Social network architecture and the tempo of cumulative cultural evolution

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Abstract

The ability to build upon previous knowledge—cumulative cultural evolution (CCE)—is a hallmark of human societies. While CCE depends on the interaction between social systems, cognition and the environment, there is increasing evidence that CCE is facilitated by larger and more structured societies. However, the relative importance of social network architecture as an additional factor shaping CCE remains unclear. By simulating innovation and diffusion of cultural traits in populations with stereotyped social structures, we disentangle the relative contributions of network architecture from those of population size and connectivity. We demonstrate that while multilevel societies can promote the recombination of cultural traits into high-value products, they also hinder spread and make products more likely to go extinct. We find that transmission mechanisms are therefore critical in determining the outcomes of CCE. Our results highlight the complex interaction between population size, structure and transmission mechanisms, with important implications for future research.

Keywords

Cultural evolution | Cultural complexity | Multilevel societies | Small-world networks | Social structure

Introduction

Cumulative cultural evolution—where iterative innovations and social transmission generate cultural accumulation over time [1-3]—is key to the human's ecological success and worldwide distribution [4,5]. While CCE fundamentally depends on the interplay between cognition and social learning mechanisms [1], it is increasingly clear that demography can modulate the rate of cultural evolution [6-9]. Large population sizes [10,11], greater population turnover, and more densely connected societies [3,12] can all provide greater innovative potential, more learning models, faster diffusion, and reduced extinction risk of useful innovations [7,13-15]. For example, increasing population density as well as migration of hunter-gatherers during the upper Paleolithic transition led to the explosion of culture that forms the basis of modern human

societies [8,15]. Yet, it remains unclear how variation in the wiring of these social connections shape the tempo of cumulative cultural evolution.

Network architecture—here defined as a social structure with a characteristic set of properties—can shape transmission of behaviours, thus setting the tempo of CCE—here defined as the rate of cultural recombination events. For example, architectures with low network connectivity (i.e. density; proportion of realised connections), high clustering (tendency of connected individuals to share the same social neighbours) and high modularity (tendency of the network to contain sets of individuals more connected to each other than with others) slow down the spread of information across populations [16-18]. Slower spread can then potentially favour greater cultural diversity by allowing multiple cultural lineages to arise in populations before any one lineage dominates [19,20]. While previous work has largely focused on how new behaviours spread through a social network [16,17] to establish cultures [20,21] and how cultural traits can generate a feedback shaping network structure [18,22], more recently it has been argued that emergent network properties could affect CCE [12,14,19] by shaping how new traits are produced, recombined, and maintained [14]. For example, partial connectivity facilitates the emergence of multiple cultural lineages in parallel [20], which is required for achieving cultural accumulation, but partially-connected networks suffer from cultural loss if connectivity is too low for new innovations to spread [14]. By contrast, full connectivity facilitates rapid spread of new innovations, but can prevent the accumulation of alternative cultural traits [12,14]. However, within a given level of connectivity, how connections are structured—the social network architecture—could also impact CCE by influencing how fast and widely information can spread.

Because network architecture can shape the effect of connectivity on diffusion dynamics [23], those architectures that balance the ability for cultural accumulation together with the recombination of different cultural traits should have a selective advantage in facilitating CCE [19]. Multilevel societies, such as those in modern hunter-gatherers, feature high clustering and nested modularity. These network properties are expected to favour CCE by allowing coexistence of multiple cultural traits in different parts of the network, and for different cultural lineages to come into contact to allow combinations from lineages to produce new traits [19]. Multilevel societies have been

demonstrated to accelerate CCE when compared to fully connected networks [19]. However, when considering their potential for facilitating CCE, multilevel and fully-connected networks represent possible endpoints along a continuum of possible architectures. Here, we ask how a range of social network architectures can affect the tempo of CCE within a given population size and number, or density, of social connections within that population. Our approach allows us to explicitly disentangle the relative contribution of network architecture from those of connectivity and population size.

Results

We generated networks with six different architectures—random, small-world, lattice, modular, modular lattice, and multilevel—capturing different levels and combinations of clustering and modularity (**Fig. 1A**). We expressed these network architectures in populations with different sizes and densities of connections (average degree), where all individuals in the network had the same degree. We then used the agent-based model implemented by Migliano et al. [19] (hereafter model 1), inspired by the experiment of Derex & Boyd [12], to explore how network architecture affects time to cultural recombination (i.e. tempo) and the diversity of cultural traits. Briefly, this model allows innovations of cultural products to take place along two cultural lineages, with the knowledge of new products being spread to all social connections (one-to-many diffusion). Once a

high level of product diversity has been reached in both lineages, agents can recombine each lineage's products into one with a final higher payoff product (hereafter 'recombination').

