predicted ancestral diversity, predicted by migratory distance from East Africa, accounting for continent fixed effects and potential geographical confounders:[27]

$$CD_e = \alpha + \beta D_e + \tau Z_e + \zeta_k + \epsilon_e,$$

where CD_e is the degree of folkloric or musical diversity in ethnic group e. The independent variable D_e is the migratory distance from the cradle of humanity to the homeland of ethnic group e, Z_e is a vector of confounding geographical controls, including absolute latitude, mean caloric suitability, standard deviation in caloric suitability, and a small island indicator, and ζ_k is a continent fixed effect.[28] The coefficient of interest, β, is expected to be negative.

The analysis is conducted using available samples of indigenous ethnic groups with documented measures of folkloric or musical diversity, as well as subsamples excluding African ethnic groups.[29]

Norms, Values, and Attitudes in National Populations. A linear regression model examines the association between ancestral diversity, captured by migratory distance from the cradle of humanity in Africa, and contemporary cultural diversity, accounting for continent fixed effects and potential ancestral geographical confounders. In particular, the regression model is:

[27] The distribution of motifs across indigenous ethnic groups is highly skewed: half of the groups contain fewer than 62 motifs, whereas the top 1% contain more than 450 (Table A.2). The baseline analysis therefore uses the logarithm of folkloric diversity and, for comparability, applies the same transformation to musical diversity. Estimation in levels yields qualitatively similar results (Table A.5).

[28] In Cantometrics, each song is coded along the same 37 musical dimensions, and musical diversity counts the distinct feature categories observed across the songs assigned to an ethnic group. A larger song sample therefore mechanically expands the opportunity to observe additional categories. We consequently condition on the number of songs to compare musical repertoires at a given sampling intensity. Berezkin's source count, by contrast, records the number of bibliographic titles consulted for each tradition. Titles are not standardized sampling units: publications differ substantially in their scope and in the number of narratives and motifs they document. The number of titles therefore does not provide an analogous adjustment for sampling exposure and may partly reflect substantive variation in the extent and richness of a tradition's documentation. Nevertheless, in our preferred specification, controlling for it strengthens the result: the coefficient on migratory distance becomes larger in absolute magnitude and considerably more precisely estimated, increasing both its economic and statistical significance.

[29] As discussed in Appendix A.4, uncertainty regarding the location of human origins within Africa may affect the estimates; the analysis therefore includes and excludes African ethnic groups.

$$CD_{v,c} = \alpha + \beta D_c + \tau Z_c + \delta_v + \zeta_k + \epsilon_{v,c},$$

where $CD_{v,c}$ represents the dispersion of responses to social norm v in country c; the independent variable, D_c, is the ancestry-adjusted migratory distance from East Africa to country c; Z_c is a vector of ancestry-adjusted geographical controls; δ_v is a social-norm fixed effect; and ζ_k is a continent fixed effect. The coefficient of interest, β, is hypothesized to be negative.

Norms, Values, and Attitudes Among Second-Generation Migrants. A linear regression model examines the association between ancestral diversity, captured by migratory distance from the cradle of humanity in Africa, and cultural diversity among second-generation migrants, accounting for a host-country fixed effect and potential geographical confounders in their ancestral homelands. In particular, the following linear regression model is estimated:

$$CD_{v,h,c} = \alpha + \beta D_h + \tau Z_h + \delta_v + \zeta_k + \theta_c + \epsilon_{v,h,c},$$

where the dependent variable, $CD_{v,h,c}$, represents the dispersion of responses to social norm v among second-generation migrants from ancestral homeland h who were born and reside in host country c; the independent variable, D_h, is the ancestry-adjusted migratory distance from East Africa to ancestral homeland h; Z_h is a vector of ancestry-adjusted geographical controls in the homeland; δ_v is a social-norm fixed effect; ζ_k is a continent fixed effect; and θ_c is a host-country fixed effect. The coefficient of interest, β, is hypothesized to be negative.[30]

Visual Representations in National Populations. A linear regression model examines the association between ancestral diversity, captured by migratory distance from the cradle of humanity in Africa, and visual conceptual diversity within contemporary countries, accounting for continent fixed effects and potential ancestral geographical confounders. In particular, the following linear regression model is estimated:

$$VCD_c = \alpha + \beta D_c + \tau Z_c + \zeta_k + \epsilon_c,$$

where VCD_c represents visual conceptual diversity in country c, measured as the mean pairwise cosine distance between visual representations of common concepts; D_c, is the ancestry-adjusted migratory distance from East Africa to country c; Z_c is a vector of ancestry-adjusted geographical controls; and ζ_k is a continent fixed effect. The coefficient, β, is hypothesized to be negative.

5.3 Findings

Folklore and Music. Table III presents the estimated relationship between ancestral population diversity, as captured by migratory distance from the cradle of humanity, and folkloric diversity. This relationship is illustrated in Figure 9.

[30] Standard errors are clustered at the ancestral-homeland level, since the main independent variable, ancestry-adjusted migratory distance from East Africa, varies at that level.

The estimates in Column (1) reveal a highly significant, unconditional negative association between migratory distance from the cradle of humanity and folkloric diversity. Column (2) shows that the negative association between migratory distance from the cradle of humanity and folkloric diversity is present within continents. Column (3) demonstrates that accounting for various potentially confounding geographical factors does not alter the qualitative association or its statistical significance. Finally, consistent with the uncertainty surrounding the exact origin of humans within Africa, Column (4) shows that the estimated association increases in absolute value and becomes more statistically significant when African ethnic groups are excluded from the analysis.

Table III: The Out-of-Africa Migration and Folkloric Diversity

	Folkloric Diversity			
	(1)	(2)	(3)	(4)
Migratory distance	−0.18***	−0.58***	−0.45***	−0.62***
from the cradle of humanity	(0.043)	(0.15)	(0.16)	(0.17)
Continent FE		✓	✓	✓
Geographical controls			✓	✓
Exclusion of Africa				✓
Dep. var. mean	87	87	87	93
Observations	958	958	956	813
Adjusted R^2	0.018	0.20	0.24	0.24

Notes: The table presents a significant negative association between migratory distance from East Africa and folkloric diversity among indigenous ethnic groups. Migratory distance is measured in units of 10,000 km. Folkloric diversity is defined as the log number of motifs. Geographic controls include absolute latitude, ecological diversity, caloric suitability, and a small island dummy. As caloric suitability is not reported for the Polynesian islands of Kapingamarangi and Ulithi, the number of observations in Column (3) is reduced to 956. Heteroskedasticity-robust standard errors are reported in parentheses. *** Significant at the 1 percent level.

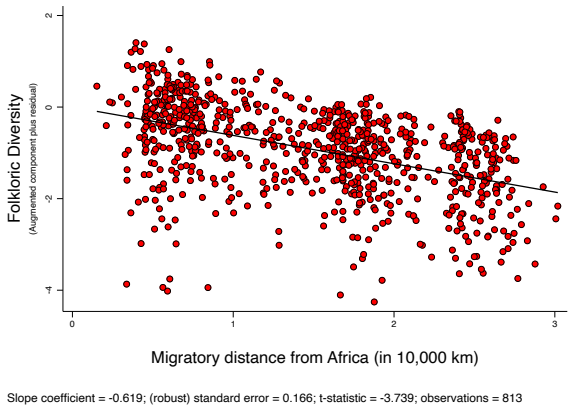


Figure 9: The Out-of-Africa Migration and Folkloric Diversity

Notes: A scatterplot of the association between folkloric diversity and migratory distance from East Africa among indigenous ethnic groups (Table III, Column (4)).

The association between ancestral diversity, as captured by prehistoric migratory distance from the cradle of humanity, and folkloric diversity is substantial. A shift from the lowest to the highest level of migratory distance in the sample is associated with a decline from the median to the 6th percentile of the folkloric-diversity distribution.

Table IV presents the results of the impact of ancestral population diversity, as captured by migratory distance from the cradle of humanity, on musical diversity, as depicted in Figure 10. The estimates in Column (1) reveal a highly significant negative association between migratory distance from the cradle of humanity and musical diversity in a parsimonious specification that controls for the logarithm of the number of songs sampled. Column (2) shows that the negative association between migratory distance from the cradle of humanity and musical diversity is present within continents. Column (3) demonstrates that accounting for various potentially confounding geographical factors does not alter the qualitative association or its statistical significance. Lastly, consistent with the uncertainty surrounding the exact origin of humans within Africa, Column (4) shows that the estimated association increases in absolute value and becomes more statistically significant when African ethnic groups are excluded from the analysis.

Table IV: The Out-of-Africa Migration and Musical Diversity

	Musical Diversity			
	(1)	(2)	(3)	(4)
Migratory distance	−0.020***	−0.071***	−0.077***	−0.12***
from the cradle of humanity	(0.0075)	(0.025)	(0.026)	(0.027)
Continent FE		✓	✓	✓
Geographical controls			✓	✓
Exclusion of Africa				✓
Dep. var. mean	79	79	79	79
Observations	825	825	824	630
Adjusted R^2	0.89	0.90	0.90	0.90

Notes: The table demonstrates a significant negative association between migratory distance from East Africa and musical diversity among indigenous ethnic groups. Migratory distance is measured in units of 10,000 km. Musical diversity is defined as the log number of musical features. All specifications control for the logarithm of the number of songs sampled from each ethnic group. The geographical controls include absolute latitude, ecological diversity, caloric suitability, and a small island dummy. As caloric suitability is not reported for the Polynesian island of Ulithi, the number of observations in Column (3) is reduced to 824. Heteroskedasticity-robust standard errors are reported in parentheses. *** Significant at the 1 percent level. ** Significant at the 5 percent level.

The association between ancestral population diversity, as captured by prehistoric migratory distance from the cradle of humanity, and musical diversity is pronounced. A shift from the lowest to the highest level of migratory distance in the sample is associated with a decline from the median to the 28th percentile of musical diversity.

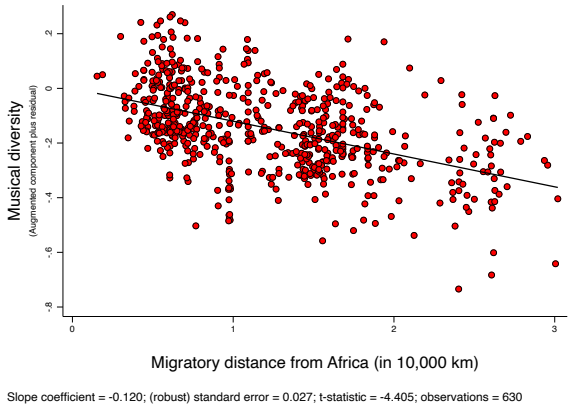
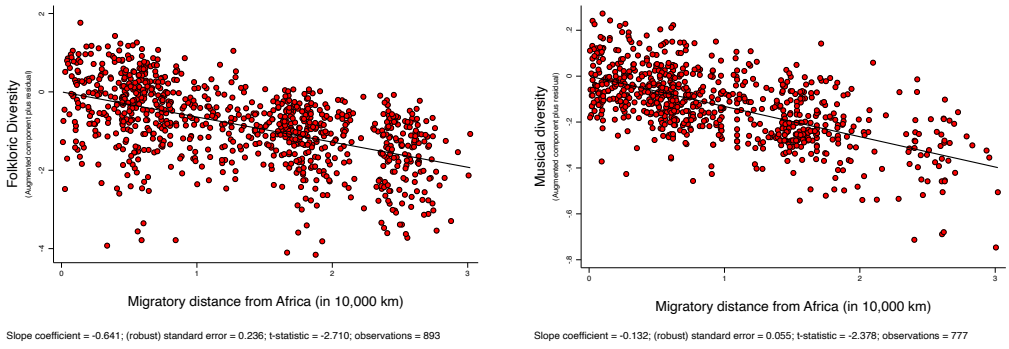


Figure 10: The Out-of-Africa Migration and Musical Diversity

Notes: The scatterplot of the association between musical diversity and migratory distance from East Africa among indigenous ethnic groups (Table IV, Column (4)).



(a) Folklore (b) Music

Figure 11: The Out-of-Africa Migration and Cultural Diversity within Indigenous Ethnic Groups: Conditional on Country fixed effects

Notes: The figure presents scatterplots depicting the association between cultural diversity and migratory distance from East Africa among indigenous ethnic groups. Panel (a) displays the scatterplot for folkloric diversity, while Panel (b) shows the scatterplot for musical diversity. Note that the number of observations is reduced compared to the baseline, as singletons—single indigenous ethnic groups in a particular country—are automatically excluded from the analysis when using Stata command *reghdfe*, as their inclusion could lead to incorrect inference (Correia, 2015).

These baseline findings regarding the association between ancestral diversity, as captured by migratory distance from the cradle of humanity, and folkloric and musical diversity are remarkably robust, holding steady across a range of robustness checks and sensitivity analyses: (a) accounting for alternative estimation methods designed for count data and uneven dispersion in the dependent variable (Table A.5); (b) implementing alternative regional fixed effects, e.g., viewing Asia and Europe as a single region and including North Africa in the Old World (Table A.7)[31], and

[31]The baseline specification uses conventional continent fixed effects. As a robustness check, Europe and Asia are combined into a single region, reflecting their contiguous landmass and extensive preindustrial flows of people, goods, and ideas. In addition, despite the more limited preindustrial flows of people, goods, and ideas between North and

(c) including country fixed effects to exploit variation within ethnicities within modern national boundaries (Figure 11).[32]

Norms, Values, and Attitudes in National Populations. Table V presents the baseline analysis of the association between ancestral diversity, as captured by migratory distance from the cradle of humanity, and cultural diversity among individuals in contemporary societies, illustrated in Figure 12. The estimates in Column (1) reveal a highly significant unconditional negative association between migratory distance from East Africa and the dispersion of social norms, values, and attitudes, as captured by the coefficient of variation. Column (2) shows that the association remains evident when identified exclusively from within-continent variation. Column (3) demonstrates that accounting for potentially confounding geographical factors does not affect its magnitude or statistical significance. Finally, Column (4) shows that excluding Africa increases the absolute magnitude and statistical significance of the estimated association.

Table V: The Out-of-Africa Migration and Contemporary Dispersion in Cultural Values within Countries

	Dispersion in cultural value			
	(1)	(2)	(3)	(4)
Ancestral migratory distance from the cradle of humanity	−0.076***	−0.096***	−0.085**	−0.12***
	(0.022)	(0.029)	(0.034)	(0.033)
Continent FE		✓	✓	✓
Geographical controls			✓	✓
Exclusion of Africa				✓
Dep. var. mean	0.56	0.56	0.56	0.55
Demographic bins	26,558	26,558	26,558	23,562
Cultural values	383	383	383	380
Countries	112	112	112	96
Adjusted R^2	0.62	0.62	0.62	0.65

Notes: The table shows a significant negative association between ancestry-adjusted migratory distance from East Africa and contemporary dispersion in cultural values within countries. Ancestry-adjusted migratory distance is measured in units of 10,000 km. Dispersion in cultural values among individuals within each society is captured by the coefficient of variation with respect to each value, accounting for cultural value fixed effects. Ancestry-adjusted geographical controls are absolute latitude, ecological diversity, caloric suitability, and a small island dummy. Heteroskedasticity-robust standard errors (clustered at the country level) are reported in parentheses. *** Significant at the 1 percent level.

The association between prehistoric migratory distance from East Africa and contemporary cultural diversity is substantial. Specifically, an increase in this distance by 20,000 km, corresponding to a shift from the lowest to the highest ancestry-adjusted migratory distance from East Africa, is

South America, replacing their separate fixed effects with a single Americas fixed effect leaves the qualitative results unchanged under the preferred specification with geographical controls and the exclusion of Africa.

[32]Spatial correlation among neighboring observations has little effect on the precision of the estimates. Similar migratory distances from East Africa do not imply geographic proximity, since prehistoric migration proceeded in multiple directions, leaving many societies with comparable migratory distances separated by thousands of kilometers. Accordingly, accounting for spatial correlation using Conley (1999) has a negligible effect on the results (Table A.6).

associated with a decline in the dispersion of cultural values from the median to the 2nd percentile of its distribution.

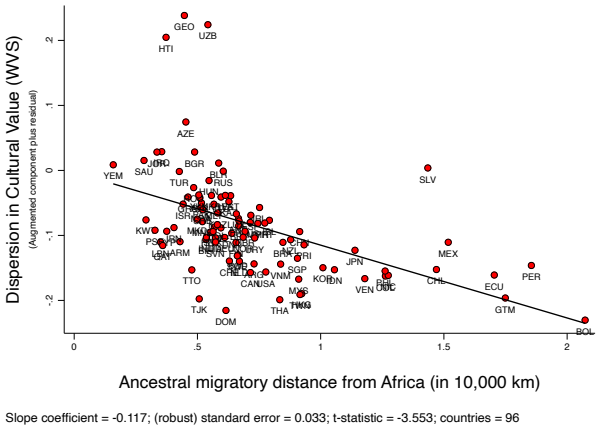


Figure 12: The Out-of-Africa Migration and Contemporary Dispersion in Cultural Values within Countries

Notes: The figure presents a scatterplot illustrating the association between contemporary dispersion in cultural values within countries and ancestry-adjusted migratory distance from East Africa (Table V, Column (4)). A non-parametric test (Lind and Mehlum, 2010) indicates that this relationship is not hump-shaped.

The baseline findings remain qualitatively unchanged when: (a) individuals are grouped by sex, age, survey wave, or educational attainment (Table B.9); (b) alternative estimation methods are employed (Figure B.1); and (c) the sample is restricted to homelands that did not experience substantial migration (Figure B.2). Furthermore, as shown in Table B.12, the association is not explained by ethnic or ethnolinguistic fractionalization.[33]

Norms, Values, and Attitudes Among Second-Generation Migrants. Table VI reports the baseline analysis of the association between ancestral diversity, as captured by migratory distance from the cradle of humanity, and cultural diversity among second-generation migrants, as depicted in Figure 13.

The estimates in Column (1) suggest a highly significant unconditional negative association between the migratory distance from East Africa to the ancestral homeland of second-generation migrants and the dispersion of their social norms, values, and attitudes. Column (2) shows that the association remains evident when identified exclusively from within-continent variation across ancestral homelands. Column (3) demonstrates that accounting for potentially confounding ancestral geographical factors does not affect its magnitude or statistical significance. Finally, Column

[33]The impact of spatial correlation among neighboring observations on the precision of the estimated effects of migratory distance from East Africa on cultural diversity is minimal. Societies with similar migratory distances from East Africa are not necessarily geographically proximate. Migration out of Africa unfolded in multiple directions, leaving many societies with comparable migratory distances separated by thousands of kilometers and therefore plausibly spatially independent. As shown in Table B.11, accounting for spatial correlation using Conley (1999) has a negligible effect on the estimates.

(4) shows that excluding Africa increases the absolute magnitude and statistical significance of the estimated association.

Table VI: The Out-of-Africa Migration and Contemporary Dispersion in Cultural Values within Populations of Second-Generation Migrants in Europe

	Dispersion in cultural value			
	(1)	(2)	(3)	(4)
Ancestral migratory distance from the cradle of humanity	−0.029**	−0.035**	−0.032**	−0.057***
	(0.013)	(0.016)	(0.014)	(0.013)
Continent FE		✓	✓	✓
Geographical controls			✓	✓
Exclusion of Africa				✓
Dep. var. mean	0.42	0.42	0.42	0.42
Demographic bins	68,381	68,381	68,381	61,288
Cultural values	119	119	119	119
Host countries	39	39	39	39
Ancestral homelands	133	133	133	99
Adjusted R^2	0.21	0.21	0.21	0.24

Notes: The table demonstrates a significant negative association between ancestry-adjusted migratory distance from East Africa and dispersion in cultural values within populations of second-generation migrants in Europe. Ancestry-adjusted migratory distance is measured in units of 10,000 km. Dispersion in cultural values among individuals from an identical ancestral origin within each European country is captured by the coefficient of variation with respect to each value, accounting for cultural value and a host-country fixed effect. Ancestry-adjusted geographical controls are absolute latitude, ecological diversity, caloric suitability, and a small island dummy. Heteroskedasticity-robust standard errors (clustered at the ancestral homeland level) are reported in parentheses. *** Significant at the 1 percent level; ** Significant at the 5 percent level.

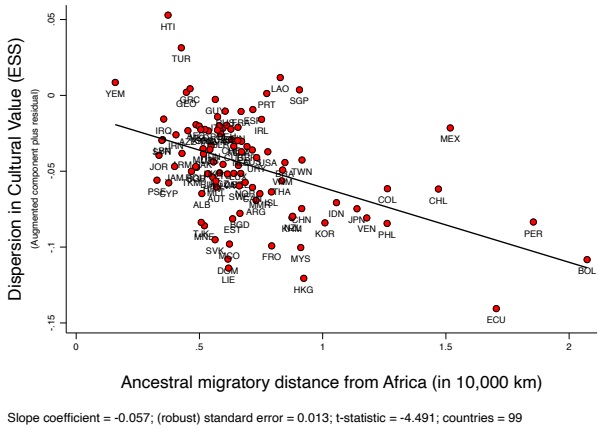


Figure 13: The Out-of-Africa Migration and Contemporary Dispersion in Cultural Values within Populations of Second-Generation Migrants in Europe

Notes: Scatterplot of the association between contemporary dispersion in cultural values and ancestry-adjusted migratory distance from East Africa across populations of second-generation migrants in Europe (Table VI, Column (4)). A non-parametric test (Lind and Mehlum, 2010) suggests that this relationship is not hump-shaped.

The association between prehistoric migratory distance from East Africa and contemporary cultural diversity among second-generation migrants is sizable. Specifically, an increase in this distance by 20,000 km, corresponding to a shift from the lowest to the highest ancestry-adjusted migratory distance from East Africa, is associated with a decline in the dispersion of cultural values from the median to the 29th percentile of its distribution.

The baseline findings remain qualitatively unchanged when: (a) individuals are grouped by sex, age, survey wave, or educational attainment (Table B.10); and (b) alternative estimation methods are employed (Figure B.1). Furthermore, as shown in Table B.14, the association is not explained by ethnic or ethnolinguistic fractionalization.

Visual Representations in National Populations. The findings reveal a pronounced and highly significant positive association between ancestral population diversity and visual conceptual diversity within contemporary nations. As reported in Table VII, ancestry-adjusted migratory distance from East Africa is negatively associated with VCD across all four strict-support specifications.

Table VII: The Out-of-Africa Migration and Visual Conceptual Diversity within Countries

	Visual Conceptual Diversity (VCD points)			
	(1)	(2)	(3)	(4)
Ancestry-adjusted migratory distance from the cradle of humanity	−0.447***	−0.495***	−0.414***	−0.395***
	(0.089)	(0.096)	(0.091)	(0.090)
Continent FE		✓	✓	✓
Geographical controls			✓	✓
Exclusion of Africa				✓
Dep. var. mean	22.75	22.75	22.75	22.75
Observations	65	65	65	62
Adjusted R^2	0.44	0.48	0.53	0.57

Notes: The dependent variable is Visual Conceptual Diversity (VCD points), defined as 100 times raw mean pairwise cosine distance averaged over the 245 concepts common to every country in the strict-support sample. Each country–concept cell contains 100 recognized drawings. Ancestry-adjusted migratory distance is measured in units of 10,000 km. Geographical controls are ancestry-adjusted absolute latitude, ecological diversity, caloric suitability, and a small island dummy. Heteroskedasticity-robust standard errors are reported in parentheses. *** Significant at the 1 percent level.

Under the preferred specification, which includes continent fixed effects and ancestry-adjusted geographical controls and excludes Africa, an additional 10,000 km of migratory distance is associated with 0.395 fewer VCD points, with a standard error of 0.090. A one-standard-deviation increase in migratory distance is therefore associated with a 0.60-standard-deviation decline in VCD. Figure 14 illustrates this relationship, while Appendix Table B.1 reports the corresponding extended-support estimates.

