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Author	Family Name	Madsen
	Particle	
	Given Name	Mark E.
	Suffix	
	Email	mark@madsenlab.org
Author	Family Name	Lipo
	Particle	
	Given Name	Carl P.
	Suffix	
	Email	Carl.Lipo@csulb.edu
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Behavioral Modernity and the Cultural
Transmission of Structured Information: The
Semantic Axelrod Model

Mark E. Madsen and Carl P. Lipo

Abstract

Cultural transmission models are coming to the fore in explaining increases in the Paleolithic toolkit richness and diversity. During the later Paleolithic, technologies increase not only in terms of diversity but also in their complexity and interdependence. As Mesoudi and O'Brien (Biolog Theory 3:63–72, 2008) have shown, selection broadly favors social learning of information that is hierarchical and structured. We believe that teaching provides the necessary scaffolding for transmission of more complex cultural traits. Here, we introduce an extension of the Axelrod (J Confl Resolut 41:203–226, 1997) model of cultural differentiation in which traits have prerequisite relationships, and where social learning is dependent upon the ordering of those prerequisites. We examine the resulting structure of cultural repertoires as learning environments range from largely unstructured imitation, to structured teaching of necessary prerequisites, and we find that in combination with individual learning and innovation, high probabilities of teaching prerequisites leads to richer cultural repertoires. Our results point to ways in which we can build more comprehensive explanations of the archaeological record of the Paleolithic as well as other cases of technological change.

Keywords

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6.1 Introduction

Although humans and our hominin ancestors have been cultural animals throughout our evolutionary history, an important change occurred in our lineage during the Middle and Upper Paleolithic. For millennia our ancestors manufactured

relatively small toolkits and their material culture was remarkably similar across continental distances and over many generations. Beginning in the Middle Paleolithic and continuing through the Upper Paleolithic, the archaeological record reflects an explosion in our cultural repertoire. Over tens of thousands of years, artifactual toolkits shift from sets of relatively few objects with multiple uses to large collections of functionally-specialized tools that, employed increasingly complex technologies and that were manufactured from an enriched range of materials. The changes in artifacts suggest that human solutions to the problems of everyday life became regionalized and differentiated. Further, the economic basis of our lives began to broaden and also, in many areas, to become specialized (Bar-Yosef 2002; d'Errico and Stringer 2011; Straus 2005).

M.E. Madsen (✉)
Department of Anthropology, University of Washington, Box 353100,
Seattle, WA 98195, USA
e-mail: mark@madsenlab.org

C.P. Lipo
Department of Anthropology and IIRMES, California State University
at Long Beach, 1250 Bellflower Blvd, Long Beach, CA 90840, USA
e-mail: Carl.Lipo@csulb.edu

While early researchers believed that the Upper Paleolithic resulted from a singular “revolution” in human evolution leading to behaviorally modern homo sapiens, this view is held by a minority of paleoanthropologists and archaeologists today (e.g., Klein 2009). Careful examination of the Middle Paleolithic archaeological record especially in Africa and the Near East suggests that this change in behavior did not occur as a single distinct event, instead occurring over a long period of time since much of the enriched material culture we later characterize as the “Upper Paleolithic” had precursors. In addition, this change now appears to be patchy and fitful, with modern features appearing and frequently being lost again (Bouzouggar et al. 2007; d’Errico and Henshilwood 2007; d’Errico and Stringer 2011; Straus 2005; McBrearty and Brooks 2000; McBrearty 2007). Nor does behavioral modernity map neatly to biological taxa and their movements, given that evidence for the precursors of fully modern behavior is abundant in deposits associated with Neanderthals in addition to modern *Homo sapiens* (Villa and Roebroeks 2014).

The “learning hypothesis” studied in this series of volumes makes the plausible claim that behavioral modernity is the product of cumulative changes in the way cultural information was acquired and retained across generations (Nishiaki et al. 2013), thus providing a potential explanation for the slow evolution of “modern” features, its patchiness in space and time, and the lack of a neat mapping between hominin taxonomy and material culture. In short, according to the learning hypothesis, behavioral modernity arose through a change or changes in the way social learning operated within hominin groups, with those groups adopting richer modes of cultural learning surviving and spreading compared to those who retained simpler forms of social learning.