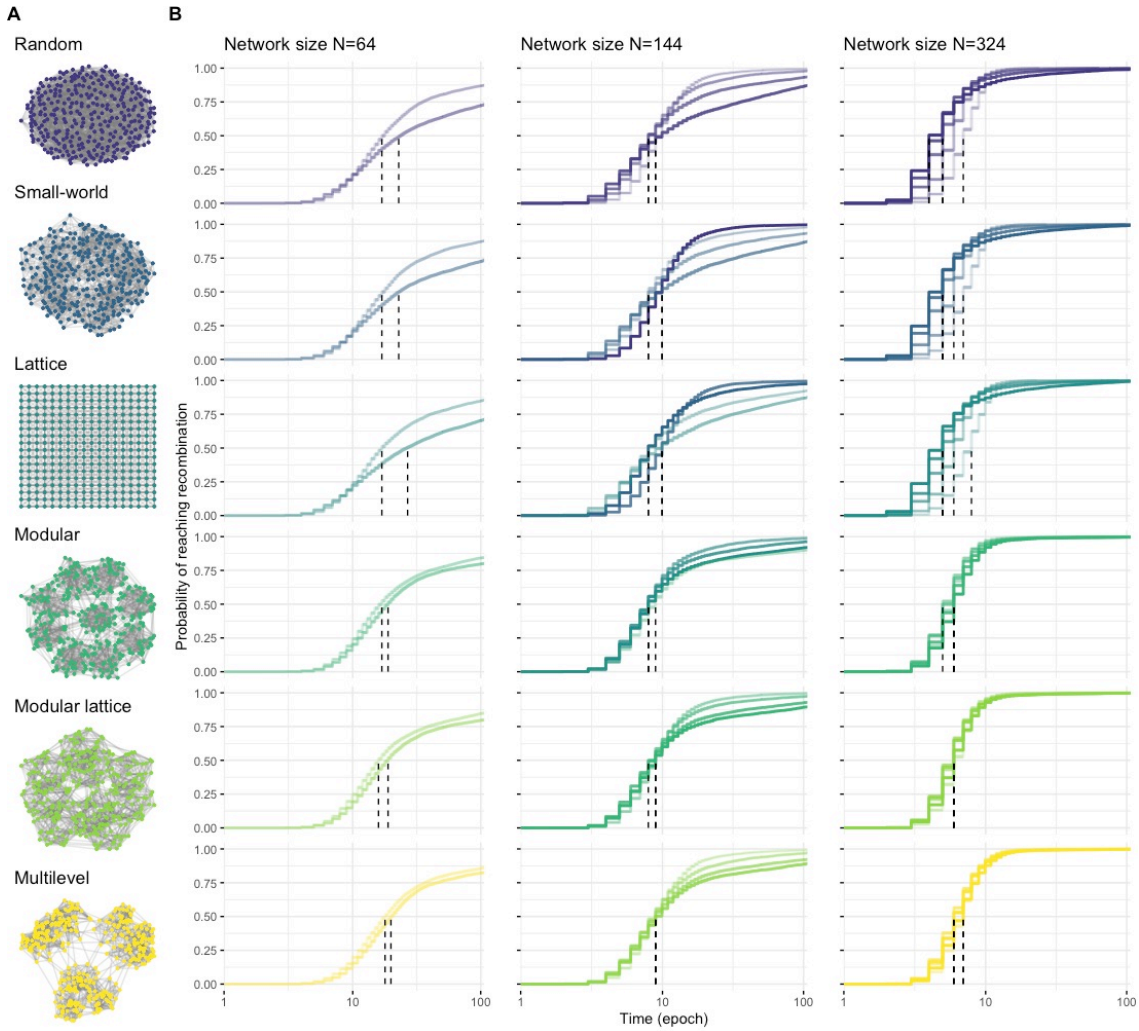

Figure 1. Social network architectures, and the time to recombination for each architecture across population sizes and levels of connectivity using model 1. (A) Network architectures vary in clustering and modularity: Random (unclustered C=0.03, non-modular Q=0.24), small-world (clustered C=0.52, medium-modular Q=0.63), lattice (clustered C=0.45, medium-modular Q=0.54), modular (unclustered C=0.23, modular Q=0.82), modular lattices (clustered C=0.41, modular Q=0.81), multilevel (clustered C=0.42, modular Q=0.83). Each binary network depicts populations with the same number of individuals (here, N=324 nodes) that have the same number of social connections (here, degree K=12 links per node; density D=0.037) but are wired differently. **(B)** Cumulative incidence of recombination events (y-axis) as a stepwise function over time (x-axis, log epochs) for small (N=64), medium (N=144), and large population sizes (N=324). The line shading represents the amount of network connectivity (node degree K, where the lighter the shade, the smaller the degree (K∈{8,12} for N=64; K∈{8,12,18,24} for N=144; K∈{8,12,18,24,30} for N=324). Vertical dashed lines indicate the median of time to

recombination (S(t)≤0.5) per network connectivity, across architectures. The time to reach recombination was truncated to 100 epochs for better visualization. Curves were calculated based on 5,000

Confirming the effects of population size and connectivity on CCE

When comparing time to recombination, we confirm that partially connected networks outperform fully connected networks [12,14,19] **(Fig. 2A)**. A generalized linear model indicated that overall fully connected networks were, on average, 65% slower (GLM, exp(β)=1.652, t=59.208, p<.001; **Table S1**) compared to the least structured network architecture of the same size (random, N=64 taken as the intercept), with similar decreases in performance independent of size. Further, we also confirm [7] that larger populations take less time (about 40% less) to reach recombination (GLM, exp(β)=0.618, t=-68.481, p<.001) compared to networks of the same architecture and connectivity (**Figs. 1B,2, Table S2**). Larger partially-connected network architectures were less variable in their time to recombination (Quartile Coefficient of Dispersion: *QCD*=0.688 for N=64; *QCD*=0.444 for N=144; *QCD*=0.273 for N=324, **Fig. 2A**). We also found that time to recombination was optimized at intermediate densities of connections, confirming that intermediate levels of connectivity can favour CCE [14], and revealing that the optimal level of connectivity varied with population size (**Fig. 1B**). In the smallest population (N=64), sparse networks outperformed the others, but this was reversed in the largest population (N=328) (**Fig. 1B**). However, differences in time to recombination were generally small (**Fig. 1B, 2A**).

simulations.