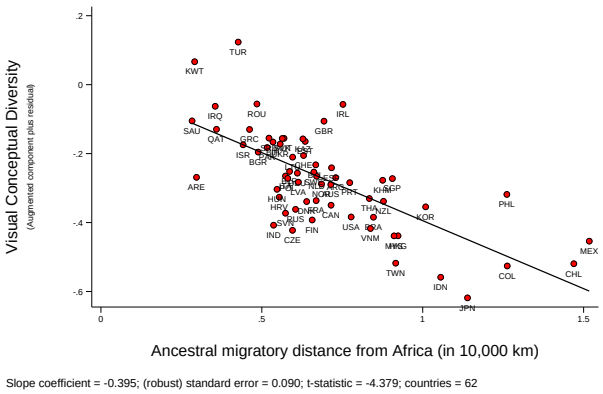


Figure 14: The Out-of-Africa Migration and Visual Conceptual Diversity within Countries

Notes: The association between visual conceptual diversity and ancestry-adjusted migratory distance from East Africa in the strict-support sample, excluding Africa. (Table VII, Column (4)). The regression includes continent fixed effects and ancestry-adjusted geographical controls.

Split-half reliability is high: scores from disjoint cell halves correlate 0.858. Appendix B.2 reports extended-support, alternative-aggregation, and semantic-domain estimates, correlations with WVS dispersion, and sensitivities to unrecognized drawings and non-overlapping months. The negative gradient persists across these checks, the sample restrictions in Figure B.3, and the fractionalization controls in Table B.13.

6. Concluding Remarks

The research advances the hypothesis that, as population movements and socioeconomic transformations exposed societies to new environments, inherited cultural traits became increasingly misaligned with prevailing conditions, setting in motion a process of cultural adaptation that fostered the compatibility between human populations and the environments they inhabited. It develops a unified theory of cultural evolution that captures this process during the formative stages of human history, characterizing cultural change as the outcome of the interplay among adaptation-based vertical transmission, horizontal diffusion, and fitness-based evolutionary selection. This framework establishes a unified foundation for the analysis of the forces that operated during the formative stages of human civilization, gave rise to the mosaic of cultural expressions across societies and variation in cultural diversity within them, and exerted an enduring influence on comparative development.

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Supplemental Appendix

Contents

A Ethnic-Level

A.1 Variable Definitions and Sources

A.1.1 Genetic Diversity

- Measured using an index commonly referred to as expected heterozygosity by population geneticists. At a given locus, this index is the probability that two alleles sampled independently from the population are different. The measure is averaged across loci and calculated from allelic frequencies, which reflect the occurrence of different gene variants (alleles) within the population. Data Source: Arbatlı et al. (2020).

A.1.2 Cultural Diversity

- **Folkloric diversity**: The total number of motifs that are prevalent in a given oral tradition (i.e., ethnic groups or clusters of ethnic groups along linguistic lines). Data Source: Berezkin (2015) and Michalopoulos and Xue (2021).

- **Folkloric distance:** For each society, we observe a binary vector indicating the presence or absence of 2,564 motifs. Pairwise distance between societies is computed using the Jaccard distance, defined as one minus the ratio of the number of shared motifs to the total number of motifs present in at least one of the two societies. Formally, for two societies i and j, the Jaccard distance is

$$1 - \frac{|M_i \cap M_j|}{|M_i \cup M_j|},$$

where M_i and M_j denote the sets of motifs observed in each society. This measure captures similarity in the composition of folkloric traditions, focusing on the overlap in observed cultural elements. Data Source: Berezkin (2015) and Michalopoulos and Xue (2021).

- **Musical diversity**: The total number of musical features that are prevalent in a given musical tradition (i.e., ethnic groups). Data Source: Lomax (1962), Lomax (2017), Wood et al. (2022), and Wainstock (2026).

- **Musical distance:** For each society, we observe a vector of 216 musical features describing stylistic and structural characteristics. Pairwise distance between societies is computed using the Jaccard distance applied to these feature vectors. As in the folkloric case, the Jaccard distance measures the share of non-overlapping features relative to the union of features present in either society. This approach emphasizes differences in the presence of musical traits, thereby capturing variation in observable musical styles across societies. Data Source: Lomax (1962), Lomax (2017), Wood et al. (2022), and Wainstock (2026).

A.1.3 Migratory Distance from the Cradle of Humanity

- The migratory distance to each ethnic group is defined as the shortest traversable path from Omo I (Ethiopia)—the site of the earliest known Homo sapiens remains in East Africa—to the geographic centroid of that group. In alignment with archaeological evidence, the migratory path permits crossings of the Bab-el-Mandeb Strait, the Strait of Hormuz, and the Bering Strait while excluding the crossing of the Strait of Gibraltar and the Himalayan mountain range. Due to the limited capacity of early humans to traverse large bodies of water, migratory paths were confined to land masses. However, considering that sea levels at the time of the exodus during the Ice Age were nearly 100 meters lower than today, along with the ability of humans to cross shallow water, we permit travel within 100 km of the shoreline. Varying the buffer to 25 km or 50 km does not alter the results. Moreover, given the uncertain dynamics of the Serial Founder Effect over long maritime distances, it is assumed that oceanic travel to remote islands has no additional impact on diversity. Yet, permitting such an impact does not qualitatively affect our findings. Data Source: Authors' computations.

A.1.4 Ecological Distance

- Ancestral ecological distance is measured as the cosine distance between vectors of geographical endowments. For each society, we construct a vector of 40 geographic traits capturing agricultural suitability, terrain, and climatic conditions. These include variables such as overall caloric suitability, crop-specific suitability measures (e.g., wheat, rice, maize), elevation, irrigation potential, and a full set of bioclimatic indicators which summarize annual trends, seasonality, and extreme environmental conditions derived from temperature and precipitation data (e.g., annual means, seasonal variation, and conditions in wettest/driest or warmest/coldest periods).

  Pairwise distance between societies is computed using the cosine distance:

$$1 - \frac{G_i \cdot G_j}{\|G_i\| \, \|G_j\|},$$

where G_i and G_j denote the vectors of geographic traits for societies i and j. Cosine distance captures differences in the composition of ecological environments, independent of scale, by measuring the angle between the corresponding vectors. Data Source: Authors' computations.

A.1.5 Geographical Controls

- **Absolute latitude**: The absolute value of the latitude of the geodesic centroid of each indigenous ethnic group. Data Source: Authors' computation.
- **Caloric Suitability**: The maximum potential caloric yield attainable in each indigenous ethnic group, given the set of crops that are suitable for cultivation in the pre-1500 period. Data Source: Galor and Özak (2016).
- **Ecological Diversity**: Standard deviation of caloric suitability within the territory of each indigenous ethnic group. Data Source: Authors' computation based on Galor and Özak (2016).
- **Island**: A dummy variable that captures whether the indigenous ethnic group is located on a small island country as defined by the United Nations M49 classification. Data Source: United Nations Statistics Division.

A.2 Summary Statistics

Table A.1: The Out-of-Africa Migration and Diversity within Indigenous Ethnic Groups: Summary Statistics

	Mean	SD	Median	Min	Max	N
Expected heterozygosity	0.72	0.05	0.73	0.55	0.8	207
Migratory distance (km)	7448.94	7394.53	4351.75	182.46	28345.7	207
Absolute latitude	15.15	15.09	8.81	0.04	68.9	207
Caloric suitability (mean)	6094.02	2808.23	6298.59	0.00	12060.7	207
Caloric suitability (std)	1035.00	863.89	931.89	0.00	4313.0	207
Island	0.13	0.33	0.00	0.00	1.0	207

Notes: The table provides for all variables used in the data analysis the mean, the standard deviation (SD), the median, the minimum value (MIN), the maximum value (MAX), and the number of observations (N).

Table A.2: The Out-of-Africa Migration and Folkloric Diversity within Indigenous Ethnic Groups: Summary Statistics

	Mean	SD	Median	Min	Max	N
Number of motifs	87.23	88.09	62	1	598.0	958
Migratory distance (km)	13048.90	8035.41	12,742	105	30186.1	958
Absolute latitude	27.53	19.34	24	0	77.5	958
Caloric suitability (mean)	5959.41	4020.75	6,323	0	19167.5	956
Caloric suitability (std)	707.68	802.03	425	0	4352.3	956
Island	0.05	0.22	0	0	1.0	958
Folkloric distance	0.96	0.04	0.97	0	1.0	457446
Ecological distance	1.00	0.50	1.07	0	1.9	457446

Notes: The table provides for all variables used in the data analysis the mean, the standard deviation (SD), the median, the minimum value (MIN), the maximum value (MAX), and the number of observations (N).

Table A.3: The Out-of-Africa Migration and Musical Diversity within Indigenous Ethnic Groups: Summary Statistics

	Mean	SD	Median	Min	Max	N
Number of musical features	79.45	32.26	78	34	175.0	825
Migratory distance (km)	9787.91	6888.46	7,670	67	30192.5	825
Absolute latitude	23.03	17.77	19	0	70.5	825
Caloric suitability (mean)	6318.03	3238.52	7,126	0	17250.6	824
Caloric suitability (std)	817.12	787.62	609	0	4290.1	824
Island	0.14	0.35	0	0	1.0	825
Musical distance	0.67	0.12	0.68	0	1.0	339076
Ecological distance	0.99	0.49	1.07	0	1.9	339076

Notes: The table provides for all variables used in the data analysis the mean, the standard deviation (SD), the median, the minimum value (MIN), the maximum value (MAX), and the number of observations (N).

A.3 The Out-of-Africa Migration and Ancestral Diversity

A.3.1 Migratory Distance from Cradle of Humanity

The prehistoric dispersal of humankind from Africa, tens of thousands of years ago, marks one of the most momentous chapters in human history, laying the foundation for the development of human societies across the continents. This migration unfolded as a gradual, stepwise expansion in which subgroups departed from their ancestral communities to establish new settlements farther afield, carrying only a subset of the traits present in the original population. The sequential nature of this dispersal generated the well-documented Serial Founder Effect, in which subsampling, population bottlenecks, and limited interbreeding produced a marked decline in genetic and phenotypic diversity among indigenous populations that settled at greater migratory distances from the cradle of humanity in Africa.[34]

A.3.2 The Benchmark Analysis

The most comprehensive and geographically uniform dataset on inherited diversity comprises 207 distinct indigenous ethnic groups, whose global distribution is depicted in Figure A.1. This dataset offers a uniquely valuable foundation for examining the enduring imprint of humanity's migration out of Africa on patterns of population diversity.[35]

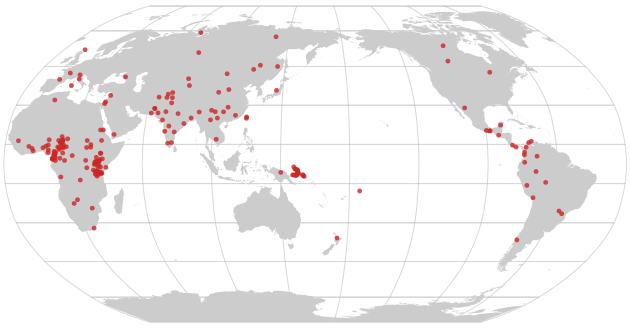


Figure A.1: Worldwide Distribution of Indigenous Ethnic Groups – Inherited Diversity

Notes: The figure depicts the locations of the 207 distinct indigenous ethnic groups for which inherited diversity is available, as constructed by Arbatlı et al. (2020).

Consistent with the Out-of-Africa hypothesis and the Serial Founder Effect, a markedly significant negative linear relationship exists between inherited diversity and migratory distance from East Africa (Figure A.2).

[34]The serial founder effect is well documented; see the extensive survey by Ashraf et al. (2021).
[35]See (Arbatlı et al., 2020).

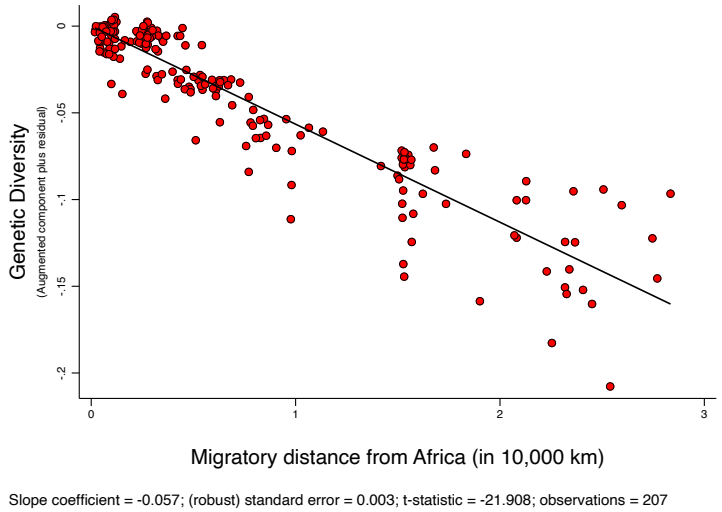


Figure A.2: The Out-of-Africa Migration and Inherited Diversity within Indigenous Ethnic Groups: Unconditional Analysis

Notes: The figure presents a scatterplot of the unconditional association between inherited diversity within ethnic groups and their migratory distance from East Africa (Table A.4, Column (1)).

Nevertheless, the validity of the hypothesis that inherited diversity declines with migratory distance from East Africa hinges on the presence of this pattern both within and across continents. Observable and unobservable continent-specific characteristics, such as geographical factors (e.g., climatic conditions and disease environments) and historical forces (e.g., conflict and colonialism) may have influenced inherited diversity and they could be correlated with migratory distance from East Africa. Therefore, the conventional analysis should incorporate continental fixed effects, isolating within-continent variation when estimating the impact of the out-of-Africa migration on inherited diversity.

Moreover, several geographical characteristics may have shaped inherited diversity in each ethnic homeland, including: (i) absolute distance from the equator, given its negative association with biodiversity and, plausibly, population diversity; (ii) geographical isolation, which tends to reduce inherited biological variation and increase vulnerability to population bottlenecks and drift (Ashraf and Galor (2011); Galor and Özak (2016)); (iii) the agricultural suitability of the land, which influences community size and the potential for interaction across groups; and (iv) ecological diversity, which shapes intra-group trade and contact (Michalopoulos (2012); Fenske (2014); Dickens (2022)) and may thereby affect the flow of inherited traits across populations. As migratory distance from East Africa may be linked to these geographical determinants of inherited diversity, the estimated effect should account for these characteristics to mitigate omitted variable bias.

Lastly, in line with the traditional view in the out-of-Africa literature, we associate the cradle of humanity with East Africa and thus estimate the impact of migratory distance from East Africa on inherited diversity. Although there is some uncertainty regarding the specific regions within the African continent where humans originated (e.g., Ragsdale et al. (2023)), since humans appear to have dispersed to the rest of the globe via East Africa, different points of origin within the continent would only result in augmenting the distances to all ancestral homelands outside Africa by the same constant, sustaining the qualitative relationship between migratory distance and inherited diversity. However, given the uncertainty about humanity's dispersal patterns within Africa, the estimated effect is more precise when Africa is excluded from the sample.

A.3.3 The Augmented Empirical Model

Recognizing the potential limitations of the benchmark analysis, we estimate an augmented linear regression model that examines the effect of migratory distance from East Africa on inherited diversity across ethnic groups, accounting for continental fixed effects and potential geographical confounders. This analysis employs both the most extensive sample of indigenous ethnic groups with documented data on ancestral diversity and a subsample excluding ethnic groups from the African continent. Specifically, we estimate the model:

$$GD_e = \alpha + \beta D_e + \tau Z_e + \delta_c + \epsilon_e.$$

In this model, the baseline dependent variable, GD_e, represents the degree of inherited diversity within ethnic group e. The independent variable, D_e, captures the migratory distance from East Africa to ethnic group e. The term Z_e is a vector of geographical characteristics that may confound the analysis, including absolute latitude, mean caloric suitability, standard deviation in caloric suitability, and a small island dummy. Finally, δ_c is a continent fixed effect.

The analysis is first conducted on the most extensive sample of indigenous ethnic groups for which documented data on inherited diversity are available. However, because migratory distance from East Africa is an imprecise predictor of inherited diversity among ethnic groups located within Africa, the impact of the out-of-Africa migration is subsequently examined in a restricted sample that excludes African groups. This refinement reduces measurement error in migratory distance from humanity's cradle and yields a more accurate estimate of the effect of the prehistoric dispersal on inherited diversity.

Table A.4: The Out-of-Africa Migration and Inherited Diversity within Indigenous Ethnic Groups

	Genetic Diversity			
	(1)	(2)	(3)	(4)
Migratory distance from the cradle of humanity	−0.057***	−0.039***	−0.050***	−0.061***
	(0.0026)	(0.0081)	(0.010)	(0.014)
Continent FE		✓	✓	✓
Geographical controls			✓	✓
Exclusion of Africa				✓
Dep. var. mean	0.72	0.72	0.72	0.69
Observations	207	207	207	106
Adjusted R^2	0.86	0.88	0.88	0.74

Notes: The table demonstrates a significant negative effect of migratory distance from East Africa on inherited diversity among indigenous ethnic groups. Migratory distance is measured in units of 10,000 km. Inherited diversity is measured by expected heterozygosity, the probability that two alleles sampled independently from a population are different at a given locus, averaged across loci. Geographical controls include absolute latitude, ecological diversity, caloric suitability, and a small-island dummy. Heteroskedasticity-robust standard errors are reported in parentheses. *** Significant at the 1 percent level. ** Significant at the 5 percent level. * Significant at the 10 percent level.

A.4 Robustness Checks and Sensitivity Analyses

A.4.1 Estimation Method and Spatial Correlation

Table A.5: The Out-of-Africa Migration and Cultural Diversity within Indigenous Ethnic Groups: Robustness to Estimation Method

	Number of Motifs				Number of Musical Features			
	Log-Linear	Linear	Poisson	Negative Binomial	Log-Linear	Linear	Poisson	Negative Binomial
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
Migratory distance from the cradle of humanity	−0.62***	−59.1***	−0.76***	−0.77***	−0.12***	−9.78***	−0.13***	−0.12***
	(0.17)	(13.7)	(0.15)	(0.14)	(0.027)	(2.28)	(0.030)	(0.029)
Dep. var. mean	93	93	93	93	79	79	79	79
Observations	813	813	813	813	630	630	630	630
Adjusted R^2	0.24	0.39	.	.	0.90	0.88	.	.

Notes: The table establishes that the impact of the out-of-Africa migration on folkloric and musical diversity is robust to alternative estimation methods such as linear regression, Poisson, and negative binomial regressions. Migratory distance is measured in units of 10,000 km. Folkloric diversity is defined as the number of motifs. Musical diversity is defined as the number of musical features. All specifications account for geographical controls (i.e., absolute latitude, ecological diversity, caloric suitability, and a small island dummy) and continent fixed effects. Music specifications further control for the logarithm of the number of songs sampled from each ethnic group. The analysis excludes ethnic groups in Africa. Heteroskedasticity-robust standard errors are reported in parentheses. *** Significant at the 1 percent level. ** Significant at the 5 percent level. * Significant at the 10 percent level.

Table A.6: The Out-of-Africa Migration and Diversity within Indigenous Ethnic Groups: Robustness to Spatial Correlation

	Genetic Diversity		Folkloric Diversity		Musical Diversity	
	(1)	(2)	(3)	(4)	(5)	(6)
Migratory distance from the cradle of humanity	−0.061***	−0.061***	−0.62***	−0.62***	−0.12***	−0.12***
	(0.014)	(0.015)	(0.17)	(0.16)	(0.027)	(0.038)
Conley SE		✓		✓		✓
Observations	106	106	813	813	630	630
Adjusted R^2	0.74	.	0.24	.	0.90	.

Notes: The table shows that the impact of the out-of-Africa migration on diversity remains significant when accounting for spatial correlations across ethnic groups using the method of Conley (1999). Migratory distance is measured in units of 10,000 km. All specifications incorporate geographical controls (absolute latitude, ecological diversity, caloric suitability, and a small-island indicator) and continent fixed effects. Music specifications further control for the logarithm of the number of songs sampled from each ethnic group. The analysis excludes ethnic groups within Africa. Conley standard errors (500 km cutoff) are reported in parentheses. *** Significant at the 1 percent level. ** Significant at the 5 percent level. * Significant at the 10 percent level.

A.4.2 Alternative Regional Fixed Effects

Table A.7: The Out-of-Africa Migration and Diversity within Indigenous Ethnic Groups: Alternative Regional fixed effects

	Genetic Diversity			Folkloric Diversity			Musical Diversity		
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
Migratory distance from the cradle of humanity	−0.039***	−0.039***	−0.041***	−0.58***	−0.87***	−0.93***	−0.071***	−0.052**	−0.072***
	(0.0081)	(0.0082)	(0.0076)	(0.15)	(0.15)	(0.15)	(0.025)	(0.024)	(0.024)
Regions:									
Africa	✓	✓		✓	✓		✓	✓	
Asia	✓			✓			✓		
Europe	✓			✓			✓		
Eurasia		✓			✓			✓	
Old World			✓			✓			✓
Sub-Saharan Africa			✓			✓			✓
North America	✓	✓	✓	✓	✓	✓	✓	✓	✓
South America	✓	✓	✓	✓	✓	✓	✓	✓	✓
Oceania	✓	✓	✓	✓	✓	✓	✓	✓	✓
Dep. var. mean	0.72	0.72	0.72	87.23	87.23	87.23	79.45	79.45	79.45
Observations	207	207	207	958	958	958	825	825	825
Adjusted R^2	0.88	0.87	0.88	0.20	0.14	0.16	0.90	0.90	0.90

Notes: This table shows that the impact of the out-of-Africa migration on diversity is unaffected by alternative definitions of continental groupings. Migratory distance is measured in units of 10,000 km. All specifications include the regional fixed effects indicated in the table. Music specifications further control for the logarithm of the number of songs sampled from each ethnic group. Heteroskedasticity-robust standard errors are reported in parentheses. *** Significant at the 1 percent level. ** Significant at the 5 percent level. * Significant at the 10 percent level.

B Contemporary Analysis

B.1 Variable Definitions and Sources

B.1.1 Cultural Diversity

- **Dispersion in social norms:** The coefficient of variation in individual responses to each survey question. Data Source: WVS-EVS and ESS.

- **WVS distance:** Cultural distance between countries is measured using the fixation index (F_{st}) applied to survey responses from the World Values Survey, following Muthukrishna et al. (2020). The F_{st} statistic captures the extent of between-country variation in the distribution of beliefs, values, and attitudes relative to total variation. Intuitively, it measures how different two populations are in terms of the frequencies of responses across a large set of survey questions, rather than differences in mean responses. Values of F_{st} range from 0 (identical distributions) to 1 (complete separation), and the statistic is computed by comparing the average pairwise differences in responses within and across populations. This approach treats survey responses as cultural "alleles," allowing for a theoretically grounded measure of cultural differentiation that accounts for the full distribution of beliefs and behaviors. Data Source: Muthukrishna et al. (2020).

- **Visual conceptual distance:** Cultural distance between countries is measured using the mean cosine distance between visual representations of the same concepts across countries net of average visual dissimilarity within the two countries. This isolates differences between countries' average representations from their internal dispersion. The pairwise index averages equally over the concepts common to every country in the sample. Data Source: *Quick, Draw!* (Google Creative Lab, 2017).

B.1.2 Ancestral Migratory Distance from the Cradle of Humanity

- The migratory distance to each ancestral homeland is defined as the shortest traversable path from Omo I (Ethiopia)—the site of the earliest known Homo sapiens remains in East Africa—to the modern capital city of the ancestral homeland. In alignment with archaeological evidence, the migratory path permits crossings of the Bab-el-Mandeb Strait, the Strait of Hormuz, and the Bering Strait while excluding the crossing of the Strait of Gibraltar and the Himalayan mountain range. Due to the limited capacity of early humans to traverse large bodies of water, migratory paths were confined to land masses. However, considering that sea levels at the time of the exodus during the Ice Age were nearly 100 meters lower than today, along with the ability of humans to cross shallow water, we permit travel within 100 km of the shoreline. Varying the buffer to 25 km or 50 km does not alter the results. Moreover, given the uncertain dynamics of the Serial Founder Effect over long maritime distances, it is assumed that oceanic travel to remote islands has no additional impact on diversity. Yet, permitting such an impact does not qualitatively affect our findings. Data Source: Authors' computations.[36]

[36]Since the ancestral homeland may consist of populations that are themselves from different ancestries, the ancestry-adjusted migratory distance from East Africa to the ancestral homeland captures the weighted average of the migratory distances from East Africa of each of these ancestral populations, accounting for the proportional representation of these deeper ancestral populations in the ancestral homeland, using the migration matrix of Putterman and Weil (2010). If the ancestral homeland is not in the matrix, we keep the unadjusted migratory distance only if the homeland is in the Old World given the drastic changes in the composition of populations of the New World in the post-1500 period.