Within the umbrella of the learning hypothesis, there are many ways in which social learning and thus intergenerational cultural transmission could have changed, and an increasing amount of research is focused upon formulating and testing different models. One class of studies is focused upon factors exogenous to the learning or imitation process itself. Shennan (2000, 2001) proposed that population size has a powerful effect on diversity within cultural transmission processes, which Henrich showed in the case of toolkit element loss during a Tasmanian population bottleneck (Henrich 2004). In a similar line of reasoning, Kuhn (2013) argues that low population size and density put Neanderthals in a situation where innovations spread slowly and ultimately led to their demise relative to modern humans. Furthermore, a growing set of experimental studies clearly show a relationship between accumulation of complex cultural traits and the number of cultural “models” from whom individuals can learn (Muthukrishna et al. 2014; Derex et al. 2013; Kempe and Mesoudi 2014). Not all studies have shown a strong

association between population size and cultural diversity, however. Collard and colleagues, find little association in a linked series of comparative studies (Collard et al. 2011, 2013a,b,c). Finally, in his analysis of the overall evolutionary rate, Aoki (2013) found that innovation rates were more important than population size to determining the rate of evolution in a population.

To us, this body of work indicates that while population size is an important parameter in mathematical models, it may be better understood as a second-order effect in the real world, interacting with a myriad of other factors and thus often dominated by those factors. Another important factor is the structure of bands or demes into larger regional metapopulations. Network topology, for example, is known to have a substantial effect upon contagion or diffusion processes (e.g., Castellano et al. 2009; Smilov and Kocarev 2012). Thus, it is likely that regional structure has critical effects on the outcomes we can expect from a single social “learning rule.” Along these lines, Premo (2012) has examined whether metapopulation dynamics that include local extinction and recolonization might provide an improved account for the retention and expansion of diversity.

A second group of studies has focused upon endogenous changes to social learning processes. Many authors in this volume series, for example, have looked at aspects of the way individuals learn skills and acquire information (Aoki 2013; Nishiaki et al. 2013). We know that learning and teaching styles vary across human groups, and formal modeling efforts are beginning to make clear that such variation has evolutionary consequences that might lead to a rapid expansion of the human cultural repertoire (Nakahashi 2013). Those populations which increased the amount or effectiveness of teaching would have a fitness advantage over those who relied upon imitation and “natural pedagogy” in passing along technological and foraging knowledge (Csibra and Gergely 2011; Fogarty et al. 2011; Terashima 2013). Demography and population structure would then play an important role in reinforcing the fitness differences which different learning strategies would create, as pointed out by Kuhn (2013).

Ultimately, a full “learning explanation” for behavioral modernity will be multifaceted, including demographic and spatial changes as well as changes to the mechanisms of social learning and technological innovation themselves. Sterelny (2012, p. 61) sums up this kind of multifactorial approach to behavioral modernity well:

...the cultural learning characteristic of the Upper Paleolithic transition and later periods of human culture—social transmission with both a large bandwidth and sufficient accuracy for incremental improvement—requires individual cognitive adaptations for cultural learning, highly structured learning environments, and population structures that both buffer existing resources effectively and support enough specialization to generate a supply of innovation.

In research designed to explore how the structure of a learning environment affects the results of social learning, Creanza and colleagues (2013), Aoki (2013), Nakahashi (2013), and Castro and colleagues (2014) developed models that examine how explicit teaching (as opposed to simple imitation) affects the overall evolutionary rate or cultural diversity in a population. Castro et al. for example, find that cumulative cultural transmission requires active teaching in order to achieve fidelity across generations. Our work in this chapter follows these authors, focusing on the nature of transmitted information itself and the effects of teaching upon the richness of structured technological knowledge.

In particular, we suggest that when knowledge is structured such that skills and information must be learned in sequences, high fidelity learning environments are critical to evolving ever-richer cultural repertoires, of the type seen in behaviorally modern assemblages. To formalize this idea, we construct a model which:

- Represents cultural traits as hierarchically structured, in order to study increases in complexity,
- Has a learning rule sensitive to the order in which cultural traits are acquired, with multiple levels of fidelity, and
- Has a mechanism (such as homophily) that allows cultural differentiation endogenous to the model.

As we alter the “learning environment” in our models from less to more frequent teaching of traits and their prerequisites, we expect to see greater diversity, larger structured sets of traits persisting in the population, and greater differentiation of the population into “different” cultural configurations. We also expect that individual innovation, independent of the social learning context, will play a role in the accumulation of cultural complexity by allowing a population to explore increasingly large spaces of technological design possibilities; this expectation is concordant with Aoki’s (2013) result in Volume I of this series.