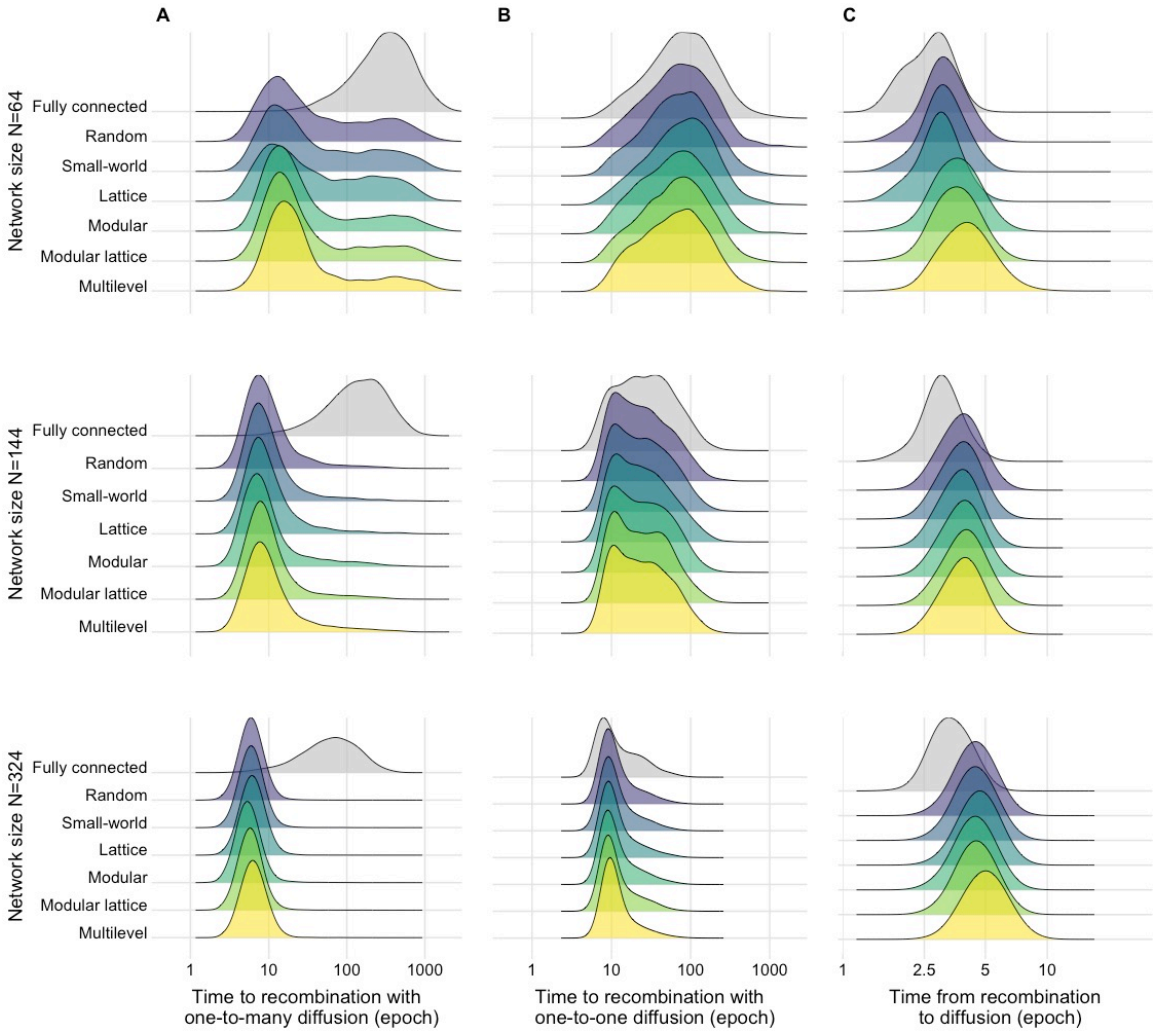

Figure 2. Time to recombination and time from recombination to diffusion across network architectures with varying sizes but a fixed degree. Comparison of the performance across the range of network architectures of the same degree (here K=12 link per node) and fully connected networks of the same size (N=64, N=144, and N=324 nodes, K=63, 143, and 323 respectively). **(A)** Time to recombination (log epochs) from 5,000 simulations with model 1 that uses a broadcast (one-to-many) diffusion dynamic. **(B)** Time to recombination (log epochs) from 5,000 simulations with model 2 that uses a dyadic (one-to-one) diffusion dynamic. **(C)** Difference between the time to recombination and the time to diffusion, where time to diffusion corresponds to the latency until the majority of the individuals in the population has information about the final higher-payoff product, from 5,000 simulations using model 2 (one-to-one diffusion). All ridges were plotted with the same bandwidth (0.18).

Architectures favouring CCE under some conditions disfavour CCE under other conditions

Under the one-to-many diffusion mechanism (model 1), multilevel, modular, and modular lattice architectures had relatively shorter times to recombination in smaller populations with greater connectivity and in larger populations with less connectivity (**Fig. 3A**). However, such network architectures performed worse than lattice, small world, and random architectures in smaller populations with less connectivity and in larger populations with greater connectivity (**Fig. 3A**). Multilevel, modular, and modular lattice architectures were optimal at lower and higher levels of connectivity in medium-sized populations (N=144, **Fig. 3A**), although connectivity generally had a lesser impact for these architectures relative to random, small-world, and lattice architectures (**Fig. 1B**). Surprisingly, multilevel performed the worst in seven out of the 11 size and connectivity combinations (**Fig. 3A**) despite having the highest clustering and modularity—properties that have been predicted to favour CCE [19]. The modular lattice architecture (which had similar modularity and clustering to multilevel architecture) performed best in the other four combinations (**Fig. 3A**). Thus, no one network architecture proved optimal, with those favoured under some conditions being disfavoured under other conditions.

The large variation in the time to recombination (**Fig. 2**) within a given combination of network architecture, population size, and density of connections suggests that the outcomes of a simulation were predominantly driven by stochastic events. The impact of such stochasticity is best revealed by the bimodal outcome for partially connected networks, which arises most often in smaller populations **(Fig. 2A)**. This bimodality occurs because there are fewer independent innovation events when there are fewer individuals, which increases the chance that cultural products all emerge from the same lineage and, therefore, that this single lineage spreads to the whole population before the other lineage is innovated. Tracking the diversity of products over time (**Figs. 4,S1**) highlights how the stochasticity in early events can affect cultural diversity, and therefore the outcomes of CCE, even within the same network architecture. Overall, measuring the tempo of CCE under one-to-many diffusion (model 1) revealed differences in the best performing architecture across population sizes and levels of connectivity (**Fig. 2A,3A**); however, these

between-architecture differences were small (range = 0.886-1.145; **Fig. 3A**), compared to the large variance in the time to recombination within architecture (**Fig. 2A**).