B.1.3 Ancestral Geographical Controls

- **Absolute latitude**: The ancestry-adjusted absolute value of the latitude of the geodesic centroid of each country. Data Source: Authors' computation.
- **Caloric Suitability**: The ancestry-adjusted maximum potential caloric yield attainable in each country, given the set of crops that are suitable for cultivation in the pre-1500 period. Data Source: Galor and Özak (2016).
- **Ecological Diversity**: The ancestry-adjusted standard deviation of caloric suitability within the territory of each country. Data Source: Authors' computation based on Galor and Özak (2016).
- **Island**: The ancestry-adjusted dummy variable that captures whether each country is classified as a small island country under the United Nations M49 classification. Data Source: United Nations Statistics Division.

B.1.4 Ancestral Ethnic Fragmentation Controls

- **Ethnic Fractionalization:** The index captures the probability that two individuals in a country belong to distinct ethnic groups. Data Source: Alesina et al. (2003).
- **Ethnolinguistic Fractionalization:** The index captures the probability that two individuals in a country belong to distinct ethnic groups, with each pair weighted by the linguistic distance between the groups. This is also known as the Greenberg index. Data Source: Desmet et al. (2009).

B.2 Visual Conceptual Diversity and Distance

This appendix develops the visual conceptual diversity and distance measures used in the analysis. Both begin with the expected visual distance between two contributions responding to the same prompt. The country index pairs contributions from the same country. The country-pair index compares contributions across two countries and removes their average within-country dispersion.

B.2.1 Data, representation, and support

Quick, Draw! is an online game in which a contributor receives an English word and has 20 seconds to draw the requested concept. The public record contains the prompt, vector strokes, a stable drawing identifier, creation time, recognition status, and a two-letter country code inferred from the contribution's IP location. The complete public release contains 50,426,266 drawings across 345 concepts. Among these contributions, 46,136,816, or 91.5 percent, were recognized by the game as the prompted concept. The initial coverage audit contains 217 non-missing country and territory codes.

Each vector drawing is uniformly scaled and centered on a common white canvas. A fixed, pretrained DINOv2 model (Oquab et al., 2024) maps the rendered image into a 384-dimensional feature vector. No country label, QuickDraw prompt, migratory distance, or outcome in this paper enters the fixed mapping applied to the drawings. Every feature vector is normalized to unit Euclidean length. The cosine distance between two representations z_i and z_j is therefore $1 - z_i' z_j$, which increases as the visual representations diverge.[37]

The primary construction uses recognized drawings. It requires at least 100 eligible drawings in a country–concept cell, at least 250 eligible concepts for a country, and at least 20 eligible countries

[37]The implementation uses the 384-dimensional pooled representation from a pinned DINOv2-small model. Every source drawing is centered and scaled on a 224 by 224 canvas with a fixed margin and stroke width before the same image normalization is applied. The exact model revision is recorded in the replication material.

for a concept. Iterative application of these joint support conditions retains 65 countries, all 345 concepts, and 22,248 country–concept cells. Exactly 100 drawings are retained in each cell, yielding 2,224,800 drawings. An extended profile requires at least 50 drawings in a cell, 200 concepts for a country, and 15 countries for a concept. It retains 76 countries, all 345 concepts, 25,892 cells, and 2,520,760 drawings.

Within each eligible cell, a reproducible lottery based only on country, concept, original record identifier, and a fixed seed retains the 100 lowest-ranked drawings or all eligible drawings when fewer than 100 are available. Drawing content and visual representations do not enter the lottery.

B.2.2 Within-country estimand and Rao interpretation

Fix country c and concept k. Let Z_{ck} and Z^*_{ck} be independent draws from the distribution of unit-normalized visual representations among observed contributions in that cell. Cell diversity is

$$Q_{ck} = \mathbb{E}\big[1 - Z'_{ck} Z^*_{ck}\big]. \tag{25}$$

Both representations in every pair have the same country and concept. Thus, Q_{ck} is a within-country, within-concept population moment. It gives the expected visual distance between two independently sampled contributions from country c that respond to prompt k. Since the vectors have unit length,

$$1 - z'z^* = \frac{1}{2}\|z - z^*\|_2^2, \tag{26}$$

so the statistic can also be read as total dispersion in the normalized visual feature space.

Equation (25) is a continuous Rao-diversity measure (Rao, 1982). To see its relation to familiar diversity indices, suppose that visual expressions belong to discrete forms $g = 1, \ldots, G$, with population shares p_g and distance d_{gh} between forms. Then

$$Q_{ck} = \sum_{g=1}^{G} \sum_{h=1}^{G} p_g p_h d_{gh}. \tag{27}$$

If $d_{gh} = 1$ for unlike forms and $d_{gh} = 0$ for identical forms, equation (27) reduces to

$$Q_{ck} = 1 - \sum_{g=1}^{G} p_g^2, \tag{28}$$

the probability that two independent draws have different forms. This is the familiar fractionalization, Simpson-diversity, or expected-heterozygosity structure (Simpson, 1949). The visual measure retains graded distances in a continuous representation space, permitting two forms to be slightly or substantially different. A prompted concept plays the role of a locus, a drawing is a realization at that locus, and Q_{ck} is the expected distance between two realizations sampled from within the same population.

B.2.3 Between-country estimand and within–between decomposition

Let $\mu_{ck} = \mathbb{E}[Z_{ck}]$ denote the mean visual representation for country c and concept k. Unit normalization gives

$$Q_{ck} = 1 - \|\mu_{ck}\|_2^2. \tag{29}$$

For countries a and b, the expected cross-country distance for concept k is

$$C_{abk} = \mathbb{E}\big[1 - Z'_{ak} Z_{bk}\big] = 1 - \mu'_{ak}\mu_{bk}. \tag{30}$$

The cross-country distance can be large because the countries have different average representations or because drawings are internally dispersed within them. Let

$$W_{abk} = \frac{Q_{ak} + Q_{bk}}{2} \tag{31}$$

denote their average within-country diversity. The between-country component is

$$B_{abk} = C_{abk} - W_{abk} \tag{32}$$

$$= \frac{1}{2}\|\mu_{ak} - \mu_{bk}\|_2^2 \geq 0. \tag{33}$$

Thus, $C_{abk} = W_{abk} + B_{abk}$. The adjustment removes the internal dispersion that would otherwise make a visually heterogeneous country appear distant from every other country. The remaining component is the separation between the countries' mean visual representations.

Because W_{abk} is the sum of one term for each country, replacing B_{abk} by C_{abk} leaves the estimated coefficients on pair-level covariates unchanged in regressions with separate country fixed effects. We report B_{abk} because its scale has a direct between-country interpretation.

If the two country distributions receive equal weight, Rao diversity in their pooled distribution is

$$T_{abk} = W_{abk} + \frac{B_{abk}}{2}. \tag{34}$$

This is the continuous counterpart of the familiar decomposition of expected heterozygosity into within-population and between-population components. The visual conceptual distance used in the analysis is the level B_{abk}, averaged across concepts. The WVS F_{ST} measure instead expresses between-country variation relative to total variation. The two outcomes therefore share a within–between interpretation while retaining their natural scales.

B.2.4 Sample estimator and covariance identity

For a retained cell containing n_{ck} normalized representations, the sample analogue of equation (25) is the second-order U-statistic

$$\widehat{Q}_{ck} = \frac{1}{\binom{n_{ck}}{2}} \sum_{i<j} \left(1 - z_{ick}' z_{jck}\right). \tag{35}$$

Under random sampling within the cell, this estimator is unbiased for Q_{ck}. A cell with 100 drawings contains 4,950 unordered pairs, although those pairs are dependent because each drawing appears repeatedly. The empirical support remains 100 drawings.

Let $\bar{z}_{ck} = n_{ck}^{-1} \sum_i z_{ick}$. Unit normalization implies

$$\sum_{i<j} z_{ick}' z_{jck} = \frac{1}{2}\left(\left\|\sum_i z_{ick}\right\|_2^2 - n_{ck}\right), \tag{36}$$

$$\widehat{Q}_{ck} = \frac{n_{ck}}{n_{ck} - 1}\left(1 - \|\bar{z}_{ck}\|_2^2\right). \tag{37}$$

If S_{ck} denotes the unbiased sample covariance matrix of the normalized representations, then

$$\operatorname{tr}(S_{ck}) = \frac{1}{n_{ck}-1}\sum_i \|z_{ick} - \bar{z}_{ck}\|_2^2 = \widehat{Q}_{ck}. \tag{38}$$

Mean pairwise cosine distance, corrected lack of centroid concentration, and total within-cell feature variance are therefore identical. The covariance expression also permits computation in time proportional to the number of drawings.

For a pair of countries, the sample cross-country distance and its between-country component are

$$\widehat{C}_{abk} = \frac{1}{n_{ak}n_{bk}}\sum_{i=1}^{n_{ak}}\sum_{j=1}^{n_{bk}}\left(1 - z'_{iak}z_{jbk}\right) = 1 - \bar{z}'_{ak}\bar{z}_{bk}, \tag{39}$$

$$\widehat{B}_{abk} = \widehat{C}_{abk} - \frac{\widehat{Q}_{ak} + \widehat{Q}_{bk}}{2}. \tag{40}$$

Under independent sampling within each cell, $\widehat{C}_{abk}$ and $\widehat{B}_{abk}$ are unbiased for their population counterparts. With 100 drawings in each country–concept cell, the cross-country term averages 10,000 drawing pairs. The within-country terms retain the U-statistic correction in equation (35).

B.2.5 Country and country-pair aggregation

Let $\mathcal{C}_p$ be the countries retained in support profile p, let $\mathcal{K}_{cp}$ denote the concepts observed for country c, and define the common concept basket as

$$\mathcal{K}_p^{\cap} = \bigcap_{c\in\mathcal{C}_p} \mathcal{K}_{cp}. \tag{41}$$

The country score is

$$\mathrm{VCD}_{cp}^{100} = \frac{100}{|\mathcal{K}_p^{\cap}|}\sum_{k\in\mathcal{K}_p^{\cap}} \widehat{Q}_{ckp}. \tag{42}$$

For countries a and b, visual conceptual distance is

$$D_{abp}^{V} = \frac{100}{|\mathcal{K}_p^{\cap}|}\sum_{k\in\mathcal{K}_p^{\cap}} \widehat{B}_{abkp}. \tag{43}$$

The strict intersection contains 245 concepts for each of 65 countries, producing 15,925 cells, 1,592,500 drawings, and 2,080 country pairs. The extended intersection contains 172 concepts for each of 76 countries, producing 13,072 cells, 1,278,241 drawings, and 2,850 country pairs. Every country and country pair within a profile has the same concept composition, and every concept receives equal weight. The factor 100 is a uniform reporting scale. It converts the strict within-country mean of 0.2275 into 22.75 VCD points and the strict between-country mean of 0.002193 into 0.2193 visual-conceptual-distance points without changing ranks, standardized coefficients, test statistics, or significance levels. Every aggregated strict-support and extended-support country-pair estimate is positive.

Equation (42) has a direct two-stage interpretation. Draw one concept uniformly from the common basket, then draw two representations independently from country c's distribution for that concept. The country score is 100 times their expected visual distance. Drawings from another country never enter a within-country pair. Other countries affect the construction only by determining the common concept basket.

Equation (43) draws one representation from each country for the same uniformly selected concept and subtracts the countries' average within-country distance. Because the within-country terms are distinct-pair U-statistics, the finite-sample estimator is not algebraically identical to the squared distance between the sample mean representations. It is unbiased for 100 times one-half the squared Euclidean distance between the population mean representations, averaged across the common basket.

An alternative relative index standardizes $\widehat{Q}_{ckp}$ across countries separately within each concept and then averages the resulting concept scores. This transformation gives greater weight per raw distance unit to concepts with lower cross-country dispersion. The raw common-basket average in equation (42) therefore remains the primary index. The primary and relative indices correlate 0.981 under strict support and 0.940 under extended support. In the preferred specification, the standardized migration coefficients are -0.599 and -0.745 for the two primary indices, compared with -0.561 and -0.630 for the corresponding relative indices.

To assess semantic breadth, a descriptive, label-based partition assigns the 245 strict common prompts to 12 mutually exclusive domains covering animals, nature, people and health, food, clothing, built environments, transport, household objects, tools, technology, arts and play, and symbols and imaginary forms. All 12 preferred domain coefficients are negative. Seven have two-sided $p < 0.05$, and the same seven retain Benjamini–Hochberg $q < 0.05$ across the 12 tests. Giving every domain equal weight produces a coefficient of -0.390, with a standard error of 0.093, compared with -0.395, with a standard error of 0.090, for the primary equal-concept index.

B.2.6 Extended-support estimates

The extended-support estimates preserve the pattern obtained with the primary strict-support sample. As shown in Table B.1, the coefficient is negative and statistically significant in all four specifications. In the preferred specification, the coefficient is -0.497, with a standard error of 0.077, compared with -0.395, with a standard error of 0.090, under strict support.

Table B.1: The Out-of-Africa Migration and Visual Conceptual Diversity within Countries: Extended Support

	Visual Conceptual Diversity (VCD points)			
	(1)	(2)	(3)	(4)
Ancestry-adjusted migratory distance from the cradle of humanity	−0.474***	−0.553***	−0.507***	−0.497***
	(0.078)	(0.092)	(0.078)	(0.077)
Continent FE		✓	✓	✓
Geographical controls			✓	✓
Exclusion of Africa				✓
Dep. var. mean	22.91	22.91	22.91	22.91
Observations	76	76	76	72
Adjusted R^2	0.49	0.53	0.59	0.60

Notes: The dependent variable is Visual Conceptual Diversity (VCD points), defined as 100 times raw mean pairwise cosine distance averaged over the 172 concepts common to every country in the extended-support sample. Each country–concept cell contains between 50 and 100 recognized drawings. Ancestry-adjusted migratory distance is measured in units of 10,000 km. Geographical controls are ancestry-adjusted absolute latitude, ecological diversity, caloric suitability, and a small island dummy. Heteroskedasticity-robust standard errors are reported in parentheses. *** Significant at the 1 percent level.

B.2.7 Reliability, measurement sensitivity, and scope

The reproducible lottery permits a split-sample reliability test. Separate country indices constructed from the odd and even positions within every cell correlate 0.858 under strict support and 0.819 under extended support. The strict and extended primary country scores correlate 0.961 on their common countries. Country scores derived from non-overlapping January and March contributions correlate 0.684 in the balanced non-African temporal sample. The strict and extended indices correlate 0.358 and 0.350, respectively, with the independently constructed WVS country measure.

Recognition provides a common task-success screen, and the primary index uses drawings that the game recognized as the prompted concept. The all-drawings scores are strongly negatively correlated with country recognition rates and therefore combine variation in task success with visual dispersion. The recognized-only index remains the primary outcome. Columns (1) and (2) of Table B.2 show that fixed-support constructions admitting all drawings preserve a negative and statistically significant migration gradient under both strict and extended support. Columns (3) and (4) show that the gradient is also negative and statistically significant when VCD is constructed separately from the non-overlapping January and March contribution windows. The monthly exercise evaluates measurement stability over separate samples of drawings and is not an estimate of cultural change.

Table B.2: The Out-of-Africa Migration and Visual Conceptual Diversity: Measurement and Temporal Robustness

	Visual Conceptual Diversity (VCD points)			
	All drawings		Recognized drawings	
	Strict support	Extended support	January 2017	March 2017
	(1)	(2)	(3)	(4)
Ancestry-adjusted migratory distance from the cradle of humanity	−0.999***	−1.135***	−0.412***	−0.303***
	(0.297)	(0.239)	(0.103)	(0.100)
Continent FE	✓	✓	✓	✓
Geographical controls	✓	✓	✓	✓
Exclusion of Africa	✓	✓	✓	✓
Dep. var. mean	23.81	23.96	22.95	22.96
Observations	62	72	56	56
Adjusted R^2	0.43	0.47	0.44	0.30

Notes: The dependent variable is Visual Conceptual Diversity (VCD points). Columns (1) and (2) admit both recognized and unrecognized drawings while retaining the fixed country–concept support and cell sample sizes of the corresponding recognized-only profiles. Columns (3) and (4) use recognized drawings from non-overlapping January and March 2017 contribution windows. Within every retained temporal country–concept cell, the same number of drawings is used in both months. All specifications include continent fixed effects and ancestry-adjusted absolute latitude, ecological diversity, caloric suitability, and a small island dummy, and exclude Africa. Ancestry-adjusted migratory distance is measured in units of 10,000 km. Heteroskedasticity-robust standard errors are reported in parentheses. *** Significant at the 1 percent level.

The index captures expressed visual variation under a shared task. Country denotes the location inferred from each contribution's IP address. Contributors are self-selected, prompts are in English, and the public data do not report stable user identifiers, contributor demographics, or device characteristics. Every retained drawing therefore receives equal weight within its country–concept cell. The resulting index measures the diversity of visual representations contributed from each country and is not a representative estimate for its national population.

B.2.8 Between-country robustness

The between-country results are stable across alternative support profiles, measurement choices, and country samples. Table B.3 applies the three specifications reported in the main analysis to the extended-support profile. The coefficient on ancestral ecological distance is positive and highly significant throughout. In the specification that includes geodesic distance, the absolute difference in ancestral diversity, and their interaction with ecological distance, the interaction is negative and highly significant.

Table B.3: Ancestral Ecological Distance and Visual Conceptual Distance: Extended Support

	Visual conceptual distance		
	(1)	(2)	(3)
Ancestral ecological distance	0.038***	0.026***	0.020***
	(0.0032)	(0.0037)	(0.0039)
Absolute difference in ancestral diversity			0.033***
			(0.0065)
Ancestral ecological distance × absolute difference in ancestral diversity			−0.020***
			(0.0036)
Country FE	✓	✓	✓
Geodesic distance		✓	✓
Dep. var. mean	0.22	0.22	0.22
Observations	2848	2848	2848
Adjusted R^2	0.75	0.81	0.84

Notes: Each column reports estimates from pairwise regressions of visual conceptual distance on ancestral ecological distance. Visual conceptual distance is 100 times cross-country drawing distance net of average within-country drawing dissimilarity and averaged equally over the 172 concepts common to all 76 countries in the extended-support profile. All columns include separate country fixed effects for the two endpoints. Two-way clustered standard errors at the country endpoints are reported in parentheses. The unit of observation is a country pair. *** Significant at the 1 percent level.

Table B.4 reports the preferred specification for alternative constructions of visual conceptual distance. The first column reproduces the strict-support baseline. Columns (2) and (3) construct the measure from two disjoint sets of 50 drawings in every country–concept cell. Column (4) uses cosine distance between the countries' mean representation vectors rather than the Rao between component. Columns (5) and (6) admit both recognized and unrecognized drawings while retaining the fixed strict- and extended-support country–concept baskets. The positive coefficient on ecological distance and the negative interaction are highly significant in every construction.

Table B.4: Ancestral Ecological Distance and Visual Conceptual Distance: Alternative Measures

	Visual conceptual distance					
	Recognized drawings				All drawings	
	Baseline	Split 1	Split 2	Centroid	Strict support	Extended support
	(1)	(2)	(3)	(4)	(5)	(6)
Ancestral ecological distance	0.019***	0.019***	0.019***	0.025***	0.022***	0.022***
	(0.0042)	(0.0042)	(0.0043)	(0.0054)	(0.0044)	(0.0041)
Absolute difference in ancestral diversity	0.027***	0.029***	0.026***	0.035***	0.030***	0.038***
	(0.0062)	(0.0062)	(0.0062)	(0.0079)	(0.0066)	(0.0073)
Ancestral ecological distance × absolute difference in ancestral diversity	−0.017***	−0.017***	−0.017***	−0.022***	−0.017***	−0.021***
	(0.0038)	(0.0037)	(0.0041)	(0.0050)	(0.0039)	(0.0036)
Country FE	✓	✓	✓	✓	✓	✓
Geodesic distance	✓	✓	✓	✓	✓	✓
Dep. var. mean	0.22	0.22	0.22	0.58	0.23	0.23
Observations	2078	2078	2078	2078	2078	2848
Adjusted R^2	0.84	0.84	0.84	0.84	0.85	0.84

Notes: Each column reports the preferred pairwise specification. Columns (1)–(4) use recognized drawings. Column (1) reports the strict-support baseline. Columns (2) and (3) use disjoint halves of each 100-drawing cell. Column (4) averages cosine distance between the mean representation vectors of the two countries over the 245 common concepts. Columns (5) and (6) admit recognized and unrecognized drawings while retaining the fixed country–concept support and cell sample sizes of the corresponding recognized-only profiles. All columns include geodesic distance and separate country fixed effects for the two endpoints. Two-way clustered standard errors at the country endpoints are reported in parentheses. *** Significant at the 1 percent level.

Table B.5 shows that the preferred estimates are preserved when the analysis is restricted to country pairs observed in the WVS sample. Table B.6 reports summary statistics for the strict-support country-pair sample.

Table B.5: Ancestral Ecological Distance and Visual Conceptual Distance: Alternative Sample

	Visual conceptual distance	
	Baseline	WVS sample
	(1)	(2)
Ancestral ecological distance	0.019***	0.018***
	(0.0042)	(0.0043)
Absolute difference in ancestral diversity	0.027***	0.031***
	(0.0062)	(0.0073)
Ancestral ecological distance × absolute difference in ancestral diversity	−0.017***	−0.017***
	(0.0038)	(0.0044)
Country FE	✓	✓
Geodesic distance	✓	✓
Dep. var. mean	0.22	0.23
Observations	2078	1594
Adjusted R^2	0.84	0.83

Notes: Each column reports the preferred pairwise specification. Column (1) reports the strict-support baseline. Column (2) retains country pairs observed in the WVS analysis. Both columns include geodesic distance and separate country fixed effects for the two endpoints. Two-way clustered standard errors at the country endpoints are reported in parentheses. *** Significant at the 1 percent level.

Table B.6: Visual Conceptual Distance: Summary Statistics

	Mean	SD	Median	Min	Max	N
Visual conceptual distance	0.219	0.124	0.189	0.005	0.728	2,080
Ancestral ecological distance	0.815	0.511	0.779	0.000	1.911	2,080

Notes: The table reports summary statistics for all 2,080 country pairs in the strict-support profile before the regression estimator removes singleton observations. Visual conceptual distance is expressed in points. Ancestral ecological distance is the raw cosine distance between the countries' vectors of ancestry-adjusted geographical endowments.