In this chapter, we introduce a simulation model which combines a hierarchical trait space capable of expressing dependencies or semantic relationships between skills and information (Mesoudi and O’Brien 2008), and a modified version of Robert Axelrod’s (1997) homophilic social learning model which allows us to examine the conditions under which evolution in a hierarchical design space leads to cultural differentiation. After describing the model, we study its dynamics and provide an initial assessment of its suitability for studying the onset of behavioral modernity in the later Paleolithic. Models like this begin to move beyond diffusion dynamics, bringing the actual meaning and relations of traits into the modeling process. Hence, we call these “semantic Axelrod” models, and believe that such models form a platform for formalizing the type of multi-factor hypotheses necessary to examine major transitions in human evolution, such as “behavioral modernity.”

6.2 The Semantic Axelrod Model for Trait Prerequisites

Much of our technical knowledge, whether of stone tool manufacture, throwing clay pots, or computer repair, is built from simple tasks, bits of background knowledge, and step-by-step procedures (Neff 1992; Schiffer and Skibo 1987). These pieces of cultural information are not simply a set of alternative options, which can be mixed and matched in any combination. Instead, there are dependencies and relationships between items which affect how skills and information are learned and passed on between individuals. Some items will be related in time, as steps in a process. Others will be related by subsumption: arrowheads are a subclass of bifacial stone tools, and require many of the same production techniques as bifaces used in other projectiles. Still others will be related as sets of alternatives: choices of surface treatment for a given ceramic paste, given the firing regime selected, for example. To date, most archaeological models of tool production have focused upon temporal relations in the construction of an artifact, as in “sequence models” or “chaîneopératoire,” but it is important to remember that other representations are possible, including trees and more general graphs to capture relations of use, reworking, or discard (Bamforth and Finlay 2008; Ferguson 2008; Högberg 2008; Bleed 2001, 2002, 2008; Schiffer and Skibo 1987; Stout 2002).

Given conscious reflection, we describe and organize our knowledge and skills in many ways, but it is common (especially while learning a new skill) to think of a complex process as a “script” or “recipe” (Schank and Abelson 1977). Experts in a task or field may not represent their knowledge this way, having internalized such structures below the conscious level. Experts will often know more than one way to accomplish any given goal, and be able to repurpose and recombine methods and tools, as opposed to the simpler, more linear or tree-based recipes of the novice or student (e.g., Bleed 2002, 2008; Stout 2002). Nevertheless, it is common to teach or learn new information and skills in a stepwise manner.

In this chapter, we focus not on the execution steps of a recipe (and thus not on sequence models), but the relations between skills and information *during the learning process*. In specific, we focus upon the *prerequisite* relationships that exist between cultural traits, since the ordered dependencies between skills and information form one of the structures within social learning occurs during development (and into adulthood). Some pieces of information or skills must be in place before a person can effectively learn or practice others. Examples from our own childhoods abound: one needed to understand addition and subtraction and multiplication

before learning long division; in order to make soup, we need to understand how to simmer rather than boil, how to chop and slice, what ingredients might be combined, and so on. The fact that knowledge and skills build upon one another make prerequisite relations between cultural traits ubiquitous. In this chapter, we represent prerequisite relations as trees in the graph-theoretic sense (Diestel 2010), replacing the “nominal scale” structure of “locus/allele” models or paradigmatic classifications and some typologies (Dunnell 1971), but we emphasize that the tree models we discuss here are still classifications and thus analytic tools, designed to allow us to measure variation in the archaeological record, not reconstruct emic models of Paleolithic technologies.

Our model also requires a way of representing a changing learning environment, in ways that create higher fidelity and greater possibility for building cumulative knowledge. In real learning environments, there are many possibilities, but deliberate teaching and apprentice learning are repeatedly seen across human groups as ways that naive individuals can reliably learn the complex skills and information needed for foraging, artifact production and maintenance, and navigating an increasingly rich social world. The point of structuring the learning environment with teaching and/or apprenticeship is to give the learner skilled models to imitate, shortcut trial and error when acquiring a skill, provide a reference for needed information, and to guide individuals to put their information and skills together into appropriate sequences to accomplish an overall goal. Apprenticeship and formalized teaching provide a social learning “scaffold,” helping to lower the amount of individual trial and error learning needed to master a body of material (Wimsatt and Griesemer 2007; Wimsatt 2007).

Within a standard discrete-time simulation model of a social learning process, we can model this type of learning environment with the following modifications:

1. Represent the order in which skills and information need to be acquired as a series of trees, with vertices representing traits (either a skill or piece of information), and edges the prerequisite relations between them.
2. Disallowing individuals the ability to copy traits from a cultural model for which they do not have necessary background or prerequisites, given the relations in the applicable tree model.
3. Creating a probability that individuals, if disallowed a trait, can be taught one of the needed prerequisites instead by that cultural model, leading to the potential accumulation of fuller knowledge and skills over time.