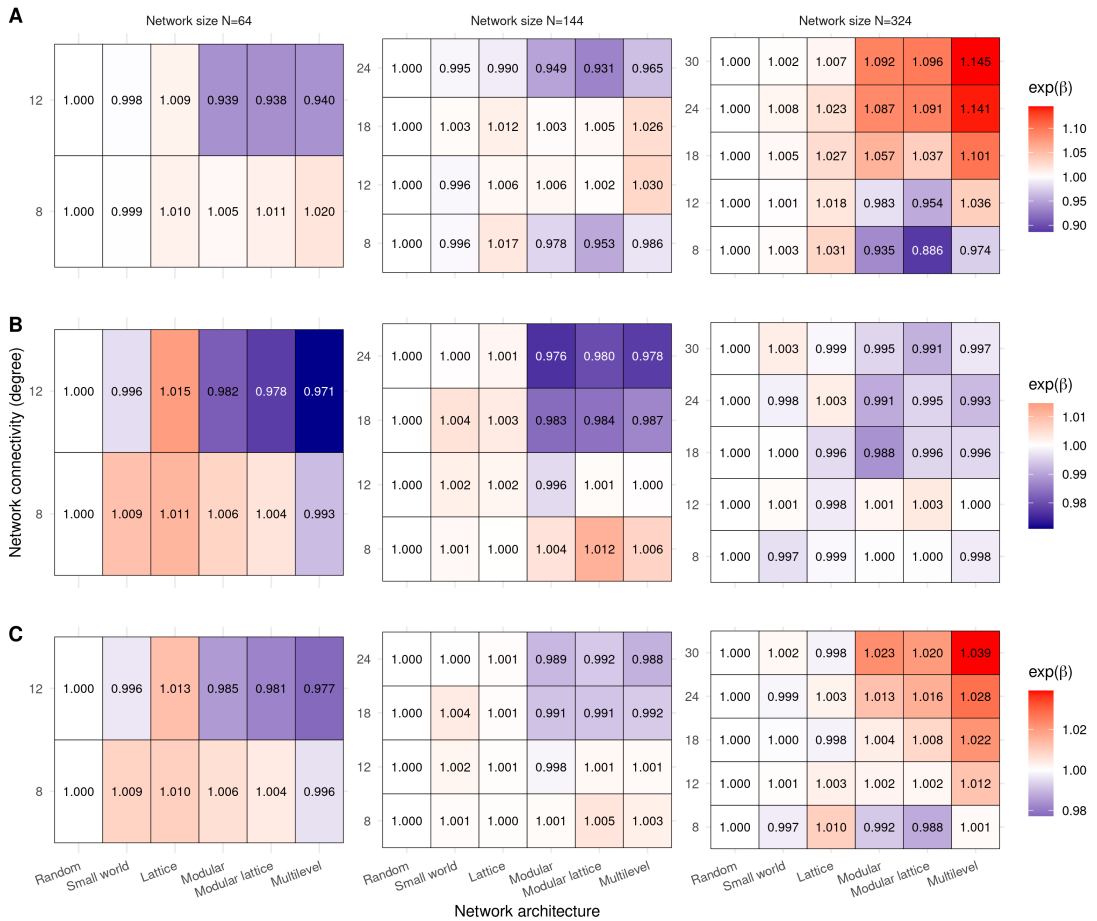

Figure 3. Relative performance of network architectures within each of the 11 combinations of population size and level of connectivity used in the simulations. Each row of each table reports the coefficient estimate of GLMs of network architecture (column) in function of the time to recombination while maintaining degree (row) and network size (box) constant. Red colours (higher coefficients) represent a poorer performance (longer latency to recombination) while blue colours represent architecture that perform better (shorter latency to recombination) for that combination of population size and level of connectivity (using random networks as the reference architecture in the GLM intercept). The relative performance of each architecture is shown for **(A)** time to recombination under a one-to-many diffusion mechanism (model 1), **(B)** time to recombination under a one-to-one diffusion mechanism (model 2), and **(C)** total time to diffusion (from simulation start until the majority of the population has information about the final higher-payoff product) under a one-to-one diffusion mechanism (model 2).

Diffusion mechanisms modify the contribution of network architecture, population size and connectivity on CCE

To identify the relative contribution of diffusion mechanisms to CCE, we extended model 1 by implementing a one-to-one diffusion mechanism (hereafter model 2). Whereas model 1 represents

an extreme scenario where information spreads instantaneously to all the contacts of a focal agent, model 2 tests another extreme in which information about discoveries spread only to a single contact at a time. Interestingly, when employing such one-to-one diffusion dynamics, fully connected networks were only estimated to be 3% slower to recombination compared to networks of the same population size (GLM, exp(β)=1.033, t=6.808, p<.001; **Table. S1**). Again, larger populations had a significantly shorter average time to recombination compared to smaller networks of the same architecture and degree (GLM, exp(β)=0.595, t=-109.094, p<.001; **Fig. 2B, Table. S2**). However, under one-to-one diffusion, the relative times to recombination of different architectures was generally more consistent than under one-to-many diffusion, both in their median times to recombination (**Fig. 2B**) and in their relative performance under a given population size and level of connectivity (**Fig. 3B**). Within a given population size, multilevel architecture typically had the shortest times to recombination when networks had greater connectivity, but there was almost no difference in performance among architectures when connectivity was low (**Fig. 3B**). Thus, in contrast to one-to-many, one-to-one diffusion increased the tempo for architectures with greater modularity and clustering (modular, modular lattice, multilevel) relative to the other architectures.

Model 2 also tracked the time for the recombination product to diffuse to the majority of the population, something which model 1 was not designed to track. The time from recombination to diffusion was shortest in fully connected networks, and increased with population size (**Fig. 2C**). When evaluating performance from the start of the simulations until the time to diffusion, population size was the main contributor to differences in outcomes (**Fig. S5**). In small populations, the contribution of the final diffusion was relatively small compared to the time to recombination, meaning that the best performing networks in achieving recombination also performed best overall (**Fig. 3C**). By contrast, in larger populations, the performance of modular and clustered network architectures (modular, modular lattice, and multilevel) all performed worse: they were the slowest at reaching final diffusion (**Fig. 3C**) despite typically reaching

recombination the fastest (**Fig. 3B**). These differences, however, remain minor relative to the variance in outcomes within each set of conditions (architecture, population size and connectivity).