B.2.9 Complete-cell illustrations

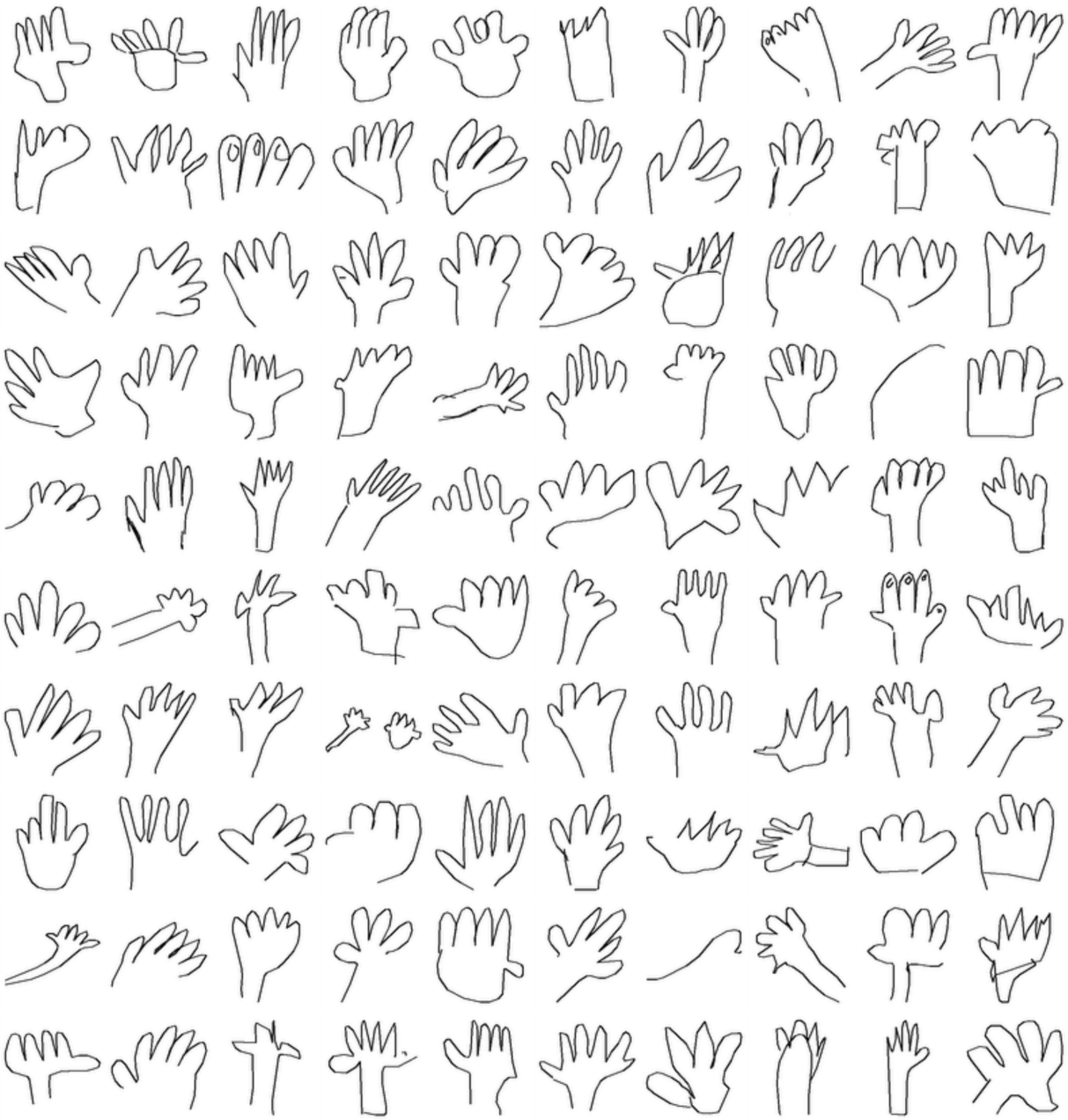
The following four pages illustrate higher and lower visual diversity for *hand* in Iraq and the Philippines and for *whale* in Saudi Arabia and Chile. Each page displays 100 recognized drawings.

Example 1 of 2: Hand

Higher visual diversity: Iraq (IQ)

All 100 recognized drawings

Mean pairwise visual distance: 0.2370

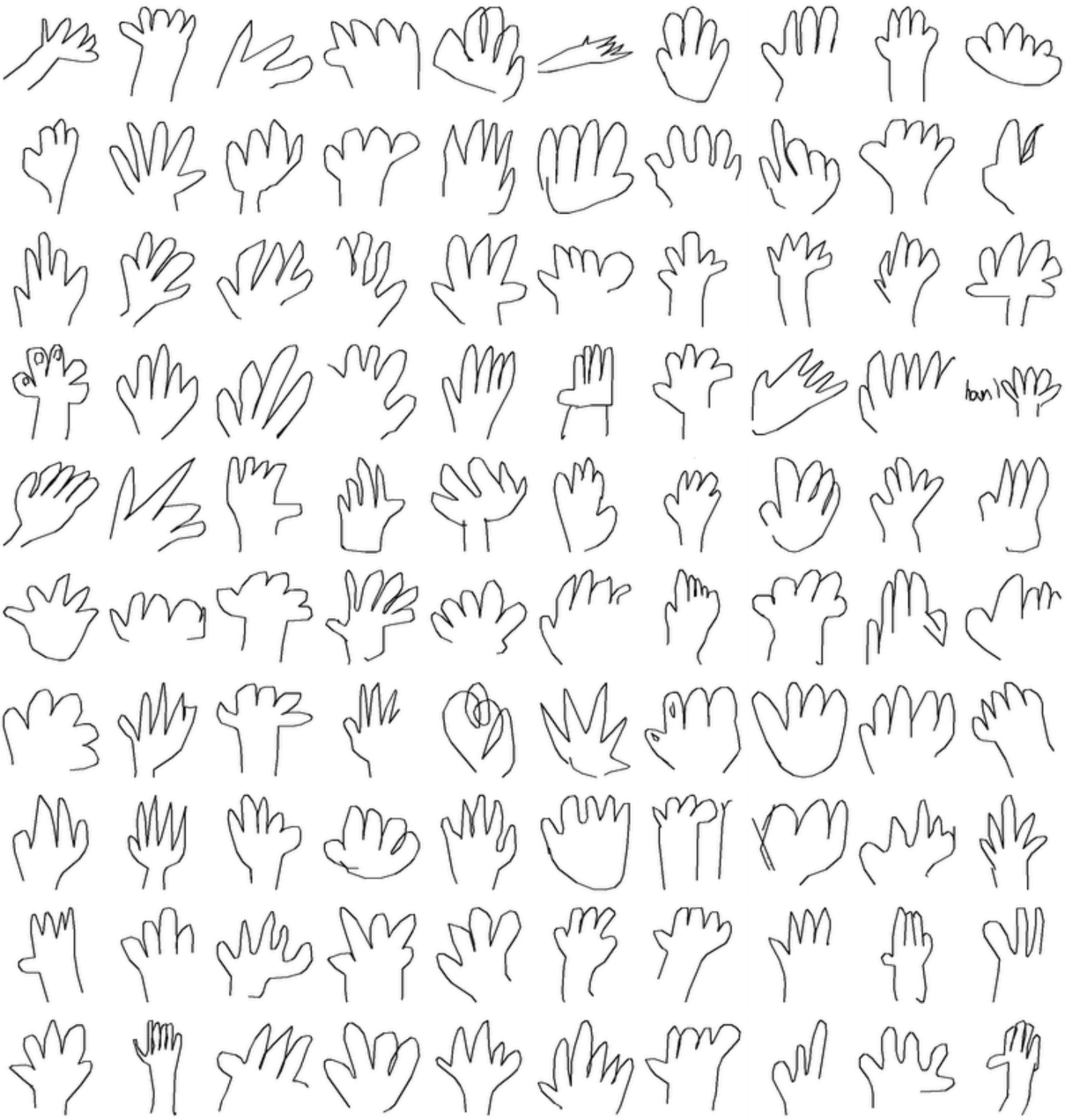


Example 1 of 2: Hand

Lower visual diversity: Philippines (PH)

All 100 recognized drawings

Mean pairwise visual distance: 0.1886

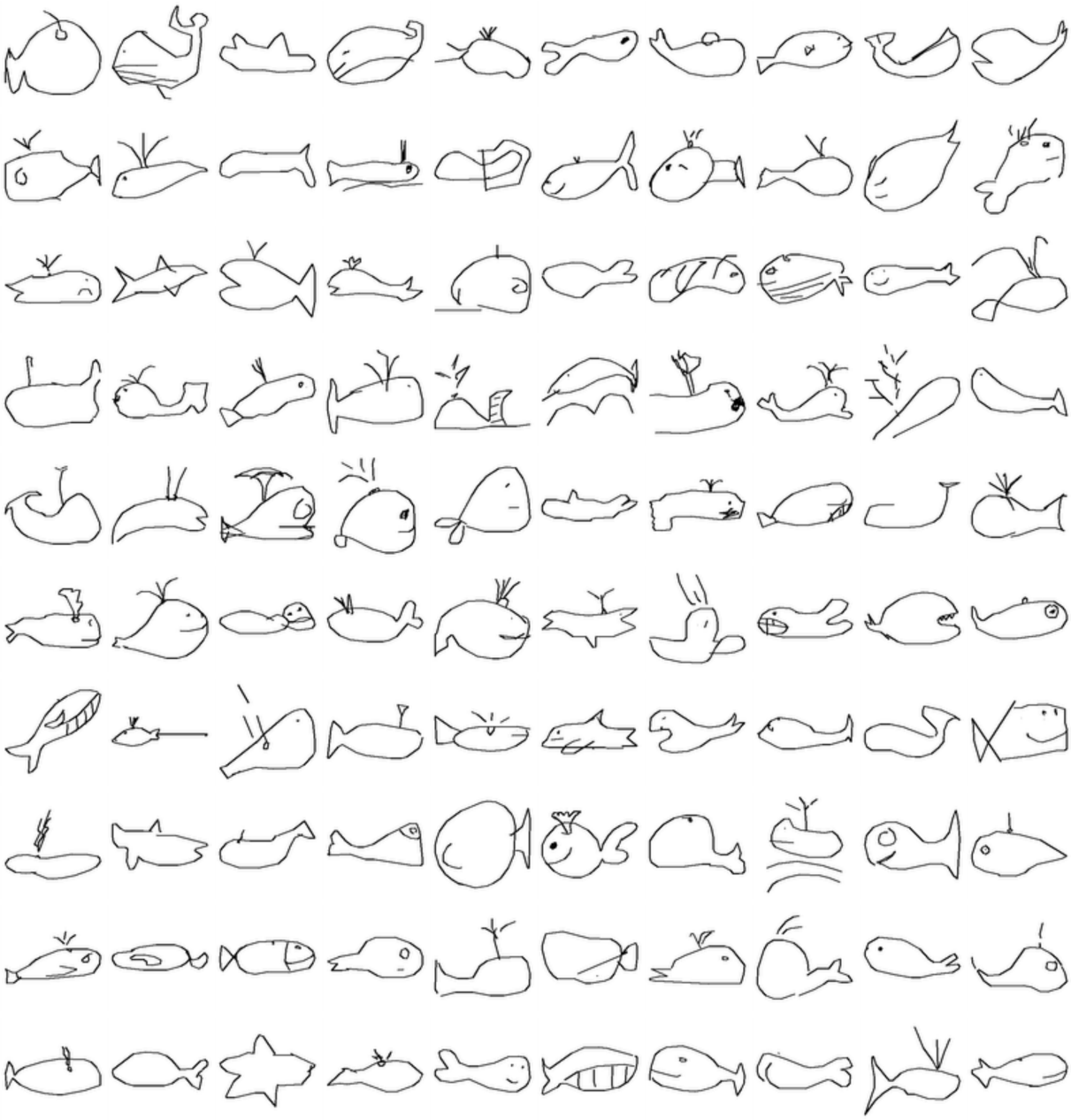


Example 2 of 2: Whale

Higher visual diversity: Saudi Arabia (SA)

All 100 recognized drawings

Mean pairwise visual distance: 0.2218

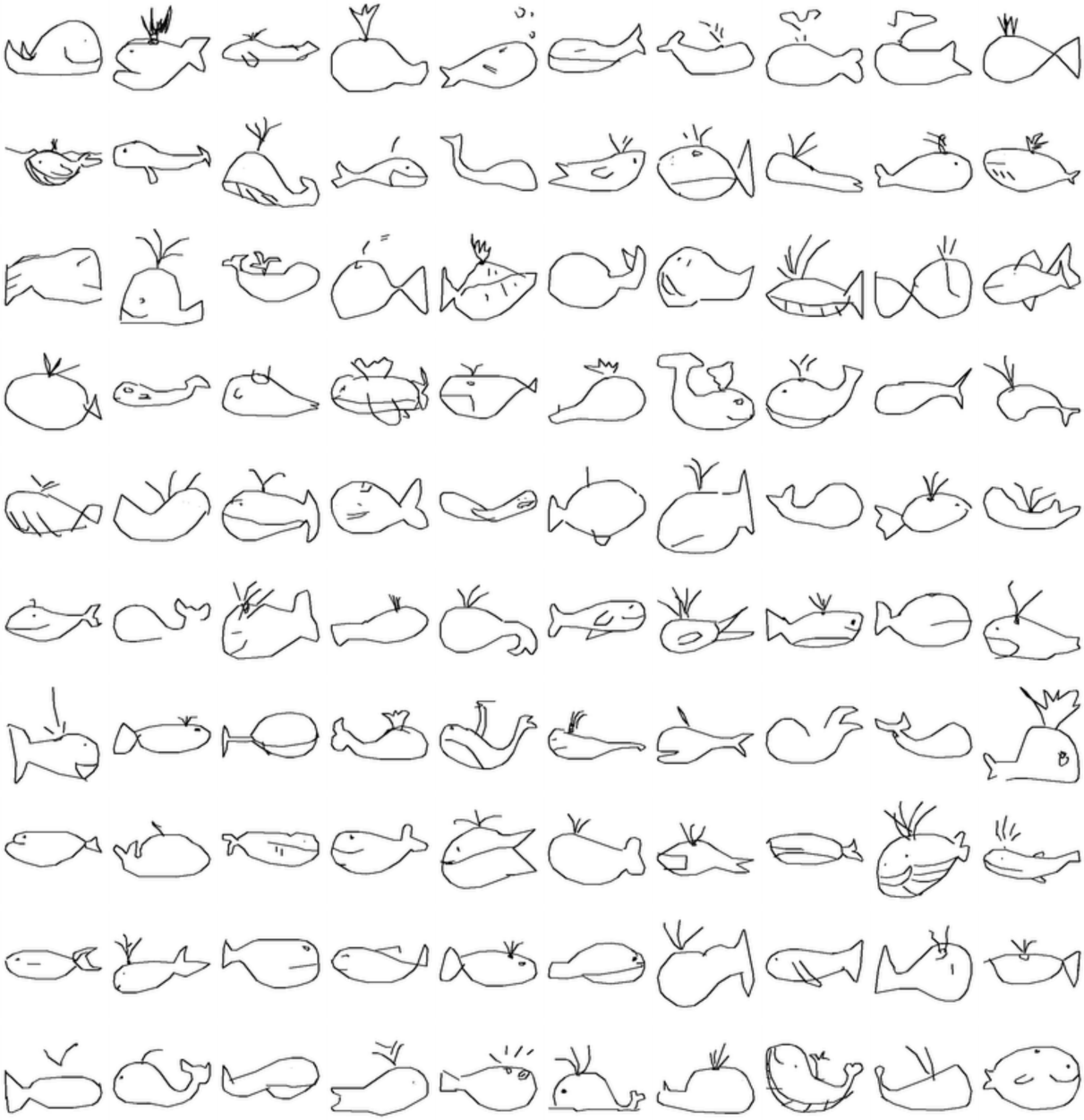


Example 2 of 2: Whale

Lower visual diversity: Chile (CL)

All 100 recognized drawings

Mean pairwise visual distance: 0.1937



B.3 Summary Statistics

Table B.7: The Out-of-Africa Migration and Contemporary Dispersion in Cultural Values within Countries: Summary Statistics

	Mean	SD	Median	Min	Max	N
A. Dispersion in cultural value						
Coefficient of variation	0.56	0.80	0	0	34.7	26,558
B. Independent variable						
Ancestral migratory distance (km)	6631.75	3585.81	5,814	595	20729.7	112
C. Ancestral geography						
Absolute latitude	35.74	14.56	38	0	64.1	112
Caloric suitability (mean)	6257.36	2810.02	7,214	0	10107.7	112
Caloric suitability (std)	1734.13	958.74	1,653	0	3993.9	112
Island	0.003	0.02	0	0	0	112
D. Ancestral ethnic fragmentation						
Ethnic fractionalization	0.39	0.24	0	0	0.9	104
Ethnolinguistic fractionalization	0.16	0.17	0	0	0.6	107
E. Pairwise distances						
WVS distance	0.14	0.08	0.12	0	0.8	4,753
Ecological distance	0.94	0.50	0.97	0	1.9	4,753

Notes: The table provides for all variables used in the data analysis the mean, the standard deviation (SD), the median, the minimum value (MIN), the maximum value (MAX), and the number of observations (N) .

Table B.8: The Out-of-Africa Migration and Contemporary Dispersion in Cultural Values within Populations of Second-Generation Migrants in Europe: Summary Statistics

	Mean	SD	Median	Min	Max	N
A. Dispersion in cultural value						
Coefficient of variation	0.42	0.34	0	0	35.6	68,381
B. Independent variable						
Ancestral migratory distance (km)	6077.70	3219.92	5,689	595	20729.7	133
C. Ancestral geography						
Absolute latitude	32.23	16.85	36	0	64.1	133
Caloric suitability (mean)	6468.11	2748.79	7,402	0	11084.6	133
Caloric suitability (std)	1697.31	946.19	1,675	0	3993.9	133
Island	0.021	0.13	0	0	1	133
D. Ancestral ethnic fragmentation						
Ethnic fractionalization	0.44	0.26	0	0	0.9	123
Ethnolinguistic fractionalization	0.16	0.16	0	0	0.6	125

Notes: The table provides for all variables used in the data analysis the mean, the standard deviation (SD), the median, the minimum value (MIN), the maximum value (MAX), and the number of observations (N) .

B.4 Robustness Checks and Sensitivity Analyses

B.4.1 Alternative Bins

Table B.9: The Out-of-Africa Migration and Dispersion in Cultural Values within Countries: Robustness to Alternative Bins

	Dispersion in cultural value			
	(1)	(2)	(3)	(4)
Ancestral migratory distance from the cradle of humanity	−0.12***	−0.11***	−0.084***	−0.12***
	(0.033)	(0.031)	(0.021)	(0.038)
Wave FE		✓	✓	✓
Age FE			✓	
Sex FE			✓	
Education FE				✓
Dep. var. mean	0.55	0.56	0.54	0.54
Demographic bins	23,562	51,006	606,369	72,051
Cultural values	380	383	383	383
Countries	96	96	96	92
Adjusted R^2	0.65	0.61	0.66	0.56

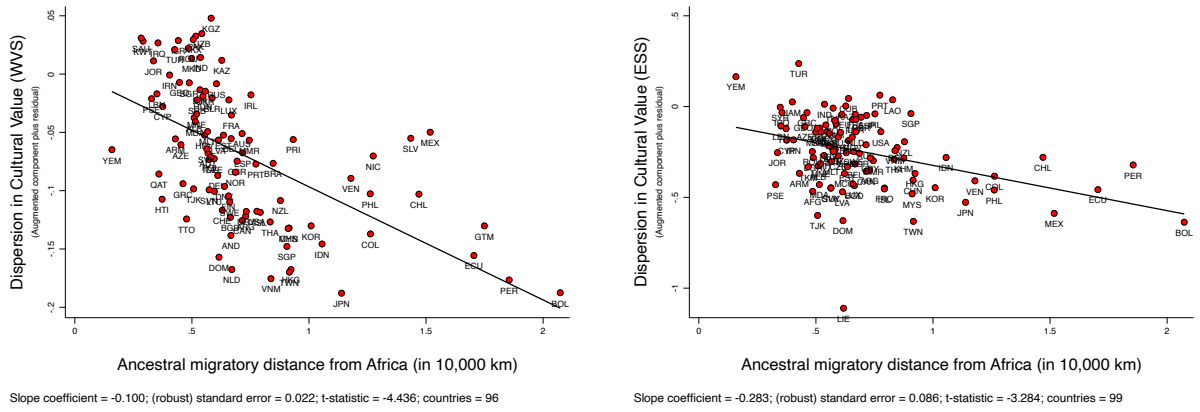
Notes: This table establishes that the impact of the out-of-Africa migration on contemporary dispersion in cultural values across countries holds irrespective of the inclusion of wave, age, and sex fixed effects. The unit of observation is a bin at the level of: (1) country, (2) country and wave, (3) country, wave, age-group, and sex, and (4) country, wave, and education. Ancestry-adjusted migratory distance is measured in units of 10,000 km. Dispersion in cultural values among individuals within each society is captured by the coefficient of variation with respect to each value, accounting for cultural value fixed effects. All specifications include ancestry-adjusted geographical controls (i.e., absolute latitude, ecological diversity, caloric suitability, and a small island dummy) as well as continent fixed effects. The analysis excludes countries in Africa. Heteroskedasticity-robust standard errors (clustered at the country level) are reported in parentheses. *** Significant at the 1 percent level. ** Significant at the 5 percent level. * Significant at the 10 percent level.

Table B.10: The Out-of-Africa Migration and Contemporary Dispersion in Cultural Values within Populations of Second-Generation Migrants in Europe: Robustness to Alternative Bins

	Dispersion in cultural value			
	(1)	(2)	(3)	(4)
Ancestral migratory distance from the cradle of humanity	−0.057***	−0.050***	−0.045**	−0.049**
	(0.013)	(0.017)	(0.019)	(0.019)
Wave FE		✓	✓	✓
Age FE			✓	
Sex FE			✓	
Education FE				✓
Dep. var. mean	0.42	0.41	0.40	0.41
Demographic bins	61,288	130,566	241,575	155,492
Cultural values	119	119	119	119
Homelands	99	92	73	89
Adjusted R^2	0.24	0.20	0.15	0.19

Notes: This table establishes that the impact of the out-of-Africa migration on contemporary dispersion in cultural values across populations of second-generation migrants in Europe holds irrespective of the inclusion of wave, age, and sex fixed effects. The unit of observation is a bin at the level of: (1) country, (2) country and wave, (3) country, wave, age-group, and sex, and (4) country, wave, and education. Ancestry-adjusted migratory distance is measured in units of 10,000 km. Dispersion in cultural values among individuals from an identical ancestral origin within each European country is captured by the coefficient of variation with respect to each value, accounting for cultural value and a host-country fixed effect. All specifications include ancestry-adjusted geographical controls (i.e., absolute latitude, ecological diversity, caloric suitability, and a small island dummy) as well as continent fixed effects. The analysis excludes countries in Africa. Heteroskedasticity-robust standard errors (clustered at the ancestral homeland level) are reported in parentheses. *** Significant at the 1 percent level. ** Significant at the 5 percent level. * Significant at the 10 percent level.

B.4.2 Estimation Method and Spatial Correlation



(a) National Populations

(b) Second-Generation Migrants in Europe

Figure B.1: The Out-of-Africa Migration and Contemporary Dispersion in Cultural Values within Modern Nations: Log-Linear Model

Notes: The figure presents a scatterplot illustrating the association between ancestry-adjusted migratory distance from East Africa and the natural logarithmic contemporary dispersion of cultural values across: (a) countries, and (b) populations of second-generation migrants in Europe.

Table B.11: The Out-of-Africa Migration and Contemporary Dispersion in Cultural Values within Countries: Robustness to Spatial Correlation

	Dispersion in cultural value	
	(1)	(2)
Ancestral migratory distance from the cradle of humanity	−0.12***	−0.12***
	(0.033)	(0.030)
Conley SE		✓
Dep. var. mean	0.55	0.55
Demographic bins	23,562	23,562
Cultural values	380	380
Countries	96	96
Adjusted R^2	0.65	.

Notes: The table establishes that the impact of the out-of-Africa migration on contemporary dispersion in cultural values across countries remains significant if spatial correlations across countries are accounted for using the method of Conley (1999).