By changing the probability that individuals learn a missing prerequisite trait, we can “tune” the learning environment. Low probabilities might correspond, for example, to a learning environment where individuals can observe others executing a production step, but are given little or no instruction or guidance on what they need to know in order to

successfully master it. High probabilities of learning prerequisites would correspond, on the other hand, to environments where individuals receive instruction, or work together with a more skilled individual who guides them toward learning the information and skills they lack. In the next section, we discuss our model of trait relationships and the learning environment in more detail.

6.2.1 Representation of Traits and Their Prerequisites

In order to represent the “prerequisite” relations between a number of cultural traits, we organize the traits into trees,¹ where nodes higher in the tree represent knowledge, skills, or concepts which are necessary for traits further down the tree. Let us consider the different skills and information necessary for the construction of a single artifact, say a dart thrown by an atlatl. An artisan will possess information about different raw materials, an understanding of what materials are suitable for specific purposes, skills and information concerning the knapping of different types of bifaces, methods of hafting bifaces into different kinds of shafts, and so on. Stout (2011) organized such knowledge into “action hierarchies,” which represent sequences of actions, sets of choices, and optional elements for the construction of a class of stone tools, drawing the representation from Moore’s (2010) graphical notation.

We should emphasize that employing tree structures to represent learning dependencies is a modeling choice. Other choices may be sensible as well. General graphs could represent webs of relations between concepts or skills, and multigraphs (replacing adjacency matrices with tensors) can represent different types of relations in a single structure (Nickel et al. 2011). For purposes of the present chapter, we are interested in the order in which people usually *learn* skills and information, rather than the order in which steps are executed. The difference is potentially significant, in that two adjacent steps in a sequence might involve very different information, tools, or skills, which can be learned in parallel without dependencies. Because, in our model, traits cannot be learned unless an individual possesses the necessary prerequisites, we introduce the idea of a “learning hierarchy,” which is a division of Stout’s action hierarchy into components which are learned with ordered dependencies, and independent components represented in separate trees. For example, one might learn about the sources of good

¹A tree is a graph with no cycles or loops. That is, a tree is a connected graph on n vertices that possesses at most $n - 1$ edges (Diestel 2010). Furthermore, in this chapter we are concerned with *rooted* trees, in which one vertex is distinguished as the “origin” of the tree, giving rise to a hierarchical structure.

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Fig. 6.1 A design space composed of 4 independent trees, each tree with branching factor 3 and depth factor 3, order 40. We also studied larger design spaces with 16 independent trees, and with larger branching and depth factors

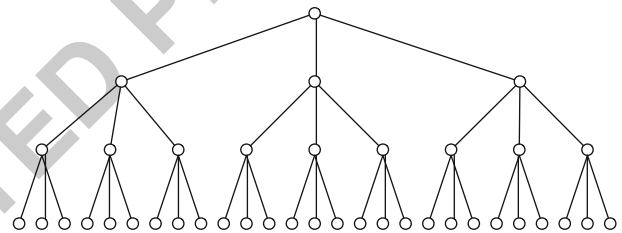
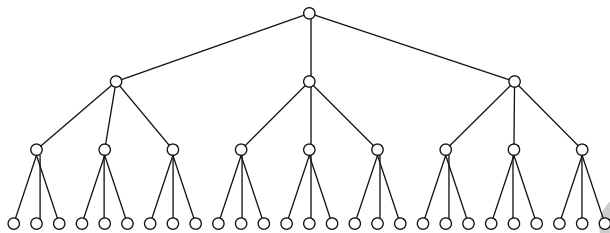
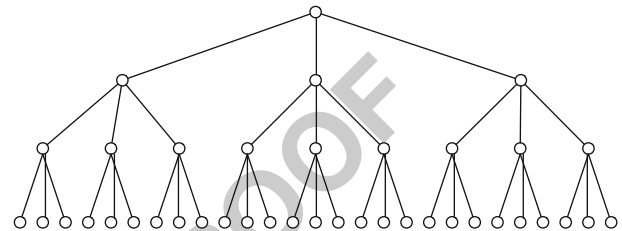
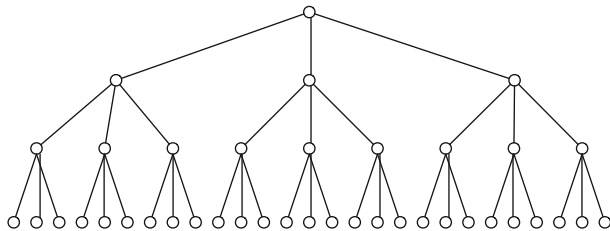
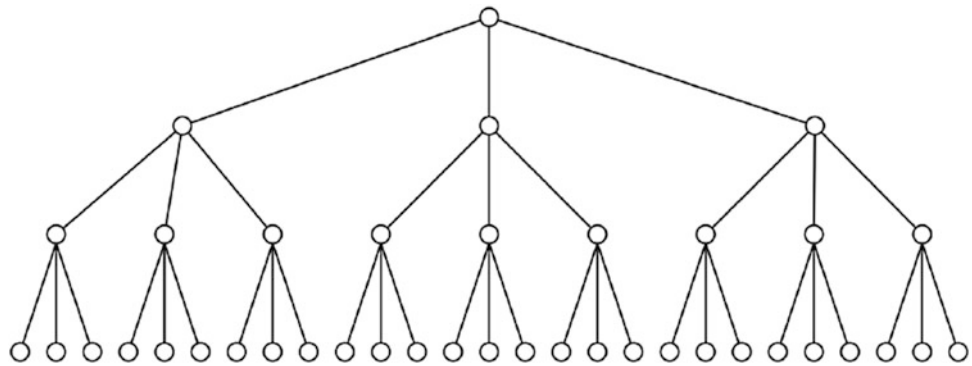