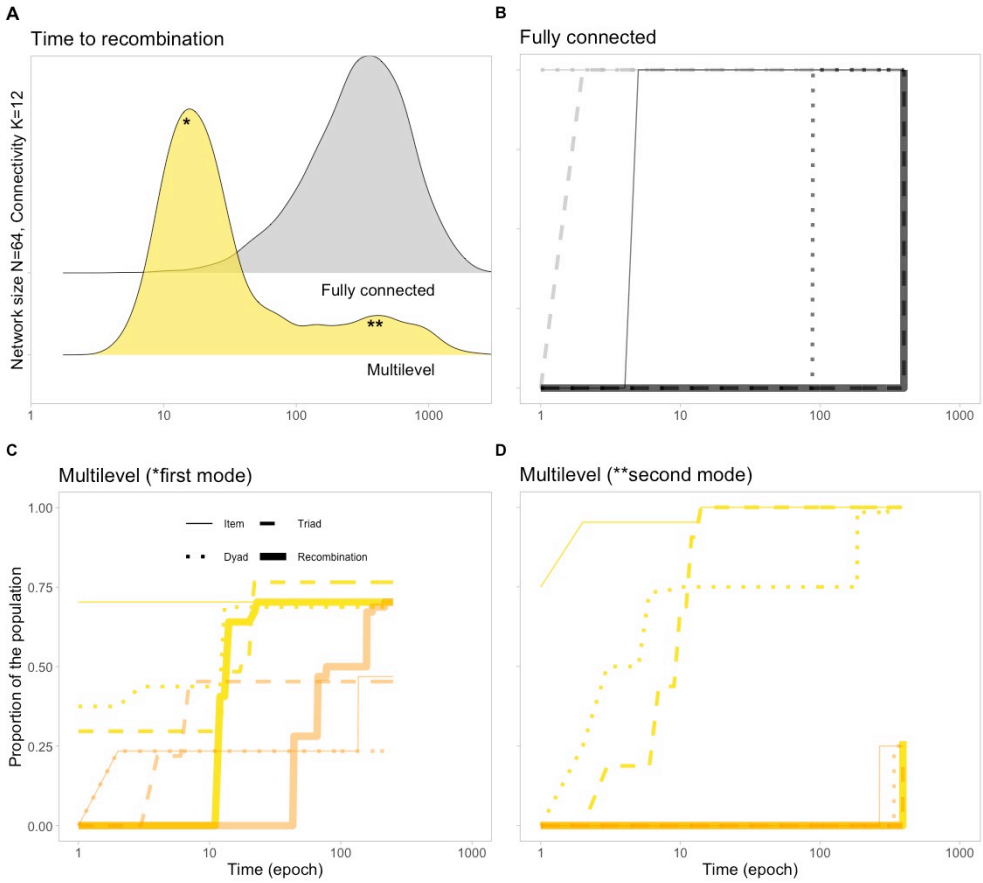

Figure 4. Cultural product diversity across time in a fully connected network and a highly structured social network architecture illustrates how early stochasticity shapes cultural outcomes. (A) Time to recombination (epochs) from 5,000 simulations with one-to-many diffusion dynamics (model 1) in multilevel and fully-connected networks (with N=64 and K=12). Following panels show cultural diversity over time from one simulation taken from the **(B)** from the mode of the fully-connected network, and the **(C)** first (*) and **(D)** second (**) modes of the distribution of results from the multilevel architecture. Cultural diversity represents the proportion of the population with one of the four possible products over time, from two independent lineages (light and dark shades): a single inventory item (1st stage; thin lines), a combination of two items (2nd stage; dotted lines), a valid combination triad of items (3rd stage; dashed lines), and the final higher payoff product, i.e. a triad recombining products from the two lineages (recombination; thick full lines).

Discussion

We revisit recent empirical and *in silico* experiments in humans to tease apart the contributions of different candidate social structures to the tempo of cumulative cultural evolution. Our results suggest that it is unlikely that one specific social network architecture consistently promotes CCE

across all population sizes, densities of social connections, or diffusion mechanisms. Rather, the relationship is nuanced; the broad distribution of outcomes from our two models indicate that the best performing architecture under some conditions can be the worst performing architecture under others. Further, the outcome of any diffusion mechanism is as likely to be affected by stochastic processes as by the architecture of the networks itself. While not at odds with previous work showing that multilevel societies can accelerate CCE [19], our results suggest that a range of other partially connected architectures could equally increase the tempo of CCE.

The fact that alternative architectures can have similar outcomes in terms of CCE has important consequences for how the social structure of societies and CCE are framed in future discussions, and where future research is directed. Current thinking is that complex, highly structured societies, such as multilevel societies, might precede recombinatory CCE in the timeline of human evolution, or that the benefits accrued from cultural evolution [22] or CCE [19] might co-evolve with clustered and modular network structures. However, our results suggest that simple patterns of spatial distribution (e.g. a lattice social network caused by distributed resources) could lead to largely equivalent effects on CCE. It follows that we might expect to find recombinatory CCE even before the evolution of complex societies. Indeed, evidence that simple, lattice-like social structures [24] can provide a substrate for recombinatorial culture might be provided by the combinatorial, spatially variable song structure of territorial passerine birds [25-29], which several authors have proposed to be a simple form of CCE [30,31].

Population size has been suggested as another major demographic factor affecting rates of CCE [3,7-9]. Our findings confirm this previous research, with our simulations showing that larger populations always have a higher rate of cultural accumulation. Population size also interacted with connectivity (which we modelled as a fixed network degree, i.e. the number of individuals' social connections [22]), with changes in connectivity having a more pronounced effect in smaller populations. This outcome is likely to arise because an increase in one unit of mean degree corresponds to a greater increase in network connectivity in smaller populations (more rapidly pushing the network towards becoming fully connected). However, in our simulations we did not vary the distribution in connectivity among individuals, which has previously been shown to

impact the properties of information cascades [32] and differences among groups in behaviours such as cooperation [33]. Skewed degree distributions, where some nodes are much more connected than others, could allow independent lineages to arise in peripheral nodes and for highly connected 'hubs' to combine the products from these lineages, thereby facilitating CCE. Thus, variation in how much or how little individuals are connected, independently of other factors (mean connectivity, population size, and network properties), is an important dimension for future studies on CCE to consider.

Fully connected networks have been commonly used to evaluate the performance of a transmission network with a given set of characteristics [3,19]. Our simulations demonstrate that the contribution of large differences in connectivity outweighs any effects pertaining to architecture, at least when information is broadcast (i.e. a one-to-many diffusion mechanism). Further, for most human societies, a fully-connected social network for a population of any reasonable size would correspond with an unrealistically high level of connectivity [34], even in the higher levels of the fractal-like human social networks [35]. Thus, we suggest that fully connected networks are uninformative null models for testing the influence of social structure on rates of CCE. Instead, random networks of similar sizes and densities of connections as a given network of interest would provide a more robust benchmark for comparing the performance of its architecture. Our results suggest, however, that any effect of network architecture on increased rate of CCE inferred from noisy field data would likely be indistinguishable from the null expectancy, as variation within architecture greatly exceeded that between architectures.

The evolutionary benefits of CCE not only rely on cultural accumulation, but also on the ability for new cultural traits to spread through populations. When we extended simulations to examine the time from recombination to the diffusion of the final higher payoff product, our results suggested that the network architecture hypothesized to improve time to recombination performance paradoxically inhibited diffusion most. These findings complement and extend the previous study by Derex et al. [12] demonstrating that populations with partially-connected network structures can suffer from cultural loss when connectivity becomes too low for new innovations to spread. Further, the relative performance of architectures can change dramatically when considering

performance in terms of acquisition of behaviour by the majority of nodes in a network, as opposed to the time when a single node has reached recombination, especially in larger populations. For example, while multilevel architecture consistently reached recombination faster than random networks under one-to-one diffusion, this architecture then restricted the final spread of higher-value cultural traits. Our results therefore suggest that multiple dimensions of performance—including every step from innovations to the final acquisition of higher-valued traits—may need to be considered when studying the role of social structure in shaping CCE and vice-versa.