B.4.3 Migration Flows and Population Composition

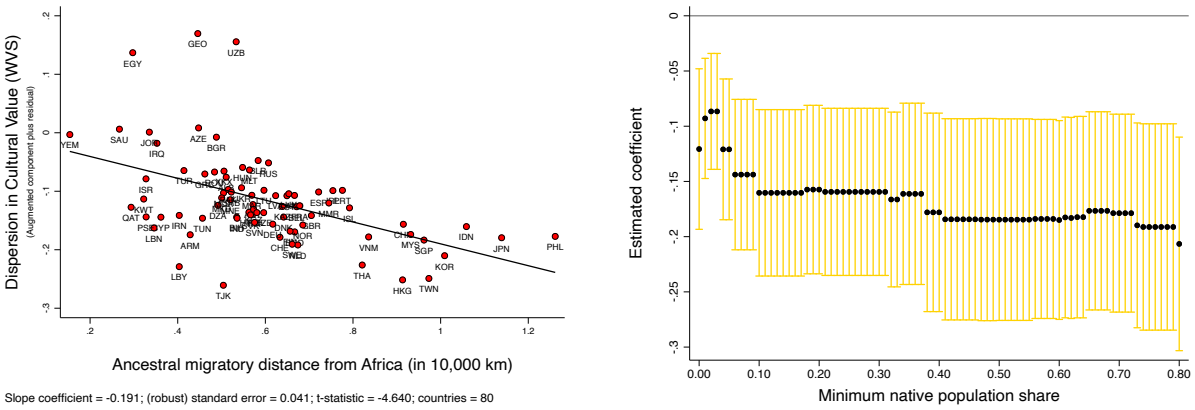


Figure B.2: The Out-of-Africa Migration and Dispersion in Cultural Values within Modern Nations: Migration Flows and Population Composition

Notes: This figure shows that the baseline findings remain qualitatively unchanged when restricting the sample to homelands that were not subjected to significant migration. The left panel illustrates the association between ancestry-adjusted migratory distance from East Africa and contemporary dispersion in cultural values across countries in the Old World. The right panel depicts the changes in the estimated coefficient in our baseline specification, as we restrict the sample to homelands to include a minimum share of indigenous population and varying level from 0 to 80%, across countries. At a 80% threshold, the sample contains 54 countries.

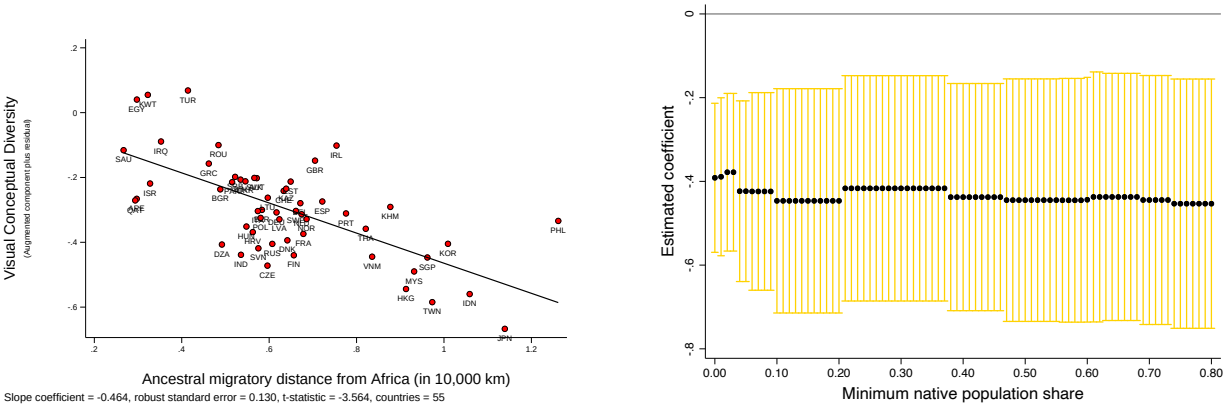
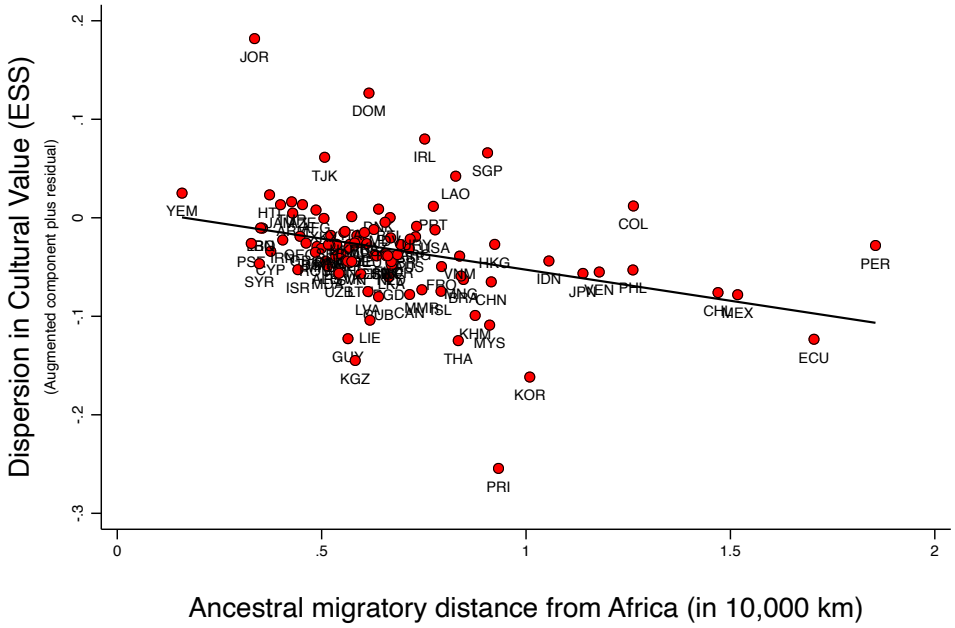


Figure B.3: The Out-of-Africa Migration and Visual Conceptual Diversity within Modern Nations: Migration Flows and Population Composition

Notes: The left panel illustrates the association between migratory distance from East Africa and visual conceptual diversity across 55 countries in the Old World, accounting for continent fixed effects and geographical controls. The right panel reports the estimated coefficient on ancestry-adjusted migratory distance in the preferred specification as the required minimum share of the native population increases from 0 to 80%. Vertical bars report 95% confidence intervals based on heteroskedasticity-robust standard errors. At a 80% threshold, the sample contains 41 countries.

B.4.4 Ancestral Origins

Since cultural transmission is typically stronger along maternal lineages, the baseline analysis of second-generation migrants uses the mother's country of birth to define ancestry. However, the impact of the out-of-Africa migration on contemporary cultural diversity is unaffected qualitatively when ancestry is instead defined by the father's country of birth (Figure B.4).



Slope coefficient = -0.044; (robust) standard error = 0.014; t-statistic = -3.027; countries = 97

Figure B.4: The Out-of-Africa Migration and Dispersion in Cultural Values Among Second-Generation Migrants in Europe: Ancestry Along Paternal Lineage

Notes: The figure presents a scatterplot of the association between contemporary dispersion in cultural values and ancestry-adjusted migratory distance from East Africa across populations of second-generation migrants in Europe based on paternal lineages, under our preferred specification, which includes continent fixed effects, ancestry-adjusted geographical controls, and excludes Africa.

B.4.5 Accounting for Fractionalization

Table B.12: The Out-of-Africa Migration and Contemporary Dispersion in Cultural Values within Countries: Accounting for Fractionalization

	Dispersion in cultural value					
	(1)	(2)	(3)	(4)	(5)	(6)
Ancestral migratory distance from the cradle of humanity	−0.11***		−0.11***	−0.11***		−0.11***
	(0.030)		(0.032)	(0.034)		(0.035)
Ethnic fractionalization		0.0038	0.00052			
		(0.011)	(0.0099)			
Ethnolinguistic fractionalization					0.0077	0.0097
					(0.010)	(0.0091)
Dep. var. mean	0.55	0.55	0.55	0.56	0.56	0.56
Demographic bins	21,891	21,891	21,891	22,368	22,368	22,368
Cultural values	379	379	379	380	380	380
Countries	88	88	88	91	91	91
Adjusted R^2	0.64	0.64	0.64	0.64	0.64	0.64

Notes: The table establishes that the impact of the out-of-Africa migration on contemporary dispersion in cultural values across countries is not explained by ethnic or ethnolinguistic fractionalization. Ancestry-adjusted migratory distance is measured in units of 10,000 km. Dispersion in cultural values among individuals within each society is captured by the coefficient of variation with respect to each value, accounting for cultural value fixed effects. All specifications include ancestry-adjusted geographical controls (i.e., absolute latitude, ecological diversity, caloric suitability, and a small island dummy) as well as continent fixed effects. The analysis excludes countries in Africa. Heteroskedasticity-robust standard errors (clustered at the country level) are reported in parentheses. *** Significant at the 1 percent level. ** Significant at the 5 percent level. * Significant at the 10 percent level.

Table B.13: The Out-of-Africa Migration and Visual Conceptual Diversity within Countries: Accounting for Fractionalization

	Visual Conceptual Diversity (VCD points)					
	(1)	(2)	(3)	(4)	(5)	(6)
Ancestry-adjusted migratory distance from the cradle of humanity	−0.37***		−0.37***	−0.38***		−0.39***
	(0.091)		(0.091)	(0.097)		(0.098)
Ethnic fractionalization		0.030	0.00064			
		(0.023)	(0.015)			
Ethnolinguistic fractionalization					0.020	−0.0042
					(0.030)	(0.024)
Continent FE	✓	✓	✓	✓	✓	✓
Geographical controls	✓	✓	✓	✓	✓	✓
Exclusion of Africa	✓	✓	✓	✓	✓	✓
Dep. var. mean	22.8	22.8	22.8	22.8	22.8	22.8
Observations	59	59	59	59	59	59
Adjusted R^2	0.55	0.35	0.54	0.56	0.35	0.55

Notes: The dependent variable is Visual Conceptual Diversity (VCD points). Columns (1)–(3) use the common sample with information on ethnic fractionalization. Columns (4)–(6) use the common sample with information on ethnolinguistic fractionalization. Both fractionalization indices are standardized. All specifications include continent fixed effects and ancestry-adjusted absolute latitude, ecological diversity, caloric suitability, and a small island dummy, and exclude Africa. Ancestry-adjusted migratory distance is measured in units of 10,000 km. Heteroskedasticity-robust standard errors are reported in parentheses. *** Significant at the 1 percent level. ** Significant at the 5 percent level. * Significant at the 10 percent level.

Table B.14: The Out-of-Africa Migration and Contemporary Dispersion in Cultural Values within Populations of Second-Generation Migrants in Europe: Accounting for Ethnic Fractionalization

	Dispersion in cultural value					
	(1)	(2)	(3)	(4)	(5)	(6)
Ancestral migratory distance from the cradle of humanity	−0.060***		−0.064***	−0.057***		−0.057***
	(0.012)		(0.013)	(0.012)		(0.012)
Ethnic fractionalization		−0.0040	−0.0064*			
		(0.0041)	(0.0035)			
Ethnolinguistic fractionalization					0.0032	0.0018
					(0.0054)	(0.0046)
Dep. var. mean	0.42	0.42	0.42	0.42	0.42	0.42
Demographic bins	58,173	58,173	58,173	58,075	58,075	58,075
Cultural values	119	119	119	119	119	119
Homelands	90	90	90	92	92	92
Adjusted R^2	0.23	0.23	0.24	0.24	0.23	0.24

Notes: The table suggests that the association between the out-of-Africa migration and contemporary dispersion in cultural values across populations of second-generation migrants in Europe is not explained by ethnic or ethnolinguistic fractionalization. Ancestry-adjusted migratory distance is measured in units of 10,000 km. Dispersion in cultural values among individuals from an identical ancestral origin within each European country is captured by the coefficient of variation with respect to each value, accounting for cultural value and a host-country fixed effect. All specifications include ancestry-adjusted geographical controls (i.e., absolute latitude, ecological diversity, caloric suitability, and a small island dummy) as well as continent fixed effects. The analysis excludes countries in Africa. Heteroskedasticity-robust standard errors (clustered at the ancestral homeland level) are reported in parentheses. *** Significant at the 1 percent level. ** Significant at the 5 percent level. * Significant at the 10 percent level.

B.5 Descriptive Figures

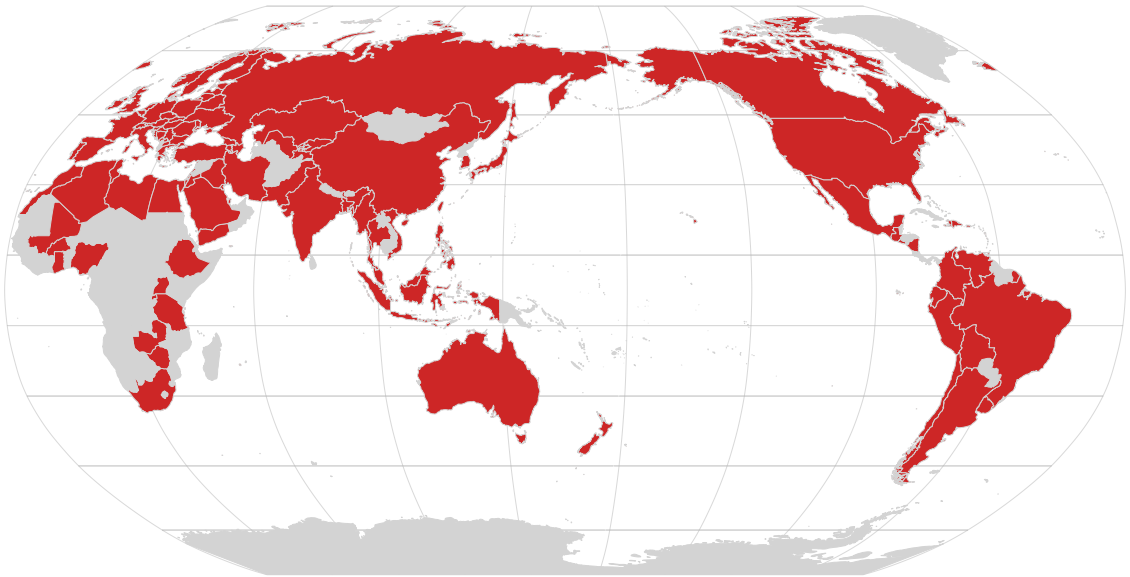


Figure B.5: Countries Included in the Analysis

Notes: This figure highlights in shaded red all the countries included in our analysis (Table V, Column (1)).

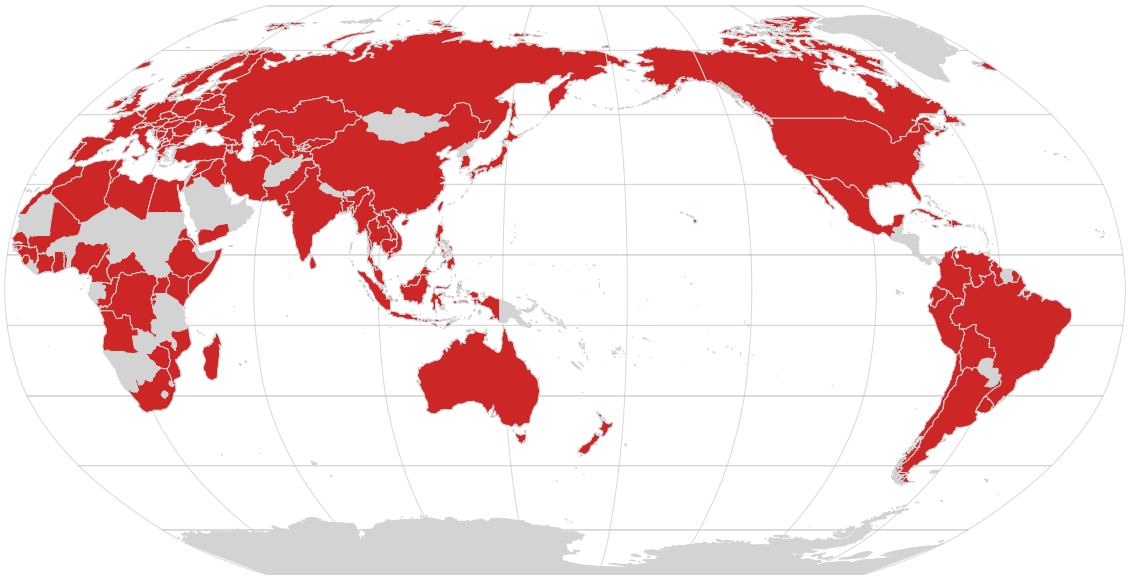


Figure B.6: Second-Generation Migrants' Homelands Included in the Analysis

Notes: This figure highlights in shaded red all the countries included in our analysis (Table VI, Column (1)).

C Proof of the Main Propositions

C.1 Proof of Proposition 1

Proof. (i): Convergence of cultural gaps.

Let $h \equiv h(e)$ and define $a \equiv (1-\mu)(1-h)(1-\delta)$, $B \equiv (1-\mu)(1-h)(1-(1-\delta))$, $C \equiv (1-\mu)h\theta^* + \mu H(\hat{\theta})$. Thus, $a, B > 0$ and $a + B = (1-\mu)(1-h) < 1$.

Since $\theta_0^j = \theta^j$, the cultural dynamics of dynasty j can be written as

$$\theta_{t+1}^j = a\theta_t^j + B\theta_0^j + C.$$

For any two dynasties $j, k \in J$ such that $\theta_0^k > \theta_0^j$, define $\Delta_t^{jk} \equiv \theta_t^k - \theta_t^j$ where $\Delta_0^{jk} > 0$. Subtracting their laws of motion, it follows that

$$\Delta_{t+1}^{jk} = a\Delta_t^{jk} + B\Delta_0^{jk}.$$

Hence, $\Delta_t^{jk} = A_t\Delta_0^{jk}$, where $A_0 = 1$ and $A_{t+1} = aA_t + B$. Defining $\bar{A} \equiv B/(1-a)$,

$$A_t = \bar{A} + (1-\bar{A})a^t.$$

Since $a \in (0,1)$ and $a + B < 1$, it follows that $\bar{A} \in (0,1)$ and therefore $0 < A_{t+1} < A_t \leq 1$. Consequently, for all $t \geq 0$,

$$0 < \Delta_{t+1}^{jk} < \Delta_t^{jk} \qquad \text{and} \qquad \lim_{t\to\infty} \Delta_t^{jk} = \bar{A}\Delta_0^{jk} \in (0, \Delta_0^{jk}).$$

(ii): Evolution of cross-dynasty dispersion.

Let $\int_J dj = 1$. Using the pairwise representation of the variance and the result that $\Delta_t^{jk} = A_t\Delta_0^{jk}$,

$$\mathrm{Var}_J(\theta_t^j) = \frac{1}{2}\int_J\int_J \left(\theta_t^k - \theta_t^j\right)^2 dj\, dk = A_t^2\,\mathrm{Var}_J(\theta_0^j).$$

Since the initial distribution is nondegenerate and $0 < A_{t+1} < A_t \leq 1$, for all $t \geq 0$,

$$0 < \mathrm{Var}_J(\theta_{t+1}^j) < \mathrm{Var}_J(\theta_t^j) \qquad \text{and} \qquad \lim_{t\to\infty} \mathrm{Var}_J(\theta_t^j) = \bar{A}^2\,\mathrm{Var}_J(\theta_0^j) \in \big(0, \mathrm{Var}_J(\theta_0^j)\big).$$

(iii): Ancestral diversity and steady-state cultural dispersion.

The dynasty-specific steady-state cultural trait satisfies

$$\bar{\theta}^j = a\bar{\theta}^j + B\theta^j + C,$$

and therefore $\bar{\theta}^j = \xi(\theta^j) = \bar{A}\theta^j + C/(1-a)$. Thus, ξ is strictly increasing and affine. Since $\theta^j = \hat{\theta} + \sigma(\omega)z^j$, where $\mathrm{Var}_J(z^j) = 1$,

$$\mathrm{Var}_J(\bar{\theta}^j) = \bar{A}^2\,\mathrm{Var}_J(\theta^j) = \bar{A}^2\sigma(\omega)^2,$$

and therefore

$$\frac{\partial \operatorname{Var}_J(\bar{\theta}^j)}{\partial \omega} = 2\bar{A}^2\sigma(\omega)\sigma'(\omega) > 0.$$

□

C.2 Proof of Proposition 2

Let

$$\mathcal{V}(\omega, b) \equiv \operatorname{Var}_p\big(\bar{\theta}^j \mid \omega, b\big) = \int_J \bar{s}^j(\omega, b)\left[\bar{\theta}^j(\omega) - \bar{\Theta}(\omega, b)\right]^2 dj, \qquad \bar{\Theta}(\omega, b) \equiv \int_J \bar{s}^j(\omega, b)\bar{\theta}^j(\omega) dj.$$

The steady-state cultural trait of dynasty j, $\bar{\theta}^j(\omega)$, is determined solely by vertical and horizontal cultural transmission and is therefore independent of the intensity of fitness-based selection, b. The parameter b affects $\mathcal{V}(\omega, b)$ only through the steady-state population shares, $\bar{s}^j(\omega, b)$.

When $b = 0$, population shares remain equal to their initial levels. Since J represents the distribution of dynasties in the founder population, the population-weighted steady-state variance coincides with the steady-state variance across dynasties. Moreover, Proposition 1 establishes that the steady-state mapping is affine, i.e., $\bar{\theta}^j = \xi_0 + \xi_1\theta^j$, where $\xi_1 \in (0, 1)$.

Since $\theta^j = \hat{\theta} + \sigma(\omega)z^j$ and $\operatorname{Var}_J(z^j) = 1$,

$$\mathcal{V}(\omega, 0) = \operatorname{Var}_J(\bar{\theta}^j \mid \omega) = \xi_1^2\sigma(\omega)^2.$$

Hence,

$$F(\omega, 0) \equiv \frac{\partial \mathcal{V}(\omega, 0)}{\partial \omega} = 2\xi_1^2\sigma(\omega)\sigma'(\omega) > 0.$$

It remains to establish that this strict inequality persists for sufficiently small positive values of b. For every finite t, the cultural traits, fitness levels, and population shares are continuously differentiable in (ω, b). In particular, the population shares evolve according to

$$s_{t+1}^j = \left[1 + b\left(1 - \frac{L_t}{\bar{L}}\right)\left(f_t^j - \bar{f}_t\right)\right] s_t^j.$$

The aggregate population law is independent of both ω and b, and Appendix J establishes that

$$\sum_{t=0}^{\infty}\left(1 - \frac{L_t}{\bar{L}}\right) < \infty.$$

Since the trait space is bounded and cultural dynamics are affine, fitness and its derivative with respect to ω are uniformly bounded. The infinite product defining $\bar{s}^j(\omega, b)$ and its derivative with respect to ω therefore converge uniformly for b in a neighborhood of zero. Hence, $\bar{s}^j(\omega, b)$, its derivative with respect to ω, and consequently

$$F(\omega, b) \equiv \frac{\partial \mathcal{V}(\omega, b)}{\partial \omega}$$

are continuous in (ω, b). Let Ω denote the compact admissible range of ancestral diversity. Since $F(\omega, 0)$ is continuous and strictly positive on Ω,

$$m \equiv \min_{\omega \in \Omega} F(\omega, 0) > 0.$$

By uniform continuity, there exists $\bar{b} > 0$ such that, for every $\omega \in \Omega$ and every $b \in [0, \bar{b})$,

$$|F(\omega, b) - F(\omega, 0)| < \frac{m}{2}.$$

It follows that

$$F(\omega, b) > F(\omega, 0) - \frac{m}{2} \geq \frac{m}{2} > 0,$$

and therefore, for every $b \in (0, \bar{b})$,

$$\frac{\partial}{\partial \omega} \operatorname{Var}_p\big(\bar{\theta}^j\big) > 0.$$

□

C.3 Proof of Proposition 3

Proof. Let $h \equiv h(e)$ and $\sigma \equiv \sigma(\omega)$. The cultural law of motion can be written as

$$\theta^j_{t+1} = q\theta^j_t + r\theta^j + C,$$

where

$$q \equiv (1-\mu)(1-h)(1-\delta), \qquad r \equiv (1-\mu)(1-h)\delta,$$

and

$$C \equiv (1-\mu)h\theta^* + \mu H(\hat{\theta}).$$

Hence, $q, r > 0$ and $q + r < 1$. Since

$$\theta^j = \hat{\theta} + \sigma z^j,$$

the cultural trait of dynasty j at every date t can be written as

$$\theta^j_t = m_t + A_t \sigma z^j,$$

where m_t is independent of σ, $A_0 = 1$, and

$$A_{t+1} = qA_t + r > 0.$$

Consequently,

$$A_t \longrightarrow \bar{A} \equiv \frac{r}{1-q} > 0,$$

and the dynasty-specific steady-state cultural trait is

$$\bar{\theta}^j = \bar{m} + \bar{A}\sigma z^j,$$

where $\bar{m}$ is independent of σ.

