Proximity and genetic networks shape the evolution of cumulative culture

Keywords: Multiplex networks, Social learning, Cultural Diffusion, Social behaviour, Cumulative culture

Extended Abstract

Culture, defined as behavioural traditions transmitted through social learning, has been documented across animal species. Human culture, however, is uniquely complex, diverse, and cumulative, as individuals build on prior innovations through recombination of knowledge [1, 2]. While cumulative culture was long considered specific to humans [3, 4], recent field studies suggest that chimpanzees, our closest living relatives, display precursors through complex tool use [5, 6]. Here, we examine the role of genetic connectivity and proximity in the emergence and spread of cumulative culture among chimpanzee populations.

Chimpanzees exhibit diverse foraging behaviours, from simple tools like using leaves to drink water, to multipart toolsets such as nut-cracking. We classified 15 observed behaviours into three categories: three nontool behaviours, nine simple tools, and three complex toolsets. Non-tool and simple tools are geographically widespread, whereas complex toolsets are more localized. To test whether this distribution reflects independent reinvention or cultural transmission across populations, we compared tool-use data with genetic connectivity spanning sub-Saharan chimpanzee populations.

We applied Bayesian logistic regressions to predict dyadic sharing of behaviours from genetic links while controlling for habitat and rainfall. Genetic connection increased the odds of sharing complex toolsets by a factor of 2.60 [95% CI: 1.21–5.48], and simple tools by 1.39 [95% CI: 0.97–1.97]. This suggests that complex tools are more likely transmitted across groups, while simple tools often arise independently.

To further quantify this relationship, we compared the structure of networks of genetic connectivity and behavioural sharing using reinforcement analysis [7]. In this method, the conditional probability of a link in one layer is estimated given its presence in another. A shared complex toolset predicted a shared genetic segment with probability $> 50\%$, whereas shared genetic markers predicted only a small fraction of cultural links (Fig. 1A–D).

We statistically validated these results by comparing real networks with 1000 randomizations of each toolset network (Fig. 1E-F). Ratios of reinforcement probabilities showed a significant deviation from chance: genetic links were nearly three times more likely to be predicted by real complex toolset links than by randomized ones (pseudomedian ratio = 2.96). By contrast, nontool (0.826) and simple tool (1.39) networks showed weaker effects (Fig. 1G-H). These findings are robust under alternative network backboning techniques.

Taken together, our results indicate that the observed distribution of chimpanzee complex toolsets reflects cultural transmission over generations, facilitated by migration and genetic connectivity. By contrast, simple tools appear less spatially patterned and likely re-emerge independently across populations. The strong link between shared genetics and shared complex cultural traits provides one of the first quantitative demonstrations of cumulative culture in non-human animals.

Understanding this interplay between genetic and cultural transmission in chimpanzees offers insights into the evolutionary roots of human cultural complexity. While chimpanzees appear to display early stages of cumulative culture, humans developed a far more expansive repertoire, possibly due to larger-scale connectivity and more sophisticated mechanisms of cultural recombination.

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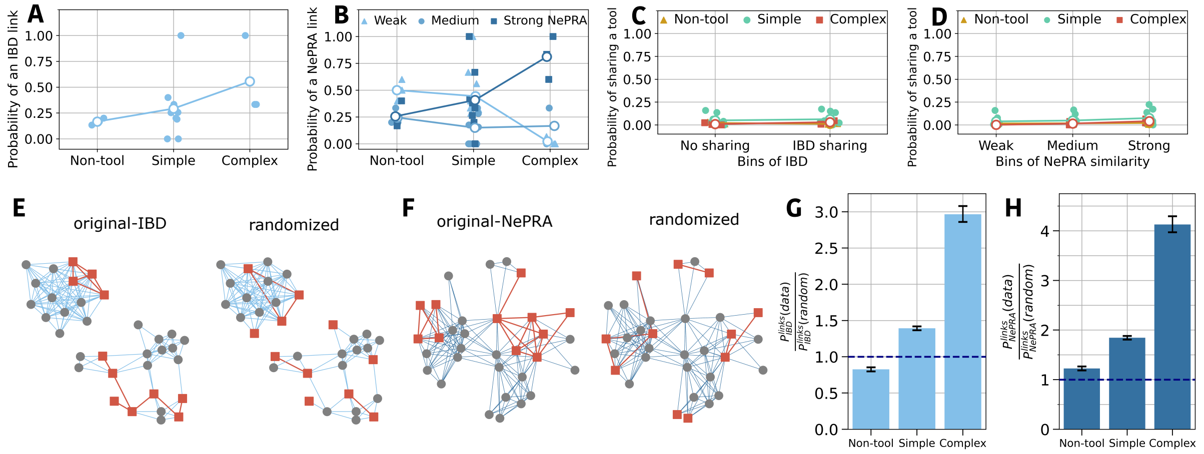

Figure 1: **Reinforcement analyses of genetic and cultural sharing networks.** (**A-B**) Probability of genetic link as a function of corresponding tool sharing link increases with complexity of tools. (**C-D**) The inverse probability of sharing a tool is unchanged with the presence and absence of genetic link. (**E-F**) Snapshots of original and randomized tool behaviour on genetic links. (**G-H**) Ratio of probabilities for original and randomized tool behaviour showing statistically significant deviation from 1 for complex tools.