Our work reinforces the need for studies of CCE to explicitly consider how network structure interacts with transmission mechanisms to form a realised transmission network. We show that a very restrictive transmission dynamics (one-to-one) mitigates the effect of network connectivity on CCE by generating a partially connected transmission network within an otherwise fully-connected social network. The consequences of transmission dynamics on CCE were demonstrated, for instance, by Migliano et al. [19] who found that CCE was faster in simulations where transmission was limited to kin-based connections (i.e. reduced connectivity). Under one-to-one diffusion, independent lineages can develop in fully-connected networks because new information is not immediately accessible to all, leading to more comparable performance between fully and partially connected networks. Thus, when simulating CCE, it is important to match the transmission dynamics with the time scale of the model. One-to-many diffusion can be realistic when each epoch represents one generation (e.g. the innovation of a new medicine [19] could take tens or hundreds of epochs to reach high recombinatory levels), while the one-to-one diffusion might be more realistic when cultural traits are simpler to recombine. The production and innovation frequency, as well as transmission biases, may further vary between species, populations, tasks and contexts. Together with network structure, innovation frequency and transmission biases may fundamentally alter the transmission dynamics—for example, conformity overrides pay-off biases [21,36] and homophily reduces social connectivity [18,37]—fuelling evolutionary feedbacks between network structure and cultural evolution [22]. Both factors will therefore alter the resulting transmission networks, potentially restricting spread of new cultural traits and slowing recombinatory CCE. More than highlighting the intricate, yet nuanced,

interplay between demography and cultural transmission, our work strengthens our emerging understanding that realised connectivity, rather than network architecture, is important for CCE [2,3].

Materials and Methods

Networks

We generated six architectures of binary social networks in which nodes represent individuals linked by social relationships: (i) small-world networks, using the Watts-Strogatz model [23] with node degree K links; (ii) random networks, by randomly connecting nodes ensuring all nodes had the same degree K; (iii) lattices, by placing nodes on a grid and connecting each to its K nearest neighbours; (iv) modular networks, by assigning nodes into nine modules, randomly connecting each to K-1 nodes from the same module and one node from another module; (v) modular lattices, as per modular networks, but where the connections within modules were lattices; and (vi) multilevel networks, as per modular lattices, but assigning nodes into three sets of three modules, and connecting each to K-2 nodes within their module, one node from each module from within its set and one node from a module outside of it. We generated networks with different sizes ($N \in \{64,144,324\}$ nodes), and densities of connections (in which $K \in \{8,12,18,24,30\}$ average links). We used these population sizes because they allowed us to partition the network into equally-sized clusters composed of equally-sized groups in which all individuals had the same degree, and in which connectivity was greater within groups and within clusters than between groups and between clusters.

Network metrics

Although all networks had comparable sizes and densities (i.e. the proportion links), the six architectures varied in levels and combinations of clustering coefficient and modularity. Clustering, C, informs the tendency of connected nodes to share the same connections with other

nodes, while modularity, Q, informs the tendency of the nodes to be organized into cohesive subsets that are more connected to each other than to the rest of the network [38].

Simulations

Our first agent-based model (model 1) followed Migliano et al. [19]. All agents were initialized with an inventory of three items from each of two lineages. In each simulation round (epoch), each focal agent was selected once, at random, and a partner randomly chosen from its social network connections. These agents combined one or two items from their inventory in proportion to their value into a triad of items. If this triad was a valid product, knowledge of that product was learned, spread immediately to all their network connections (one-to-many diffusion), and subsequently became available as an ingredient for making new products. Simulations finished once a recombination product (a triad that recombines specific products from both lineages) was first innovated. We ran 5,000 simulations for each of the network architecture types, sizes and densities of connections, recording time to achieve the recombination product (in epochs) and diversity of innovations in each epoch. An epoch was one simulation round in which each agent was selected once as a focal agent in random order.

Our second agent-based model (model 2) extended the first by changing the transmission mechanic and altering the set of valid combinations such that the model can run past the first innovation of either recombination product. Transmission of valid products now occurred between dyads of agents (one-to-one diffusion) prior to choosing items from their inventory, in contrast to the broadcast style of diffusion in model 1. Secondly, if a triad contained either recombination products, the final product was that recombination product. In the case where both recombination products were present in the triad, one was chosen as the final product at random. This allowed us to track the diffusion of recombination products beyond their innovation. We also ran 5,000 simulations for the same parameter space of model 1, recording time to recombination and time to diffusion to the majority of the network (in epochs). We implemented the agent-based models in R and Python. The code to generate the social networks, perform the simulations, the statistical analyses and the figures are available at [39]

Data analyses

To compare the performance of agents organized in different network architectures, we used time-to-event (survival) analyses [40] where time to recombination was a function of architecture and connectivity. For each population size, we used the Cumulative Incidence Function to estimate the proportion of simulations in which agents reached the recombination of each cultural lineage's products into a final high-payoff product. We used the non-parametric Kaplan-Meier product limit estimator to represent the time intervals based on observed recombination events from 5,000 simulations from model 1, calculating 95% confidence intervals with the Greenwood estimator. To measure variance in time to recombination across population sizes, we measured the quartile coefficient of dispersion (QCD=(Q3-Q1)/(Q3+Q1)), as this variable is not normally distributed and QCD offers a more robust measure.

While statistics are not typically performed on data from agent-based models since the posterior is directly sampled, we wanted to quantify the relative contributions of architecture, size and connectivity without the cumbersome descriptions of the entire distribution (which can be readily seen in **Fig. 2)**. For both models 1 and 2, we created three sets of generalized linear models (GLMs) that predicted logged time to recombination (in epochs). Time to recombination was logged to account for non-normality of residuals, and to make comparisons more fair by bringing the mean closer to the median of the distribution. All models used log link function, as the data was non-linear conditional on predictors, even after the log transformation. Also, the log link function allowed the presentation of exponentiated coefficients, which simplify the comparison to the reference (here, the random networks at the GLM intercept). The first set of GLMs used a full interaction structure to partition the relative contributions of architecture, size and connectivity to average time to recombination **(Table S1)**, excluding fully connected networks. To then compare fully connected networks to all other networks, we built a GLM using architecture and population size as predictors in a full interaction structure **(Table S2)**. Connectivity was excluded as a predictor, as all fully connected networks only have 1 possible degree ($K=N-1$). Finally, to compare differences between architectures in **Fig. 3** more precisely, we subset data by connectivity and

population size and performed a GLM with only architecture as a predictor for each subset, again excluding fully connected networks. We performed all data analyses in R [41], using 'survival' [42] and 'survminer' [43] packages.