Demographic reweighting.

Let $s_t(z;\sigma)$ denote the population distribution of dynasties indexed by z, and define its mean by

$$M_t(\sigma) \equiv \int_J z\, s_t(z;\sigma)\, dz.$$

Under the linear fitness specification,

$$f_t(z;\sigma) = 1 - \nu\left[d_t - A_t\sigma z\right], \qquad d_t \equiv \theta^* - m_t.$$

Therefore,

$$f_t(z;\sigma) - \bar{f}_t(\sigma) = \nu A_t \sigma\left[z - M_t(\sigma)\right].$$

The population distribution consequently evolves according to

$$s_{t+1}(z;\sigma) = Q_t(z;\sigma) s_t(z;\sigma),$$

where

$$Q_t(z;\sigma) \equiv 1 + c_t\sigma\left[z - M_t(\sigma)\right], \qquad c_t \equiv \kappa_t \nu A_t > 0.$$

Since

$$\int_J Q_t(z;\sigma) s_t(z;\sigma)\, dz = 1,$$

this updating rule preserves total population shares. Moreover, $Q_t(z;\sigma) > 0$ along the equilibrium path.

The mean of z evolves according to

$$\begin{aligned} M_{t+1}(\sigma) - M_t(\sigma) &= c_t\sigma \int_J z\left[z - M_t(\sigma)\right] s_t(z;\sigma)\, dz \\ &= c_t\sigma\, \mathrm{Var}_{s_t}(z) > 0. \end{aligned}$$

Since the founder distribution is nondegenerate and has mean zero,

$$M_0(\sigma) = 0,$$

and therefore

$$M_t(\sigma) > 0 \qquad \text{for every } t > 0.$$

It remains to establish that $M_t(\sigma)$ is strictly increasing in σ. Define the score of the population distribution as

$$u_t(z;\sigma) \equiv \frac{\partial \log s_t(z;\sigma)}{\partial \sigma}.$$

Since the founder distribution of z is independent of σ,

$$u_0(z;\sigma) = 0.$$

Moreover,

$$M_t'(\sigma) = \int_J z\, u_t(z;\sigma) s_t(z;\sigma)\, dz = \mathrm{Cov}_{s_t}(z, u_t(z;\sigma)).$$

Differentiating the population updating rule gives

$$u_{t+1}(z;\sigma) = u_t(z;\sigma) + \frac{c_t\left[z - M_t(\sigma) - \sigma M_t'(\sigma)\right]}{1 + c_t\sigma\left[z - M_t(\sigma)\right]}.$$

The derivative of the second term with respect to z is

$$\frac{c_t\left[1 + c_t\sigma^2 M_t'(\sigma)\right]}{\left\{1 + c_t\sigma\left[z - M_t(\sigma)\right]\right\}^2} > 0$$

whenever $M_t'(\sigma) \geq 0$. Thus, beginning with $u_0 = 0$, induction implies that $u_t(z;\sigma)$ is strictly increasing in z for every $t > 0$. Since the distribution of z is nondegenerate,

$$M_t'(\sigma) = \mathrm{Cov}_{s_t}\left(z, u_t(z;\sigma)\right) > 0.$$

Finite cumulative selection implies

$$\sum_{t=0}^{\infty} c_t < \infty.$$

The population distributions and their derivatives with respect to σ therefore converge uniformly to a nondegenerate limiting distribution $\bar{s}(z;\sigma)$. It follows that

$$\bar{M}(\sigma) \equiv \int_J z\,\bar{s}(z;\sigma)\,dz$$

satisfies

$$\bar{M}(\sigma) > 0 \qquad \text{and} \qquad \bar{M}'(\sigma) \geq 0.$$

Ancestral diversity and cultural adaptation.

The population-weighted steady-state mean cultural trait is

$$\bar{\Theta}(\omega) = \int_J \bar{s}^j(\omega)\bar{\theta}^j(\omega)\,dj = \bar{m} + \bar{A}\sigma(\omega)\bar{M}(\sigma(\omega)).$$

Since

$$\bar{A} > 0, \qquad \sigma'(\omega) > 0, \qquad \bar{M}(\sigma) > 0, \qquad \bar{M}'(\sigma) \geq 0,$$

it follows that

$$\frac{\partial\bar{\Theta}}{\partial\omega} = \bar{A}\sigma'(\omega)\left[\bar{M}(\sigma) + \sigma\bar{M}'(\sigma)\right] > 0.$$

Finally, since $\bar{\Theta} < \theta^*$,

$$\frac{\partial(\theta^* - \bar{\Theta})}{\partial\omega} = -\frac{\partial\bar{\Theta}}{\partial\omega} < 0.$$

Thus, greater ancestral diversity moves the population-weighted steady-state mean cultural trait closer to the environment-specific fitness-maximizing cultural trait.

□

C.4 Proof of Proposition 4

Proof. The scalar representation used within each society orders cultural traits along that society's adaptation path, from the common ancestral cultural predisposition toward its environment-

specific fitness-maximizing cultural trait. This one-dimensional representation does not imply that the fitness-maximizing traits associated with different ecological environments can themselves be placed on a common scalar ordering. Indeed, ecological environments are not inherently hierarchically ordered. For the purpose of cross-societal comparisons, the society-specific one-dimensional adaptation paths are therefore embedded as different directions in a two-dimensional space, emanating from the geometric representation of the common ancestral cultural predisposition, $\hat{\boldsymbol{\theta}}$. The radial dimension preserves the within-society scalar representation, while the angular dimension distinguishes the directions associated with different ecological environments.

Since all societies share the same mean ancestral cultural predisposition, $\hat{\theta}$, and ecological environments are not inherently not hierarchically ordered, the environment-specific fitness-maximizing cultural traits for all societies are assumed to lie at a common distance from $\hat{\theta}$, where this common distance is normalized to one. Thus, the fitness-maximizing cultural traits lie on a unit circle centered at $\hat{\boldsymbol{\theta}}$. For each society $r \in \{i, \ell\}$, let $\alpha_r \in [0, 2\pi)$ denote the angular position of its environment-specific fitness-maximizing cultural trait and define $\mathbf{e}_r \equiv (\cos\alpha_r, \sin\alpha_r)$. Hence,

$$\boldsymbol{\theta}^*_r \equiv \hat{\boldsymbol{\theta}} + \mathbf{e}_r,$$

where $\mathbf{e}_r$ is the unit vector pointing from $\hat{\boldsymbol{\theta}}$ toward the environment-specific fitness-maximizing cultural trait of society r. This geometric embedding does not alter the one-dimensional cultural dynamics within any society; it only permits the directions of adaptation across societies to be compared.

Let

$$\Delta\alpha_{i\ell} \equiv \min\left\{|\alpha_i - \alpha_\ell|,\, 2\pi - |\alpha_i - \alpha_\ell|\right\} \in [0, \pi]$$

denote the smaller angular separation between the two traits. Ecological distance is represented by

$$d^e_{i\ell} \equiv 1 - \mathbf{e}'_i\mathbf{e}_\ell = 1 - \cos\left(\Delta\alpha_{i\ell}\right).$$

Because $\mathbf{e}_i$ and $\mathbf{e}_\ell$ are unit vectors,

$$\|\mathbf{e}_i - \mathbf{e}_\ell\| = \sqrt{2d^e_{i\ell}}.$$

Hence, $d^e_{i\ell}$ and the chord distance between the two environment-specific traits generate the same ordering.

Let $\chi_r \in (0, 1)$ denote the normalized degree of cultural adaptation in society r, measured by the distance traveled from the common ancestral benchmark along its adaptation path. The geometric representation of its population-weighted steady-state cultural trait is therefore

$$\bar{\boldsymbol{\Theta}}^{\,r} = \hat{\boldsymbol{\theta}} + \chi_r\mathbf{e}_r.$$

Under the affine transmission specification and the common normalization of the adaptation path, Proposition 3 implies

$$\chi_r = \chi(\omega_r), \qquad \chi'(\omega_r) > 0.$$

Cultural distance is therefore

$$d^c_{i\ell} \equiv \left\|\bar{\boldsymbol{\Theta}}^{\,i} - \bar{\boldsymbol{\Theta}}^{\,\ell}\right\| = \left\|\chi_i\mathbf{e}_i - \chi_\ell\mathbf{e}_\ell\right\|.$$

Since $\|\mathbf{e}_i\| = \|\mathbf{e}_\ell\| = 1$ and $\mathbf{e}'_i\mathbf{e}_\ell = 1 - d^e_{i\ell}$,

$$\left(d^c_{i\ell}\right)^2 = \chi_i^2 + \chi_\ell^2 - 2\chi_i\chi_\ell\mathbf{e}'_i\mathbf{e}_\ell = \left(\chi_i - \chi_\ell\right)^2 + 2\chi_i\chi_\ell d^e_{i\ell}.$$

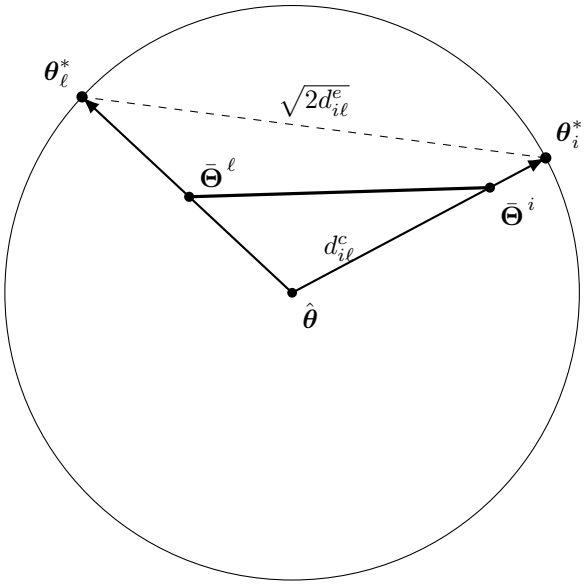


Figure C.1: Ecological distance, cultural adaptation, and cultural distance. The environment-specific fitness-maximizing cultural traits lie on the unit circle centered at the common ancestral cultural benchmark. The population-weighted steady-state cultural traits lie along the corresponding adaptation paths at normalized distances χ_i and χ_ℓ from the benchmark. Ecological distance orders the chord between the two environment-specific traits, whereas cultural distance is the chord between the two interior steady-state cultural positions.

Define the mean degree of adaptation and the absolute difference in the degrees of adaptation as

$$\bar{\chi}_{i\ell} \equiv \frac{\chi_i + \chi_\ell}{2}, \qquad d^\chi_{i\ell} \equiv |\chi_i - \chi_\ell|.$$

Since $\chi_i\chi_\ell = \bar{\chi}^2_{i\ell} - \left(d^\chi_{i\ell}\right)^2/4$, and therefore

$$(d^c_{i\ell})^2 = 2\bar{\chi}^2_{i\ell} d^e_{i\ell} + \left(1 - \frac{d^e_{i\ell}}{2}\right)\left(d^\chi_{i\ell}\right)^2.$$

All strict inequalities below are evaluated at interior admissible values and for a nondegenerate pair, so that $d^c_{i\ell} > 0$.

Part (i): Ecological distance and cultural distance.

$$\frac{\partial d^c_{i\ell}}{\partial d^e_{i\ell}} = \frac{\chi_i\chi_\ell}{d^c_{i\ell}} > 0.$$

Thus, cultural distance is strictly increasing in ecological distance.

Part (ii): Distance in ancestral diversity and cultural distance.

It is first necessary to relate distance in ancestral diversity, $d^\omega_{i\ell} = |\omega_i - \omega_\ell|$, to the difference in the societies' degrees of adaptation. χ is strictly increasing and it has a strictly increasing inverse, $g \equiv \chi^{-1}$. Without loss of generality, suppose that $\chi_i \geq \chi_\ell$. Holding $\bar{\chi}_{i\ell}$ fixed,

$$\chi_i = \bar{\chi}_{i\ell} + \frac{d^\chi_{i\ell}}{2}, \qquad \chi_\ell = \bar{\chi}_{i\ell} - \frac{d^\chi_{i\ell}}{2},$$

and therefore

$$d^{\omega}_{i\ell} = g\left(\bar{\chi}_{i\ell} + \frac{d^{\chi}_{i\ell}}{2}\right) - g\left(\bar{\chi}_{i\ell} - \frac{d^{\chi}_{i\ell}}{2}\right).$$

Differentiating with respect to $d^{\chi}_{i\ell}$ gives

$$\frac{\partial d^{\omega}_{i\ell}}{\partial d^{\chi}_{i\ell}} = \frac{1}{2}g'\left(\bar{\chi}_{i\ell} + \frac{d^{\chi}_{i\ell}}{2}\right) + \frac{1}{2}g'\left(\bar{\chi}_{i\ell} - \frac{d^{\chi}_{i\ell}}{2}\right) > 0.$$

Hence,

$$\frac{\partial d^{\chi}_{i\ell}}{\partial d^{\omega}_{i\ell}} > 0.$$

Differentiating with respect to $d^{\chi}_{i\ell}$ gives

$$\frac{\partial d^{c}_{i\ell}}{\partial d^{\chi}_{i\ell}} = \frac{\left(1 - \frac{d^{e}_{i\ell}}{2}\right) d^{\chi}_{i\ell}}{d^{c}_{i\ell}} > 0,$$

where strictness follows for $d^{\chi}_{i\ell} > 0$ and $d^{e}_{i\ell} < 2$. Hence,

$$\frac{\partial d^{c}_{i\ell}}{\partial d^{\omega}_{i\ell}} = \frac{\partial d^{c}_{i\ell}}{\partial d^{\chi}_{i\ell}} \frac{\partial d^{\chi}_{i\ell}}{\partial d^{\omega}_{i\ell}} > 0.$$

Thus, cultural distance is strictly increasing in the difference in ancestral diversity.

Part (iii): Distance in ancestral diversity and the ecological-distance gradient.

Differentiating equation (C.4) with respect to $d^{e}_{i\ell}$

$$\frac{\partial d^{c}_{i\ell}}{\partial d^{e}_{i\ell}} = \frac{\bar{\chi}^{2}_{i\ell} - \frac{\left(d^{\chi}_{i\ell}\right)^{2}}{4}}{d^{c}_{i\ell}}.$$

Differentiating this expression with respect to $d^{\chi}_{i\ell}$, holding $\bar{\chi}_{i\ell}$ fixed, yields

$$\frac{\partial^{2} d^{c}_{i\ell}}{\partial d^{e}_{i\ell} \partial d^{\chi}_{i\ell}} = -\frac{d^{\chi}_{i\ell}}{2d^{c}_{i\ell}} - \frac{\left[\bar{\chi}^{2}_{i\ell} - \frac{\left(d^{\chi}_{i\ell}\right)^{2}}{4}\right]\left(1 - \frac{d^{e}_{i\ell}}{2}\right) d^{\chi}_{i\ell}}{\left(d^{c}_{i\ell}\right)^{3}}.$$

Because

$$\bar{\chi}^{2}_{i\ell} - \frac{\left(d^{\chi}_{i\ell}\right)^{2}}{4} = \chi_{i}\chi_{\ell} > 0,$$

both terms on the right-hand side are strictly negative for interior values. Hence,

$$\frac{\partial^{2} d^{c}_{i\ell}}{\partial d^{e}_{i\ell} \partial d^{\chi}_{i\ell}} < 0.$$

Hence,

$$\frac{\partial^{2} d^{c}_{i\ell}}{\partial d^{e}_{i\ell} \partial d^{\omega}_{i\ell}} = \frac{\partial^{2} d^{c}_{i\ell}}{\partial d^{e}_{i\ell} \partial d^{\chi}_{i\ell}} \frac{\partial d^{\chi}_{i\ell}}{\partial d^{\omega}_{i\ell}} < 0.$$

Thus, the marginal effect of ecological distance on cultural distance is strictly decreasing in the difference in ancestral diversity.

□

D Learning the Environment-Specific Fitness-Maximizing Cultural Trait

At the onset of settlement, the environment-specific fitness-maximizing cultural trait, θ^*, is unknown. Members of the founder population know only that $\theta^* \in [0,1]$. They therefore know neither its value nor the direction in which cultural adaptation should proceed.

This appendix considers two alternative mechanisms through which reproductive outcomes may reveal θ^*. The first is based on experimentation with cultural practices that may depart from individuals' inherited cultural predispositions. The second does not rely on such experimentation and instead infers θ^* from differences in reproductive outcomes associated with the inherited cultural predispositions represented in the founder population. Under either mechanism, θ^* can be inferred only after reproductive outcomes in the novel environment have been realized and therefore cannot guide the initial sorting of founder populations across ecological environments.

D.1 Learning through Experimentation

As individuals seek to adapt to the novel environment, they engage in experimentation with alternative cultural practices. These practices, denoted by x, are observable actions and need not coincide with the inherited cultural predisposition of the individual who adopts them. Thus, although $\theta^j < \theta^*$ for every dynasty j, the practices that emerge through experimentation may lie on either side of θ^*.

Since all cultural traits along the equilibrium path of the baseline model lie below θ^*, the baseline fitness specification characterizes the region in which fitness declines linearly with the gap from θ^*. Experimentation, however, may generate practices above as well as below θ^*. The baseline fitness function is therefore extended symmetrically during experimentation to

$$f_0(x) = 1 - \nu|\theta^* - x|, \qquad \nu \in (0,1).$$

Thus, fitness declines linearly with the absolute distance of the experimental practice from the environment-specific optimum. For $x < \theta^*$, this formulation coincides exactly with the baseline fitness specification. Hence, the extension required for experimentation has no bearing on the evolutionary dynamics underlying Propositions 1–4.

Suppose that the distribution of experimental practices is independent of inherited cultural predispositions and has full support on $[0,1]$. Individuals with different inherited predispositions are therefore exposed to the same distribution of experimental practices and the learning process does not systematically reweight dynasties according to their inherited predispositions. Moreover, experimental practices are temporary and do not alter the inherited cultural predispositions that govern subsequent cultural evolution.

The income and fertility associated with experimental cultural practice x are

$$y_0(x) = \left[1 + \kappa_0 \left(f_0(x) - \bar{f}_0\right)\right] y_0 \qquad \text{and} \qquad n_0(x) = \frac{\gamma}{\rho} y_0(x),$$

where $\bar{f}_0$ is average fitness across the experimental practices realized in the founder population.

Hence, realized fertility is

$$n_0(x) = A - B|\theta^* - x|,$$

where

$$A \equiv \frac{\gamma}{\rho} y_0 \left[1 + \kappa_0 (1 - \bar{f}_0)\right] \qquad \text{and} \qquad B \equiv \frac{\gamma}{\rho} y_0 \kappa_0 \nu > 0.$$

Equivalently,

$$n_0(x) = \begin{cases} A - B(\theta^* - x), & x \leq \theta^*, \\ A - B(x - \theta^*), & x \geq \theta^*. \end{cases}$$

Fertility is therefore strictly increasing in the experimental cultural practice for $x < \theta^*$ and strictly decreasing for $x > \theta^*$. Consequently,

$$\theta^* = \arg \max_{x \in [0,1]} n_0(x).$$

Following the completion of the founder generation's reproductive cycle, the population observes the reproductive outcomes associated with the range of experimental cultural practices. Since both the experimental practice, x, and its associated reproductive outcome are observable, identification of θ^* does not require the inherited predisposition of the experimenting individual to be observed. The cultural practice at which fertility ceases to increase and begins to decline identifies the environment-specific fitness-maximizing cultural trait, θ^*.

Thus, under this learning mechanism, reproductive outcomes reveal θ^* after one completed generation. Once θ^* has been identified, experimentation ceases and cultural evolution proceeds according to the baseline model.

D.2 Learning from Inherited Cultural Predispositions

The second learning mechanism does not rely on experimentation with practices that depart from inherited cultural predispositions. Instead, θ^* is inferred from the reproductive outcomes associated with the inherited cultural predispositions represented in the founder population.

Under the linear fitness specification of the baseline model, this cross-sectional variation cannot identify the location of θ^*. In particular,

$$f_0^j - \bar{f}_0 = \nu \left(\theta^j - \bar{\theta}_0\right),$$

so that θ^* drops out of relative fitness and, consequently, from the variation in reproductive outcomes across dynasties. Identification from inherited predispositions therefore requires a fitness specification under which the location of θ^* affects the shape of the observed fertility schedule.

Consider the quadratic fitness specification

$$f_0^j = 1 - \frac{\nu}{2} \left(\theta^* - \theta^j\right)^2, \qquad \nu > 0.$$

The curvature of this specification permits the location of θ^* to be inferred from the reproductive outcomes associated with inherited cultural predispositions.[38]

The income and fertility of dynasty j are

$$y_0^j = \left[1 + \kappa_0 \left(f_0^j - \bar{f}_0\right)\right] y_0 \qquad \text{and} \qquad n_0^j = \frac{\gamma}{\rho} y_0^j,$$

[38] Under this alternative fitness specification, Propositions 1 and 2 remain intact, while Propositions 3 and 4 are preserved under bounded evolutionary selection.

where

$$\bar{f}_0 \equiv \int_{j\in J} s_0^j f_0^j \, dj.$$

Let

$$\bar{\theta}_0 \equiv \int_{j\in J} s_0^j \theta^j \, dj, \qquad \overline{\theta_0^2} \equiv \int_{j\in J} s_0^j (\theta^j)^2 \, dj.$$

The difference between the fitness of dynasty j and average fitness is

$$f_0^j - \bar{f}_0 = \nu\theta^* \left(\theta^j - \bar{\theta}_0\right) - \frac{\nu}{2}\left[(\theta^j)^2 - \overline{\theta_0^2}\right].$$

Hence, realized fertility is a quadratic function of the inherited cultural predisposition:

$$n_0^j = A + B\theta^j + C(\theta^j)^2,$$

where A collects terms that are independent of θ^j, $B = (\gamma/\rho)y_0\kappa_0\nu\theta^*$, and $C = -\gamma\nu y_0\kappa_0/(2\rho) < 0$.

Following the completion of the founder generation's reproductive cycle, the population observes the fertility associated with the continuum of inherited cultural predispositions represented within it. These cross-sectional outcomes identify the quadratic fertility schedule and therefore its implied maximum. In particular, the location at which the slope of the fitted fertility schedule vanishes is $\theta^* = -B/2C$.

Thus, although all inherited cultural predispositions lie below θ^*, the curvature of the observed fertility schedule permits the environment-specific fitness-maximizing cultural trait to be inferred.

Under this alternative learning mechanism, the reproductive outcomes of the founder population therefore reveal θ^* after one completed generation. As under experimentation, however, this information becomes available only after settlement and the realization of reproductive outcomes in the novel environment. Founder populations therefore cannot initially sort across ecological environments according to the alignment of their inherited predispositions with the environment-specific fitness-maximizing cultural trait.

E Robustness to Child Cultural Outcomes in Parental Preferences

This subsection shows that the qualitative results are preserved when parental utility depends directly on the expected cultural trait of the child.

Suppose parental utility depends on θ_{t+1}^j rather than on $\ln h(e_t^j)$:

$$u_t^j = (1-\gamma)\ln c_t^j + \gamma\left[\ln n_t^j + \theta_{t+1}^j - g(e_t^j)\right].$$

Cultural transmission is given by:

$$\theta_{t+1}^j = (1-\mu)\left[\theta^j + (1-h(e_t^j))(1-\delta)(\theta_t^j - \theta^j) + h(e_t^j)(\theta^* - \theta^j)\right] + \mu H(\hat{\theta}).$$

Define the cultural trait that would be transmitted before the additional adjustment generated by adaptation-based parental effort as

$$\widetilde{\theta}_t^j \equiv \theta^j + (1-\delta)(\theta_t^j - \theta^j).$$

Cultural transmission can therefore be written as

$$\theta_{t+1}^j = (1-\mu)\left[\widetilde{\theta}_t^j + h(e_t^j)\left(\theta^* - \widetilde{\theta}_t^j\right)\right] + \mu H(\hat{\theta}).$$

Optimal effort. Let $h(e_t^j) = (e_t^j)^\alpha$, $\alpha \in (0,1)$, and $g(e_t^j) = \frac{\chi}{2}(e_t^j)^2$, $\chi > 0$. Optimization with respect to e_t^j implies that

$$e_t^j = \left[\frac{(1-\mu)\alpha}{\chi}\left(\theta^* - \widetilde{\theta}_t^j\right)\right]^{\frac{1}{2-\alpha}}.$$

Hence,

$$\theta_{t+1}^j = (1-\mu)\widetilde{\theta}_t^j + \mu H(\hat{\theta}) + A\left[\theta^* - \widetilde{\theta}_t^j\right]^q,$$

where $q = 2/(2-\alpha) > 1$ and $A = (1-\mu)[(1-\mu)\alpha/\chi]^{\frac{\alpha}{2-\alpha}}$.

Qualitative properties. Let $\psi_e(\theta_t^j; \theta^j)$ be the dynamical system. Since $\widetilde{\theta}_t^j = \delta\theta^j + (1-\delta)\theta_t^j$,

$$\frac{\partial \psi_e(\theta_t^j;\theta^j)}{\partial \theta_t^j} = (1-\delta)\left[(1-\mu) - Aq\left(\theta^* - \widetilde{\theta}_t^j\right)^{q-1}\right].$$

A sufficient condition for ψ_e to be increasing and a contraction on $[0,\theta^*]$ is therefore

$$Aq(\theta^*)^{q-1} < 1-\mu.$$

Under this condition,

$$0 < \frac{\partial \psi_e(\theta_t^j;\theta^j)}{\partial \theta_t^j} < (1-\delta)(1-\mu) < 1.$$

Moreover, at the lower endpoint,

$$\psi_e(0;\theta^j) = (1-\mu)\delta\theta^j + \mu H(\hat{\theta}) + A(\theta^* - \delta\theta^j)^q > 0.$$

At the upper endpoint,

$$\theta^* - \psi_e(\theta^*;\theta^j) = \mu[\theta^* - H(\hat{\theta})] + \delta(\theta^* - \theta^j)\left[(1-\mu) - A\delta^{q-1}(\theta^* - \theta^j)^{q-1}\right] > 0.$$

Thus, ψ_e maps $[0,\theta^*]$ into itself and has a unique dynasty-specific steady state below θ^*. In addition,

$$\frac{\partial \psi_e(\theta_t^j;\theta^j)}{\partial \theta^j} = \delta\left[(1-\mu) - Aq\left(\theta^* - \widetilde{\theta}_t^j\right)^{q-1}\right] > 0.$$

Hence, the transition function preserves the ordering of dynasties by their inherited cultural predispositions. By the implicit-function theorem, the dynasty-specific steady state satisfies

$$\frac{\partial \bar{\theta}^j}{\partial \theta^j} = \frac{\partial \psi_e(\bar{\theta}^j;\theta^j)/\partial \theta^j}{1 - \partial \psi_e(\bar{\theta}^j;\theta^j)/\partial \bar{\theta}^j} > 0.$$

Feasibility. Since $A \to 0$ as $\chi \to \infty$, the sufficient condition $Aq(\theta^*)^{q-1} < 1-\mu$ holds for sufficiently large χ. Moreover, the optimal effort is interior for all admissible states if

$$\frac{(1-\mu)\alpha}{\chi}\theta^* < 1,$$

which also holds for sufficiently large χ.

Implication. The model therefore preserves a unique dynasty-specific steady state below θ^*, convergence to that steady state, order preservation, and persistent cross-dynasty dispersion. Allowing parental utility to depend explicitly on the child's expected cultural trait introduces state-dependent effort but does not alter the qualitative mechanism.

F Fitness and Endogenous Aggregate Productivity

This appendix examines an extension of the baseline framework in which aggregate productivity depends on the population-weighted cultural state. Cultural evolution remains autonomous and governed by the same affine contraction mapping as in the baseline model. Endogenous aggregate productivity does, however, alter the population path and therefore the path of the selection-intensity parameter. The analysis below establishes that cumulative selection remains finite and that the qualitative results concerning unweighted and population-weighted cultural diversity remain intact.

F.1 Endogenous Aggregate Productivity

To allow aggregate income per worker to rise as the population becomes culturally better aligned with its environment, replace the constant technology parameter A in the Malthusian production function with a term that depends on the population-weighted cultural state:

$$Y_t \;=\; A(\bar{\theta}_t)\, F(X, L_t) \;\equiv\; A(\bar{\theta}_t)\, X^{\alpha} L_t^{1-\alpha}, \qquad 0 < \alpha < 1,$$

where

$$\bar{\theta}_t \equiv \int_{j \in J} \theta_t^j \, s_t^j \, dj, \qquad A'(\cdot) > 0.$$

Income per worker is therefore

$$y_t \equiv \frac{Y_t}{L_t} = A(\bar{\theta}_t) \left(\frac{X}{L_t}\right)^{\alpha}.$$

All remaining elements of the model are unchanged. In particular, dynastic income continues to depend on relative fitness according to

$$y_t^j = \Big[1 + \kappa_t\big(f_t^j - \bar{f}_t\big)\Big]\, y_t,$$

and fertility is given by $n_t^j = (\gamma/\rho)\, y_t^j$.

Aggregating fertility across dynasties yields

$$L_{t+1} = \frac{\gamma}{\rho} y_t L_t = \frac{\gamma}{\rho} A(\bar{\theta}_t) X^{\alpha} L_t^{1-\alpha}.$$

Define the contemporaneous carrying capacity associated with the population-weighted cultural state in period t as

$$\bar{L}_t \equiv \left[\frac{\gamma}{\rho} A(\bar{\theta}_t)\right]^{1/\alpha} X.$$

The aggregate population law can therefore be written as

$$L_{t+1} = \bar{L}_t^{\alpha} L_t^{1-\alpha}.$$

Accordingly, the selection-intensity parameter is

$$\kappa_t = b\left(1 - \frac{L_t}{\bar{L}_t}\right), \qquad b \in (0,1).$$

Thus, endogenous aggregate productivity affects demographic reweighting indirectly by altering the population path and the contemporaneous carrying capacity.

F.2 Dimensionality and System Structure

Allowing y_t and κ_t to depend on the population-weighted cultural state $\bar{\theta}_t$ introduces an explicit dependence of the demographic and population dynamics on the entire cross-dynasty distribution of cultural traits and population shares. Consequently, the joint system governing $\{\theta_t^j, s_t^j\}_{j\in J}$ and L_t is high-dimensional (or infinite-dimensional when J is continuous). Importantly, however, the system remains triangular. The cultural subsystem is autonomous, while the demographic and population subsystem responds to the evolving cultural distribution but does not feed back into dynasty-specific cultural dynamics.

F.3 Autonomy of Cultural Evolution

For each dynasty $j \in J$, cultural traits evolve according to

$$\theta_{t+1}^j = \psi(\theta_t^j; \theta^j),$$

exactly as in the baseline model. Under the affine transmission specification,

$$\theta_{t+1}^j = q\theta_t^j + r\theta^j + C,$$

where $q, r > 0$, $q + r < 1$, and C is common across dynasties. The cultural evolutionary operator ψ does not depend on aggregate income, population shares, the population-weighted cultural state, or the aggregate population. Hence cultural evolution is autonomous.

As a result, all properties of the cultural dynamics established in the main text, including affinity, contraction, order preservation, and the existence of a unique dynasty-specific steady state, continue to hold. In particular, the results on monotone convergence with persistence of cross-dynasty dispersion (Proposition 1) are unaffected.

F.4 Selection and Demographic Reweighting

Population shares evolve according to

$$s_{t+1}^j = \frac{L_{t+1}^j}{L_{t+1}} = \frac{n_t^j L_t^j}{\int n_t^k L_t^k \, dk} = \frac{n_t^j}{\bar{n}_t} \, s_t^j, \qquad \bar{n}_t \equiv \int n_t^k s_t^k \, dk.$$

Using $n_t^j = (\gamma/\rho)\, y_t^j$ and the normalization $\int y_t^k s_t^k \, dk = y_t$, it follows that $\bar{n}_t = (\gamma/\rho)\, y_t$ and

$$s_{t+1}^j = \frac{y_t^j}{y_t} \, s_t^j = \Big[1 + \kappa_t \big(f_t^j - \bar{f}_t\big)\Big] \, s_t^j.$$

Aggregate income y_t therefore cancels directly from the population-share equation. Nevertheless, endogenous aggregate productivity affects demographic reweighting indirectly because it changes $\bar{L}_t$ and hence κ_t.

It remains to establish that cumulative selection is finite. Under the affine cultural law, each dynasty's cultural trait increases monotonically toward its dynasty-specific steady state. Moreover, since fitness is linear and increasing in θ_t^j along the equilibrium path, demographic selection shifts population weight toward dynasties with higher cultural traits. In particular,

$$\bar{\theta}_{t+1} - \bar{\theta}_t = \int_{j \in J} \left(\theta_{t+1}^j - \theta_t^j\right) s_{t+1}^j \, dj + \int_{j \in J} \theta_t^j \left(s_{t+1}^j - s_t^j\right) \, dj \geq 0,$$

where

$$\int_{j \in J} \theta_t^j \left(s_{t+1}^j - s_t^j\right) \, dj = \kappa_t \operatorname{Cov}_{s_t}\left(\theta_t^j, f_t^j\right) = \kappa_t \nu \operatorname{Var}_{s_t}\left(\theta_t^j\right) \geq 0.$$

Since $\bar{\theta}_t < \theta^*$, the sequence $\{\bar{\theta}_t\}_{t \geq 0}$ is bounded and therefore converges to a limit $\bar{\Theta}$. It follows that $\bar{L}_t$ is nondecreasing and converges to

$$\bar{L}_\infty = \left[\frac{\gamma}{\rho} A(\bar{\Theta})\right]^{1/\alpha} X.$$

Let

$$x_t \equiv \frac{L_t}{\bar{L}_t}.$$

If $L_0 < \bar{L}_0$, then $x_t \in (0, 1)$ for all t, and the population law implies

$$x_{t+1} = \frac{\bar{L}_t}{\bar{L}_{t+1}} x_t^{1-\alpha}.$$

Define $a_t \equiv -\ln x_t > 0$ and $d_t \equiv \ln(\bar{L}_{t+1}/\bar{L}_t) \geq 0$. Then

$$a_{t+1} = (1 - \alpha) a_t + d_t.$$

Since $\bar{L}_t$ is nondecreasing and convergent,

$$\sum_{t=0}^{\infty} d_t = \ln\left(\frac{\bar{L}_\infty}{\bar{L}_0}\right) < \infty.$$

Iterating the preceding difference equation and summing over time yields

$$\sum_{t=0}^{\infty} a_t \leq \frac{a_0}{\alpha} + \frac{1}{\alpha} \ln\left(\frac{\bar{L}_\infty}{\bar{L}_0}\right) < \infty.$$

Since $1 - x_t \leq -\ln x_t = a_t$,

$$\sum_{t=0}^{\infty} \kappa_t = b \sum_{t=0}^{\infty} (1 - x_t) \leq b \sum_{t=0}^{\infty} a_t < \infty.$$

Thus, endogenous aggregate productivity preserves finite cumulative selection and a nondegenerate limiting distribution of population shares.

F.5 Implications for the Main Results

The triangular structure of the extended system implies that cultural evolution drives demographic and population dynamics, but not conversely. Dynasty-specific cultural traits follow exactly the same affine contraction as in the baseline model. Hence, convergence with persistent unweighted cultural dispersion (Proposition 1) is unchanged.

Endogenous aggregate productivity changes the path of demographic reweighting through κ_t, but the preceding analysis establishes that cumulative selection remains finite. At $b = 0$, population shares remain equal to their founder values, and the population-weighted steady-state variance coincides with the unweighted steady-state variance. Since the affine steady-state mapping is unchanged, this variance is strictly increasing in ancestral diversity. The population path, limiting population shares, and their derivatives with respect to ancestral diversity are continuous in b in a neighborhood of zero. Consequently, by the same continuity argument used in the proof of Proposition 2, there exists $\bar{b}_A > 0$ such that, for every $b \in (0, \bar{b}_A)$, the steady-state population-weighted variance of cultural traits remains strictly increasing in ancestral diversity.

Accordingly, the qualitative results of the model remain unchanged:

- convergence with persistence of unweighted cross-dynasty cultural dispersion (Proposition 1);
- the monotone effect of ancestral diversity on long-run population-weighted cultural diversity for sufficiently limited selection (Proposition 2).

Thus, endogenizing aggregate productivity does not merely alter the level path of income per worker. It also changes the population path and the intensity of demographic selection. Nevertheless, the affine cultural dynamics imply convergence of the population-weighted cultural state, the induced carrying capacity converges, cumulative selection remains finite, and the central qualitative predictions of the theory are preserved.

G Robustness to Generalized Fitness

This section establishes the robustness of Propositions 1 and 2 to a generalized fitness structure in which dynastic fitness depends on both the distance between a dynasty's cultural trait and the environment-specific benchmark and the dispersion of cultural traits in the population. It shows, first, that dispersion-dependent fitness leaves dynasty-specific cultural dynamics and therefore unweighted long-run cultural dispersion unchanged. Second, provided that its effect on the intensity of selection is bounded, the positive association between ancestral diversity and population-weighted long-run cultural dispersion remains valid when selection is sufficiently limited.

For expositional convenience, the analysis considers $j \in \{1, \ldots, J\}$, which allows the dynamic system to be represented in a finite-dimensional state space. The same argument extends to the

continuous-type formulation because it relies on the autonomy of the cultural subsystem and finite cumulative selection.

G.1 Generalized Fitness

In the baseline framework, dynastic fitness depends solely on the proximity of a dynasty's cultural trait to the environment-specific fitness-maximizing benchmark. In particular,

$$f_t^j = 1 - \nu \left(\theta^* - \theta_t^j \right),$$

where $\theta_t^j \in (0, \theta^*)$ denotes the cultural trait of dynasty j at time t and $\nu > 0$.

The fitness function is generalized by allowing aggregate cultural dispersion to affect fitness levels. Suppose that dynastic fitness at time t is given by

$$f_t^j = A(\sigma_t^2) \left[1 - \nu \left(\theta^* - \theta_t^j \right) \right] - C(\sigma_t^2),$$

where $\sigma_t^2 \equiv \mathrm{Var}_p(\theta_t^j)$ denotes the contemporaneous population-weighted variance of cultural traits, and $A(\sigma_t^2) > 0$ and $C(\sigma_t^2) \geq 0$ are continuously differentiable functions that depend only on aggregate cultural dispersion and are therefore common across dynasties. Suppose, moreover, that on the feasible range of cultural dispersion,

$$0 < \underline{A} \leq A(\sigma_t^2) \leq \overline{A} < \infty.$$

The term $A(\sigma_t^2)$ captures how cultural dispersion scales the productivity or survival returns associated with cultural alignment, through complementarities, knowledge spillovers, or risk-sharing, while $C(\sigma_t^2)$ captures dispersion-related losses in social cohesion.

For any given distribution of cultural traits, this formulation preserves the ordinal ranking of dynasties by proximity to θ^*. For any two dynasties j, k,

$$f_t^j - f_t^k = A(\sigma_t^2) \nu \left(\theta_t^j - \theta_t^k \right),$$

so relative fitness comparisons are governed exclusively by proximity to θ^*.

As a result, the direction of selection across dynasties is unchanged, although its intensity is scaled by $A(\sigma_t^2)$. In particular, since the additive term $C(\sigma_t^2)$ cancels from relative fitness, the effective selection intensity is

$$\widetilde{\kappa}_t \equiv \kappa_t A(\sigma_t^2).$$

Since cumulative selection is finite in the baseline model,

$$\sum_{t=0}^{\infty} \widetilde{\kappa}_t \leq \overline{A} \sum_{t=0}^{\infty} \kappa_t < \infty.$$

Thus, dispersion-dependent fitness preserves finite cumulative selection and nondegenerate limiting population shares. As established below, all qualitative results derived in the baseline model, including the contraction of pairwise cultural differences, the persistence of long-run cultural dispersion, and the monotone relationship between ancestral diversity and population-weighted cultural diversity for sufficiently limited selection, remain intact.

G.2 Triangular Structure of the Dynamic System

Consider the joint evolution of cultural traits and population shares. Cultural traits evolve according to the dynasty-specific law of motion

$$\theta_{t+1}^j = \psi(\theta_t^j; \theta^j), \qquad j = 1, \ldots, J,$$

where $\psi(\cdot)$ depends only on dynasty-specific cultural predispositions and the parameters governing cultural transmission.

Population shares evolve according to the demographic updating rule

$$s_{t+1}^j = \Phi_j(s_t, f_t),$$

where $f_t = (f_{1t}, \ldots, f_{Jt})$ denotes the vector of dynastic fitness levels, which depend on the vector of dynasty-level cultural traits $\{\theta_t^j\}_{j=1}^J$ and aggregate cultural dispersion through the generalized fitness specification introduced above.

Let the state vector be

$$x_t \equiv \left(\theta_t^1, \ldots, \theta_t^J, s_t^1, \ldots, s_t^J\right)^\top.$$

The dynamic system can be written as

$$x_{t+1} = F(x_t),$$

where the first J components of $F(\cdot)$ correspond to cultural evolution and the remaining J components to demographic updating.

The defining feature of the system is its triangular structure. Cultural evolution is autonomous and depends only on dynasty-level cultural traits and predispositions. Formally,

$$\frac{\partial \theta_{t+1}^j}{\partial s_t^k} = 0 \quad \text{for all } j, k, \qquad \frac{\partial \theta_{t+1}^j}{\partial f_{kt}} = 0 \quad \text{for all } j, k, \qquad \frac{\partial \theta_{t+1}^j}{\partial \sigma_t^2} = 0.$$

The dynamic system can be written as a mapping

$$x_{t+1} = F(x_t), \qquad x_t \equiv \left(\theta_t^1, \ldots, \theta_t^J, s_t^1, \ldots, s_t^J\right)^\top.$$

If F is differentiable, its Jacobian $DF(x_t)$ has the block-triangular form (Galor, 2007)

$$DF(x_t) = \left(\begin{array}{cccc|cccc} \frac{\partial \psi(\theta_t^1;\theta^1)}{\partial \theta_t^1} & 0 & \cdots & 0 & 0 & 0 & \cdots & 0 \\ 0 & \frac{\partial \psi(\theta_t^2;\theta^2)}{\partial \theta_t^2} & \cdots & 0 & 0 & 0 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \frac{\partial \psi(\theta_t^J;\theta^J)}{\partial \theta_t^J} & 0 & 0 & \cdots & 0 \\ \hline \frac{\partial s_{t+1}^1}{\partial \theta_t^1} & \frac{\partial s_{t+1}^1}{\partial \theta_t^2} & \cdots & \frac{\partial s_{t+1}^1}{\partial \theta_t^J} & \frac{\partial s_{t+1}^1}{\partial s_t^1} & \frac{\partial s_{t+1}^1}{\partial s_t^2} & \cdots & \frac{\partial s_{t+1}^1}{\partial s_t^J} \\ \frac{\partial s_{t+1}^2}{\partial \theta_t^1} & \frac{\partial s_{t+1}^2}{\partial \theta_t^2} & \cdots & \frac{\partial s_{t+1}^2}{\partial \theta_t^J} & \frac{\partial s_{t+1}^2}{\partial s_t^1} & \frac{\partial s_{t+1}^2}{\partial s_t^2} & \cdots & \frac{\partial s_{t+1}^2}{\partial s_t^J} \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots \\ \frac{\partial s_{t+1}^J}{\partial \theta_t^1} & \frac{\partial s_{t+1}^J}{\partial \theta_t^2} & \cdots & \frac{\partial s_{t+1}^J}{\partial \theta_t^J} & \frac{\partial s_{t+1}^J}{\partial s_t^1} & \frac{\partial s_{t+1}^J}{\partial s_t^2} & \cdots & \frac{\partial s_{t+1}^J}{\partial s_t^J} \end{array}\right).$$

Consequently, population shares, fitness, and aggregate cultural dispersion do not feed back into the evolution of cultural traits. The cultural subsystem is therefore autonomous and identical to that analyzed in the baseline model, implying that all properties established for ψ, including order preservation and contraction, continue to hold. As a result, the introduction of dispersion-dependent fitness does not alter the existence, ordering, or stability of cultural steady states.

G.3 Robustness of Unweighted and Population-Weighted Cultural Diversity

Proposition A1 (Robustness of Unweighted and Population-Weighted Cultural Diversity)**.** *Suppose cultural evolution is governed by the baseline affine law of motion,*

$$\theta_{t+1}^j = \psi(\theta_t^j;\theta^j),$$

whose dynasty-specific fixed-point mapping is affine and strictly increasing:

$$\bar{\theta}^j = \xi_0 + \xi_1 \theta^j, \qquad \xi_1 \in (0,1).$$

Suppose population shares evolve according to

$$s_{t+1}^j = \left[1 + \kappa_t\left(f_t^j - \bar{f}_t\right)\right] s_t^j, \qquad \kappa_t = b\left(1 - \frac{L_t}{\bar{L}}\right), \qquad j = 1,\ldots,J,$$

and dynastic fitness is given by the dispersion-dependent specification

$$f_{jt} = A(\sigma_t^2)\left[1 - \nu\left(\theta^* - \theta_t^j\right)\right] - C(\sigma_t^2), \qquad \sigma_t^2 \equiv \mathrm{Var}_p(\theta_t^j),$$

where $\nu > 0$, and A and C are continuously differentiable and

$$0 < \underline{A} \le A(\sigma_t^2) \le \overline{A} < \infty, \qquad C(\sigma_t^2) \ge 0.$$

Then:

1. *For each dynasty j, $\theta_t^j \to \bar{\theta}^j$ as $t \to \infty$.*
2. *If $\theta^j > \theta^k$, then $\bar{\theta}^j > \bar{\theta}^k$.*
3. *The long-run unweighted dispersion of cultural traits across dynasties is identical to that in the baseline model and is strictly increasing in ancestral diversity. Moreover, there exists $\bar{b}_A > 0$ such that, for every $b \in (0, \bar{b}_A)$, the steady-state population-weighted variance of cultural traits is strictly increasing in ancestral diversity.*

Proof. By the triangular structure established in the preceding subsection, the cultural subsystem is autonomous: the evolution of $(\theta_t^1, \ldots, \theta_t^J)$ is governed solely by $\theta_{t+1}^j = \psi(\theta_t^j; \theta^j)$ and is independent of (s_t, f_t, σ_t^2). Hence the cultural dynamics are identical to those in the baseline model. Since $\psi(\cdot; \theta^j)$ is a contraction mapping, each dynasty's sequence $\{\theta_t^j\}_{t \geq 0}$ converges to the unique fixed point $\bar{\theta}^j$, proving (i). Since $\psi(\cdot; \theta)$ is order-preserving, the ordering of fixed points across dynasties follows, proving (ii). Since the set of limiting cultural traits $\{\bar{\theta}^j\}_{j=1}^J$ is unchanged by dispersion-dependent fitness, the long-run unweighted dispersion of cultural traits is identical to that in the baseline model and is therefore strictly increasing in ancestral diversity.

It remains to establish the population-weighted result. Let

$$V_A(\omega, b) \equiv \sum_{j=1}^{J} \bar{s}_A^j(\omega, b) \left[\bar{\theta}^j(\omega) - \bar{\Theta}_A(\omega, b)\right]^2, \qquad \bar{\Theta}_A(\omega, b) \equiv \sum_{j=1}^{J} \bar{s}_A^j(\omega, b) \bar{\theta}^j(\omega),$$

where $\bar{s}_A^j(\omega, b)$ denotes the limiting population share under generalized fitness.