Competing interests

The authors have no competing interests with this study

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Supporting Material for:

Social network architecture and the tempo of cumulative cultural evolution

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Table S1. Generalized linear models (GLMs) for agent-based model 1 (with one-to-many diffusion mechanism) and model 2 (one-to-one diffusion), in which time to recombination (time to recombination, measured as log(epoch+1)) is predicted by an interaction between population size and architecture. Coefficients and standard errors are exponentiated, as these GLMs used a log link function. Connectivity was not included, as this contains the same information as population size for fully connected networks. Intercepts represents random networks of population size N=64. (*p<0.1; **p<0.05; ***p<0.01)

	model1		model2	
	Estimate	p-value	Estimate	p-value
Constant	3.425***	-0.003	4.205***	-0.002
graphsmall_world	0.999***	-0.004	1.003***	-0.002
graphlattice	1.010***	-0.004	1.013***	-0.002
graphmodular	0.970***	-0.004	0.994***	-0.002
graphmodular_lattice	0.972***	-0.004	0.991***	-0.002
graphmultilevel	0.977***	-0.004	0.982***	-0.002
graphfull	1.652***	-0.003	1.033***	-0.003
pop_size144	0.715***	-0.004	0.759***	-0.002
pop_size324	0.512***	-0.004	0.587***	-0.003
graphsmall_world:pop_size144	0.999***	-0.005	0.999***	-0.003
graphlattice:pop_size144	0.996***	-0.005	0.989***	-0.003
graphmodular:pop_size144	1.013***	-0.005	0.996***	-0.003
graphmodular_lattice:pop_size144	0.999***	-0.005	1.003***	-0.003
graphmultilevel:pop_size144	1.024***	-0.005	1.011***	-0.003
graphfull:pop_size144	1.206***	-0.005	0.994***	-0.005
graphsmall_world:pop_size324	1.005***	-0.006	0.997***	-0.004
graphlattice:pop_size324	1.012***	-0.006	0.986***	-0.004
graphmodular:pop_size324	1.059***	-0.006	1.001***	-0.004
graphmodular_lattice:pop_size324	1.036***	-0.006	1.006***	-0.004
graphmultilevel:pop_size324	1.100***	-0.006	1.015***	-0.004
graphfull:pop_size324	1.406***	-0.006	0.980***	-0.005
Observations	345,000		345,000	
Log Likelihood	-446,718.40		-378,097.40	
Akaike Information Criterion	893,478.70		756,236.80	

Table S2. Generalized linear models (GLMs) for agent-based model 1 (with one-to-many diffusion mechanism) and model 2 (one-to-one diffusion), in which time to recombination (time to recombination, measured as log(epoch+1)) is predicted by an interaction between population size, network architecture, and connectivity (i.e. average network degree). Coefficients and standard errors are exponentiated, as these GLMs used a log link function. Full networks were excluded. Intercepts represent random networks of population size *N*=64, average degree of *K*=8. (*p<0.1; **p<0.05; ***p<0.01)

	model1		model2	
	Estimate	p-value	Estimate	p-value
Constant	3.196***	-0.004	4.168***	-0.002
graphsmall_world	0.999***	-0.005	1.009***	-0.003
graphlattice	1.010***	-0.005	1.011***	-0.003
graphmodular	1.005***	-0.005	1.006***	-0.003
graphmodular_lattice	1.011***	-0.005	1.004***	-0.003
graphmultilevel	1.020***	-0.005	0.993***	-0.003
pop_size144	0.724***	-0.007	0.756***	-0.004
pop_size324	0.618***	-0.007	0.595***	-0.005
degree12	1.143***	-0.005	1.018***	-0.003
degree18	0.847***	-0.01	0.996***	-0.006
degree24	0.831***	-0.01	0.995***	-0.006
degree30	0.856***	-0.01	0.992***	-0.006
graphsmall_world:pop_size144	0.997***	-0.009	0.992***	-0.006
graphlattice:pop_size144	1.007***	-0.009	0.989***	-0.006
graphmodular:pop_size144	0.973***	-0.009	0.998***	-0.006
graphmodular_lattice:pop_size144	0.942***	-0.009	1.008***	-0.006
graphmultilevel:pop_size144	0.967***	-0.009	1.014***	-0.006
graphsmall_world:pop_size324	1.004***	-0.01	0.987***	-0.007
graphlattice:pop_size324	1.021***	-0.01	0.988***	-0.007
graphmodular:pop_size324	0.930***	-0.011	0.993***	-0.007
graphmodular_lattice:pop_size324	0.876***	-0.011	0.996***	-0.007
graphmultilevel:pop_size324	0.955***	-0.01	1.005***	-0.007
graphsmall_world:degree12	0.999***	-0.007	0.987***	-0.005
graphlattice:degree12	1.000***	-0.007	1.004***	-0.005
graphmodular:degree12	0.934***	-0.007	0.976***	-0.005
graphmodular_lattice:degree12	0.928***	-0.007	0.974***	-0.005
graphmultilevel:degree12	0.922***	-0.007	0.978***	-0.005
graphsmall_world:degree18	1.002***	-0.014	1.003***	-0.008
graphlattice:degree18	0.996***	-0.013	0.997***	-0.008
graphmodular:degree18	1.131***	-0.014	0.988***	-0.008
graphmodular_lattice:degree18	1.170***	-0.014	0.996***	-0.008
graphmultilevel:degree18	1.130***	-0.013	0.998***	-0.008
graphsmall_world:degree24	1.005***	-0.014	1.002***	-0.008
graphlattice:degree24	0.992***	-0.014	1.003***	-0.008
graphmodular:degree24	1.163***	-0.014	0.991***	-0.008
graphmodular_lattice:degree24	1.231***	-0.014	0.996***	-0.008
graphmultilevel:degree24	1.172***	-0.013	0.995***	-0.008
graphsmall_world:degree30	0.999***	-0.014	1.006***	-0.008
graphlattice:degree30	0.977***	-0.013	1.000***	-0.008
graphmodular:degree30	1.168***	-0.013	0.996***	-0.008
graphmodular_lattice:degree30	1.237***	-0.014	0.992***	-0.008
graphmultilevel:degree30	1.175***	-0.013	0.999***	-0.008
pop_size144:degree12	0.864***	-0.009	0.992***	-0.006
pop_size324:degree12	0.796***	-0.011	0.975***	-0.007
pop_size144:degree18	1.251***	-0.012	1.023***	-0.007
pop_size144:degree24	1.426***	-0.012	1.030***	-0.007
graphsmall_world:pop_size144:degree12	1.000***	-0.013	1.014***	-0.008
graphlattice:pop_size144:degree12	0.989***	-0.013	0.998***	-0.008
graphmodular:pop_size144:degree12	1.101***	-0.013	1.017***	-0.008
graphmodular_lattice:pop_size144:degree12	1.134***	-0.013	1.016***	-0.008
graphmultilevel:pop_size144:degree12	1.133***	-0.013	1.016***	-0.008
graphsmall_world:pop_size324:degree12	0.999***	-0.015	1.017***	-0.01
graphlattice:pop_size324:degree12	0.989***	-0.015	0.995***	-0.01
graphmodular:pop_size324:degree12	1.125***	-0.015	1.027***	-0.01
graphmodular_lattice:pop_size324:degree12	1.160***	-0.016	1.030***	-0.01
graphmultilevel:pop_size324:degree12	1.154***	-0.015	1.024***	-0.01
graphsmall_world:pop_size144:degree18	1.005***	-0.017	1.000***	-0.01