When $b = 0$, population shares remain equal to their founder levels. Since the steady-state mapping is affine,

$$\bar{\theta}^j = \xi_0 + \xi_1 \theta^j, \qquad \xi_1 \in (0, 1),$$

and $\theta^j = \hat{\theta} + \sigma(\omega) z^j$, where the founder distribution of z^j has mean zero and variance one,

$$V_A(\omega, 0) = \xi_1^2 \sigma(\omega)^2.$$

Hence,

$$F_A(\omega, 0) \equiv \frac{\partial V_A(\omega, 0)}{\partial \omega} = 2\xi_1^2 \sigma(\omega) \sigma'(\omega) > 0.$$

Under generalized fitness, the population shares evolve according to

$$s_{t+1}^j = \left[1 + b\left(1 - \frac{L_t}{\bar{L}}\right) A(\sigma_t^2) \left(\widetilde{f}_t^j - \bar{\widetilde{f}}_t\right)\right] s_t^j,$$

where

$$\widetilde{f}_t^j \equiv 1 - \nu\left(\theta^* - \theta_t^j\right), \qquad \bar{\widetilde{f}}_t \equiv \sum_{j=1}^{J} s_t^j \widetilde{f}_t^j.$$

The term $C(\sigma_t^2)$ cancels from relative fitness, while $A(\sigma_t^2)$ scales the intensity of selection. Since

$$\sum_{t=0}^{\infty} \left(1 - \frac{L_t}{\bar{L}}\right) A(\sigma_t^2) \leq \overline{A} \sum_{t=0}^{\infty} \left(1 - \frac{L_t}{\bar{L}}\right) < \infty,$$

cumulative selection remains finite.

For every finite t, cultural traits, fitness levels, and population shares are continuously differentiable in (ω, b). Since the trait space and the feasible range of cultural dispersion are compact, the baseline fitness component and A, together with their derivatives, are uniformly bounded. The infinite product defining $\bar{s}_A^j(\omega, b)$ and its derivative with respect to ω therefore converge uniformly for b in a neighborhood of zero. Hence, $\bar{s}_A^j(\omega, b)$, its derivative with respect to ω, and

$$F_A(\omega, b) \equiv \frac{\partial V_A(\omega, b)}{\partial \omega}$$

are continuous in (ω, b).

Let Ω denote the compact admissible range of ancestral diversity. Since $F_A(\omega, 0)$ is continuous and strictly positive on Ω,

$$m_A \equiv \min_{\omega \in \Omega} F_A(\omega, 0) > 0.$$

By uniform continuity, there exists $\bar{b}_A > 0$ such that, for every $\omega \in \Omega$ and every $b \in [0, \bar{b}_A)$,

$$|F_A(\omega, b) - F_A(\omega, 0)| < \frac{m_A}{2}.$$

It follows that

$$F_A(\omega, b) > F_A(\omega, 0) - \frac{m_A}{2} \geq \frac{m_A}{2} > 0.$$

Therefore, for every $b \in (0, \bar{b}_A)$,

$$\frac{\partial}{\partial \omega} \operatorname{Var}_p\big(\bar{\theta}^j\big) > 0.$$

This establishes the robustness of Proposition 1 with respect to unweighted cultural dispersion and of Proposition 2 with respect to population-weighted cultural dispersion. □

H Time-Varying Population-Weighted Horizontal Transmission

This appendix examines the robustness of the main results to an extension in which horizontal cultural transmission depends on the time-varying population-weighted cultural state rather than on the initial mean cultural predisposition, $\hat{\theta}$. The extension does not preserve the autonomy of dynasty-specific cultural levels, since the population-weighted cultural state depends on population shares. Under the affine transmission specification, however, pairwise cultural dynamics remain autonomous, while the aggregate component follows a stable scalar recursion. As a result, Propositions 1 and 2 remain valid.

H.1 Motivation

In the baseline framework, horizontal transmission is modeled as exposure to a society-wide benchmark summarized by $H(\hat{\theta}) = \lambda\hat{\theta}$, where $\hat{\theta}$ reflects the initial mean cultural predisposition inherited from founding populations. This formulation captures diffusion through socially embedded and codified cultural expressions, such as folklore, music, institutions, and shared narratives, that evolve slowly and summarize historically accumulated predispositions.

An alternative interpretation emphasizes contemporaneous peer exposure, under which individuals are influenced by the prevailing distribution of cultural traits in the population. Under this interpretation, horizontal transmission naturally depends on the time-varying population-weighted cultural state. The extension considered below formalizes this alternative channel and establishes that it preserves the qualitative results concerning unweighted and population-weighted cultural diversity.

H.2 Cultural Dynamics with Time-Varying Population-Weighted Horizontal Transmission

Let the population-weighted mean realized cultural trait at time t be

$$\bar{\Theta}_t \equiv \int \theta_t^k \, s_t^k \, dk,$$

where s_t^k denotes the population share of dynasty k. Horizontal transmission is now given by

$$H_t = \lambda \bar{\Theta}_t.$$

Under the affine transmission specification, cultural evolution within dynasty j follows

$$\theta_{t+1}^j = q\theta_t^j + r\theta^j + C + \mu\lambda\bar{\Theta}_t,$$

where

$$q \equiv (1-\mu)(1-h)(1-\delta), \qquad r \equiv (1-\mu)(1-h)\delta, \qquad C \equiv (1-\mu)h\theta^*.$$

Hence, $q, r > 0$ and $q + r < 1$. Assume

$$q + \mu\lambda < 1.$$

This condition ensures stability of the aggregate cultural component. As in the baseline model, suppose that cultural traits remain below θ^* along the equilibrium path. A sufficient condition for the interval $[0, \theta^*]$ to be invariant is

$$\mu(\lambda - 1)\theta^* < r\left(\theta^* - \widetilde{\theta}\right),$$

where $\widetilde{\theta}$ is the upper bound of the support of inherited cultural predispositions.

Because $\bar{\Theta}_t$ depends on the entire distribution $\{\theta_t^k, s_t^k\}_k$, dynasty-specific cultural levels are not autonomous. As shown below, however, the affine structure separates the evolution of pairwise cultural differences from the aggregate component.

H.3 Invariance of Pairwise Cultural Dynamics

Consider any two dynasties j, k. Using the extended cultural dynamics,

$$\theta_{t+1}^k - \theta_{t+1}^j = q\left(\theta_t^k - \theta_t^j\right) + r\left(\theta^k - \theta^j\right) + \mu\lambda\left(\bar{\Theta}_t - \bar{\Theta}_t\right).$$

The aggregate term cancels identically, implying

$$\Delta_{t+1}^{jk} \equiv \theta_{t+1}^k - \theta_{t+1}^j = q\Delta_t^{jk} + r\left(\theta^k - \theta^j\right).$$

Since $q \in (0, 1)$,

$$\Delta_t^{jk} \longrightarrow \frac{r}{1-q}\left(\theta^k - \theta^j\right).$$

Implication. Pairwise cultural gaps contract toward positive dynasty-specific steady-state gaps and preserve the ordering of dynasties by their inherited cultural predispositions. Therefore, Proposition 1 remains valid without modification.

Equivalently, cultural traits can be written as

$$\theta_t^j = m_t + a_t \theta^j,$$

where $m_0 = 0$, $a_0 = 1$, and

$$a_{t+1} = q a_t + r.$$

Thus,

$$a_t \longrightarrow \bar{a} \equiv \frac{r}{1-q} > 0.$$

The coefficient governing cross-dynasty cultural dispersion is therefore identical to that in the baseline model.

H.4 Steady-State Characterization and Aggregate Stability

Let

$$\bar{\theta}_t^p \equiv \int \theta^j s_t^j \, dj$$

denote the population-weighted mean inherited cultural predisposition. Since

$$\bar{\Theta}_t = m_t + a_t \bar{\theta}_t^p,$$

the common component evolves according to

$$m_{t+1} = (q + \mu\lambda) m_t + C + \mu\lambda a_t \bar{\theta}_t^p.$$

Population shares converge because, as shown below, their law of motion is identical to that in the baseline model and cumulative selection is finite. Hence,

$$\bar{\theta}_t^p \longrightarrow \bar{\theta}^p$$

for some limiting population-weighted mean inherited predisposition $\bar{\theta}^p$. Since $a_t \to \bar{a}$ and $q + \mu\lambda < 1$, the recursion for m_t is stable and

$$m_t \longrightarrow \bar{m} \equiv \frac{C + \mu\lambda \bar{a} \bar{\theta}^p}{1 - q - \mu\lambda}.$$

Consequently, each dynasty's cultural trait converges to

$$\bar{\theta}^j = \bar{m} + \bar{a} \theta^j,$$

and the population-weighted cultural state converges to

$$\bar{\Theta} = \bar{m} + \bar{a} \bar{\theta}^p = \frac{C + r \bar{\theta}^p}{1 - q - \mu\lambda}.$$

Thus, aggregate stability follows from the condition $q + \mu\lambda < 1$. The steady-state mapping from inherited cultural predispositions to realized cultural traits remains affine and strictly increasing, with the same slope $\bar{a} = r/(1-q)$ as in the baseline model. Time-varying horizontal transmission alters only the common intercept.

H.5 Dimensionality and Tractability

Allowing horizontal transmission to depend on $\bar{\Theta}_t$ renders the joint system high-dimensional, since each dynasty's cultural level depends on the contemporaneous distribution of cultural traits and population shares. The system is therefore not triangular in dynasty-specific cultural levels and population shares.

The affine structure nevertheless permits an exact decomposition. Pairwise cultural differences evolve autonomously according to a one-dimensional stable recursion, while the common component m_t follows a scalar recursion driven by the population-weighted mean inherited predisposition. Since population shares converge and $q + \mu\lambda < 1$, the common component also converges. The high-dimensional system therefore reduces to autonomous pairwise dynamics and a stable aggregate component.

Accordingly, the increased dimensionality affects neither the existence nor the ordering of dynasty-specific steady states, nor the persistence of cross-dynasty cultural dispersion.

H.6 Demographic Reweighting

Population shares evolve according to the demographic updating rule of the baseline model:

$$s_{t+1}^j = \left[1 + \kappa_t \left(f_t^j - \bar{f}_t\right)\right] s_t^j, \qquad \bar{f}_t \equiv \int f_t^k s_t^k \, dk.$$

Under the linear fitness specification and the maintained condition $\theta_t^j < \theta^*$,

$$f_t^j = 1 - \nu \left(\theta^* - \theta_t^j\right),$$

and therefore

$$f_t^j - \bar{f}_t = \nu \left(\theta_t^j - \bar{\Theta}_t\right).$$

Since $\theta_t^j = m_t + a_t \theta^j$ and $\bar{\Theta}_t = m_t + a_t \bar{\theta}_t^p$,

$$f_t^j - \bar{f}_t = \nu a_t \left(\theta^j - \bar{\theta}_t^p\right).$$

The common cultural component m_t cancels from relative fitness. Moreover, a_t follows exactly the same recursion as in the baseline model. Hence, given identical initial population shares, the entire path of demographic reweighting is identical to that in the baseline model.

Since the aggregate population law is unchanged, Appendix J implies

$$\sum_{t=0}^{\infty} \kappa_t < \infty.$$

Population shares therefore converge to the same nondegenerate limiting distribution as in the baseline model.

H.7 Implications for the Main Results and Concluding Remark

Allowing horizontal transmission to depend on the time-varying population-weighted cultural state preserves the qualitative implications concerning unweighted and population-weighted cultural diversity. In particular:

- Proposition 1 is unaffected because pairwise cultural dynamics are invariant to the aggregate state and converge to the same steady-state gaps as in the baseline model.
- Proposition 2 remains valid because the slope of the affine steady-state mapping and the entire path of population shares are identical to those in the baseline model. Consequently, long-run population-weighted cultural dispersion is unchanged.

The extension does not retain a triangular structure in cultural levels and population shares. Instead, the affine transmission specification yields an exact decomposition into autonomous pairwise cultural dynamics and a stable aggregate component. Under $q + \mu\lambda < 1$, the population-weighted cultural state converges, while relative fitness and demographic reweighting remain identical to those in the baseline model. Accordingly, representing horizontal transmission as exposure to the initial mean cultural predisposition, $\hat{\theta}$, provides a transparent benchmark without restricting the central predictions concerning cultural diversity.

I Heterogeneous Labor Productivity

This section extends the baseline framework by allowing individual labor productivity to increase with fitness. Since dynasties with higher fitness acquire larger population shares during the transition, evolutionary selection increases the representation of more productive individuals. This raises aggregate productivity and permits the ecological niche to support a larger steady-state population. Nevertheless, steady-state income per worker remains unchanged. The analysis below redefines the carrying capacity and the intensity of selection consistently with the evolving level of population-weighted labor productivity and establishes that cumulative selection remains finite.

I.1 Effective Labor and Aggregate Production

Let $q_t^j > 0$ denote the labor productivity of an adult belonging to dynasty j in period t. Labor productivity is assumed to increase with the fitness of the dynasty:

$$q_t^j = Q(f_t^j), \qquad Q'(f) > 0.$$

The units of labor productivity are normalized so that population-weighted average productivity in the founder population equals one:

$$\bar{q}_0 \equiv \int_J q_0^j s_0^j \, dj = 1.$$

This normalization applies only to the founder population. Since population shares subsequently evolve through differential reproductive success, population-weighted average productivity need not remain equal to one.

Aggregate effective labor in period t, Q_t, is

$$Q_t \equiv \int_J q_t^j L_t^j \, dj = \bar{q}_t L_t,$$

where

$$\bar{q}_t \equiv \int_J q_t^j s_t^j \, dj$$

is population-weighted average labor productivity.

Aggregate production is therefore

$$Y_t = (AX)^{\alpha} Q_t^{1-\alpha} = (AX)^{\alpha} \left(\bar{q}_t L_t\right)^{1-\alpha}, \qquad 0 < \alpha < 1.$$

Income per worker is consequently

$$y_t \equiv \frac{Y_t}{L_t} = \left(\frac{AX}{L_t}\right)^{\alpha} \bar{q}_t^{1-\alpha}.$$

Thus, for a given population size, an increase in the population share of more productive dynasties raises average labor productivity, aggregate output, and income per worker.

As in the baseline model, income is distributed across dynasties according to relative fitness:

$$y_t^j = \left[1 + \kappa_t \left(f_t^j - \bar{f}_t\right)\right] y_t,$$

where

$$\bar{f}_t \equiv \int_J f_t^j s_t^j \, dj.$$

Population-weighted mean income remains equal to y_t, since

$$\int_J \left[1 + \kappa_t \left(f_t^j - \bar{f}_t\right)\right] s_t^j \, dj = 1.$$

I.2 Population and Compositional Dynamics

The optimal number of children of an adult belonging to dynasty j remains

$$n_t^j = \frac{\gamma}{\rho} y_t^j.$$

The population of dynasty j therefore evolves according to

$$L_{t+1}^j = \frac{\gamma}{\rho} \left[1 + \kappa_t \left(f_t^j - \bar{f}_t\right)\right] y_t L_t^j.$$

Aggregating across dynasties gives

$$L_{t+1} = \frac{\gamma}{\rho} y_t L_t.$$

Using equation (I.1), the aggregate population law of motion is

$$L_{t+1} = \frac{\gamma}{\rho} (AX)^{\alpha} \bar{q}_t^{1-\alpha} L_t^{1-\alpha}.$$

Define the carrying capacity associated with population-weighted average labor productivity in period t as

$$\bar{L}_t \equiv \left(\frac{\gamma}{\rho}\right)^{1/\alpha} AX \bar{q}_t^{(1-\alpha)/\alpha}.$$

The aggregate population law can therefore be written as

$$L_{t+1} = \bar{L}_t^{\alpha} L_t^{1-\alpha}.$$

Accordingly, the intensity of selection is defined consistently with the contemporaneous carrying capacity:

$$\kappa_t = b\left(1 - \frac{L_t}{\bar{L}_t}\right), \qquad b \in (0,1).$$

Thus, for a given population size, an increase in average labor productivity raises income per worker, mean fertility, the carrying capacity, and population growth.

The population share of dynasty j evolves according to

$$s_{t+1}^j = \left[1 + \kappa_t\left(f_t^j - \bar{f}_t\right)\right] s_t^j.$$

Hence, dynasties with above-average fitness increase their population shares, whereas dynasties with below-average fitness experience declining shares. Since labor productivity increases with fitness, this demographic reweighting increases the representation of more productive dynasties and thereby raises population-weighted average productivity.

To establish the evolution of the carrying capacity, observe that

$$\begin{aligned}\bar{q}_{t+1} - \bar{q}_t &= \int_J \left(q_{t+1}^j - q_t^j\right) s_{t+1}^j \, dj + \int_J q_t^j \left(s_{t+1}^j - s_t^j\right) dj \\ &= \int_J \left(q_{t+1}^j - q_t^j\right) s_{t+1}^j \, dj + \kappa_t \operatorname{Cov}_{s_t}\left(q_t^j, f_t^j\right).\end{aligned}$$

Under the affine cultural dynamics, each dynasty's cultural trait moves monotonically toward its dynasty-specific steady state. Since fitness is increasing in the cultural trait along the equilibrium path and $Q'(f) > 0$, $q_{t+1}^j \geq q_t^j$. Moreover,

$$\operatorname{Cov}_{s_t}\left(q_t^j, f_t^j\right) \geq 0,$$

since $q_t^j = Q(f_t^j)$ and Q is increasing. Starting from $L_0 < \bar{L}_0$, it follows inductively that $\kappa_t \geq 0$, $\bar{q}_{t+1} \geq \bar{q}_t$, and $\bar{L}_{t+1} \geq \bar{L}_t$. Indeed, if $L_t < \bar{L}_t$, then

$$\frac{L_{t+1}}{\bar{L}_{t+1}} = \frac{\bar{L}_t}{\bar{L}_{t+1}} \left(\frac{L_t}{\bar{L}_t}\right)^{1-\alpha} < 1.$$

Since cultural traits and fitness are bounded, labor productivity is bounded. Hence, $\{\bar{q}_t\}_{t\geq 0}$ is nondecreasing and bounded and therefore converges:

$$\bar{q}_t \longrightarrow \bar{q}.$$

Consequently,

$$\bar{L}_t \longrightarrow \bar{L} \equiv \left(\frac{\gamma}{\rho}\right)^{1/\alpha} A X \bar{q}^{(1-\alpha)/\alpha}.$$

It remains to establish finite cumulative selection. Let

$$x_t \equiv \frac{L_t}{\bar{L}_t} \in (0,1).$$

The population law of motion implies that

$$x_{t+1} = \frac{\bar{L}_t}{\bar{L}_{t+1}} x_t^{1-\alpha}.$$

Define

$$a_t \equiv -\ln x_t > 0, \qquad d_t \equiv \ln\left(\frac{\bar{L}_{t+1}}{\bar{L}_t}\right) \geq 0.$$

Then

$$a_{t+1} = (1-\alpha)a_t + d_t.$$

Since $\bar{L}_t$ is nondecreasing and converges to $\bar{L}$,

$$\sum_{t=0}^{\infty} d_t = \ln\left(\frac{\bar{L}}{\bar{L}_0}\right) < \infty.$$

Iterating the recursion for a_t and summing over time gives

$$\sum_{t=0}^{\infty} a_t \leq \frac{a_0}{\alpha} + \frac{1}{\alpha}\ln\left(\frac{\bar{L}}{\bar{L}_0}\right) < \infty.$$

Since $1 - x_t \leq -\ln x_t = a_t$,

$$\sum_{t=0}^{\infty} \kappa_t = b\sum_{t=0}^{\infty}(1-x_t) \leq b\sum_{t=0}^{\infty} a_t < \infty.$$

Thus, cumulative selection remains finite. Given the same admissibility restriction as in the baseline model ensuring that the demographic updating factors remain positive, the boundedness of fitness differences and equation (I.2) imply that population shares converge to a non-degenerate limiting distribution.

I.3 Steady-State Population and Income

The affine cultural dynamics imply that dynasty-specific cultural traits converge. Hence, dynasty-specific fitness and labor productivity converge:

$$q_t^j \to \bar{q}^j.$$

Finite cumulative selection implies that population shares converge:

$$s_t^j \to \bar{s}^j.$$

Population-weighted average productivity therefore converges to

$$\bar{q} \equiv \int_J \bar{q}^j \bar{s}^j \, dj.$$

Conditional on the limiting level of average productivity, $\bar{q}$, the steady-state population satisfies

$$\bar{L} = \left(\frac{\gamma}{\rho}\right)^{1/\alpha} AX\bar{q}^{(1-\alpha)/\alpha}.$$

The steady-state population in the baseline model with homogeneous labor is

$$\bar{L}^0 = \left(\frac{\gamma}{\rho}\right)^{1/\alpha} AX,$$

and thus, $\bar{L}/\bar{L}^0 = \bar{q}^{(1-\alpha)/\alpha}$. Hence, if cultural adaptation and evolutionary selection raise long-run average productivity above its normalized founder-population level, so that $\bar{q} > 1$, then $\bar{L} > \bar{L}^0$. Greater average labor productivity therefore permits the ecological niche to support a larger steady-state population. Nevertheless, steady-state income per worker remains unchanged. Hence, $\frac{L_{t+1}}{L_t} = (\gamma/\rho)y_t$. At any positive steady state, $L_{t+1} = L_t = \bar{L}$, and thus $\bar{y} = (\rho/\gamma)$.

Thus, allowing individual labor productivity to increase with fitness affects the transitional paths of output, income, population, the carrying capacity, and the intensity of selection. It permits the ecological niche to support a larger steady-state population whenever $\bar{q} > 1$, but it does not alter steady-state income per worker. As in the baseline Malthusian framework, the gains from greater productivity are ultimately absorbed by population growth.

I.4 Implications for Cultural Evolution

The extension has no bearing on dynasty-specific cultural dynamics. The affine law of motion governing cultural transmission remains unchanged, so convergence with persistent unweighted cultural dispersion continues to hold.

The productivity-dependent carrying capacity changes the path of selection intensity. Nevertheless, the preceding analysis establishes that cumulative selection remains finite and that population shares converge to a non-degenerate limiting distribution. At $b = 0$, population shares remain equal to their founder-population values, and the population-weighted steady-state variance coincides with the unweighted steady-state variance, which is strictly increasing in ancestral diversity. Since the population and demographic dynamics are continuous in b, the continuity argument used in the proof of Proposition 2 implies that, for sufficiently limited selection, greater ancestral diversity continues to generate greater long-run population-weighted cultural diversity.

Thus, the extension preserves the central qualitative implications regarding cultural evolution under the same limited-selection condition as in the baseline framework. Evolutionary selection toward more productive cultural traits permits the ecological niche to support a larger steady-state population, while steady-state income per worker remains at the Malthusian subsistence level.

J Finite Cumulative Selection

Lemma 1 (Finite cumulative selection)**.** *Along the equilibrium population path,*

$$\sum_{t=0}^{\infty} \kappa_t \leq -\frac{b}{\alpha} \ln\left(\frac{L_0}{\bar{L}}\right) < \infty.$$

Proof. Given the population law of motion,

$$L_{t+1} = \frac{\gamma}{\rho}(AX)^{\alpha} L_t^{1-\alpha},$$

where the steady-state population is $\bar{L} = (\gamma/\rho)^{1/\alpha} AX$, it follows that

$$x_{t+1} = x_t^{1-\alpha},$$

where $x_t \equiv L_t/\bar{L}$. Hence, $x_t = x_0^{(1-\alpha)^t}$, and $x_0 \equiv (L_0/\bar{L}) \in (0,1)$. Since

$$\kappa_t = b(1 - x_t),$$

it follows that

$$\kappa_t = b\left[1 - x_0^{(1-\alpha)^t}\right].$$

Let $a \equiv -\ln x_0 > 0$. Then

$$\kappa_t = b\left[1 - e^{-a(1-\alpha)^t}\right].$$

Since

$$1 - e^{-z} \leq z \qquad \text{for all } z \geq 0,$$

it follows that

$$\kappa_t \leq ba(1-\alpha)^t.$$

Therefore,

$$\sum_{t=0}^{\infty} \kappa_t \leq ba \sum_{t=0}^{\infty} (1-\alpha)^t = \frac{ba}{\alpha} = -\frac{b}{\alpha} \ln\left(\frac{L_0}{\bar{L}}\right) < \infty.$$

□