graphlattice:pop_size144:degree18	0.999***	-0.017	1.006***	-0.01
graphmodular:pop_size144:degree18	0.907***	-0.017	0.991***	-0.01
graphmodular_lattice:pop_size144:degree18	0.902***	-0.017	0.977***	-0.01
graphmultilevel:pop_size144:degree18	0.921***	-0.017	0.982***	-0.01
graphsmall_world:pop_size144:degree24	0.994***	-0.017	0.997***	-0.01
graphlattice:pop_size144:degree24	0.981***	-0.017	0.998***	-0.01
graphmodular:pop_size144:degree24	0.835***	-0.017	0.981***	-0.01
graphmodular_lattice:pop_size144:degree24	0.794***	-0.017	0.973***	-0.01
graphmultilevel:pop_size144:degree24	0.836***	-0.017	0.977***	-0.01
Observations	330,000		330,000	
Log Likelihood	-423,477.80		-359,565.20	
Akaike Information Criterion	847,087.60		719,262.30	

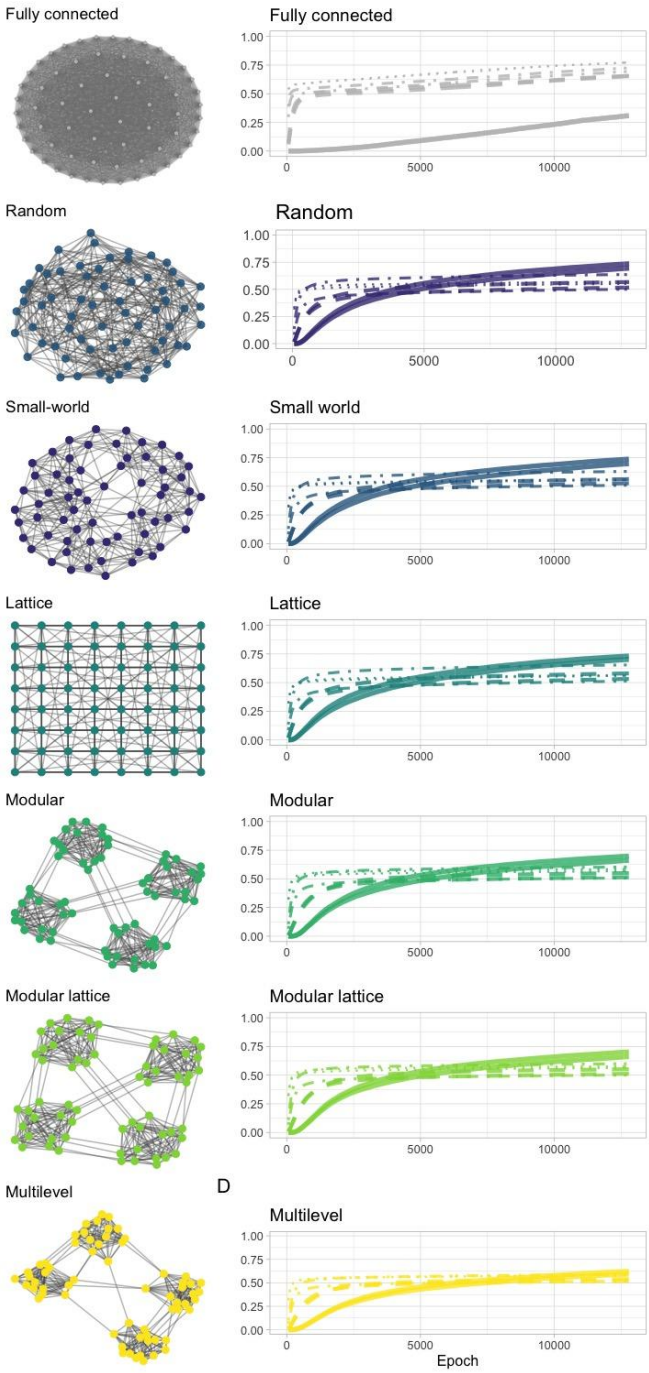

Figure S1. Cultural trait diversity across social network architectures and proposed null models. Comparison of the diversity of cultural traits along the network architecture spectrum, across populations of same size (N=64 nodes) and connectivity (average degree K=12 links) in relative to a fully connected network of the same size (N=64, K=63). Cultural innovation diversity across network architectures measured as the proportion of the population with one of the four possible traits over time: a single inventory item (dotted lines), a single combination of two items (dashed and dotted lines), a valid combination of three items (triad; dashed lines), and a recombination product (a triad that recombines specific products from both lineages; thick lines). The inventory items came from two independent lineages, represented by lines of the same type.