Fig. 6.2 A single trait tree, represented by a balanced tree with branching factor 3 and depth factor 3, order 40. In our model, nodes higher in the tree represent prerequisites for nodes lower down the tree. Each instance of the model will have several or many of these trees in the design space

lithic raw materials, independent of learning how to perform different percussion techniques. In our model, each of these independent areas is represented by a separate tree of traits.

In each simulation model, we begin with a trait or “design space” that incorporates several independent sets of traits (O’Brien et al. 2010). The overall design space of a simulation model is thus a forest,² composed of several trees (Fig. 6.1). For each tree in a learning hierarchy, we employ balanced trees which have the same number of nodes at each level, to provide a simplified model of a design space with which to begin our exploration of this class of social learning model, although real design spaces are undoubtedly more complex in their geometry. Each tree in our model is specified by a branching factor r and depth h . As a result, each trait tree in the design space has $\sum_{i=0}^h r^i$ traits.

The tree depicted in Fig. 6.2 thus has 40 vertices, for example. In this chapter, we examine both small (4 trees) and larger (16 trees) design spaces, to see how learning may dif-

fer in problems involving design spaces of different size and complexity. We examine trees with combinations of branching and depth factors of 3 and 5. Thus, a design space with 4 trees with branching and depth factors of 3 (as in Fig. 6.2) would have 160 traits, whereas a design space with 16 trees of branching and depth factors of 5 would have a total of 62,496 traits.³ Even the small design spaces we consider here create a large space for cultural change and differentiation, given the number of possible trees one can construct on even 40 vertices.⁴ In the experiments reported here, the overall

³We initially chose 6 as the limit on branching and depth factors, but found that we cannot calculate certain symmetry statistics, such as the size of the automorphism group, on trees that large using existing tools. Even a tree with $r = 5, h = 6$ has over $10^{1.623}$ possible symmetries, and an attempt to calculate the symmetries for $r = 6, h = 6$ did not complete given the memory limits of the computers we had available.

⁴If we consider each trait to be unique and non-interchangeable, the number of unique trees with unique vertex labels is n^{n-2} by Cayley’s theorem (Diestel 2010). For example, for each trait tree of 40 vertices, there are roughly 10^{60} possible trees. Even if we consider traits to be interchangeable (e.g., we look at the abstract topology of trees rather than the details of individual traits), there are at least 10^{16}

²A forest is a graph composed of multiple components, each of which is a tree.

size of the design space remains constant over time, which is a simplifying assumption as we develop this class of structured information models. In future work, we will explore the role of invention in episodically creating large new regions of design space for the evolving population to explore.

Given the total “design space” represented by a forest of trait trees, each individual in our model is initialized with a small number of “initial” traits. Initial traits are chosen randomly but heavily weighted towards the roots of the trees to represent the fact that our knowledge starts out basic and sparse. In general, all of the design spaces modeled here are larger than populations will explore within the bounds of a simulation run. In the next sections we describe the social learning model, modified from Robert Axelrod’s original, by which each simulated population evolves within this tree-structured design space, and will return to the specifics of how an initial culture repertoire is chosen.

6.2.2 The Axelrod Model of Social Learning and Differentiation

Robert Axelrod (1997) formulated a model aimed at studying the conditions under which simple learning rules could lead to cultural differentiation, rather than a single fixed state (which is the result of simpler neutral or diffusion models). This makes it useful as a starting point for understanding phenomena such as behavioral modernity, in our view. Axelrod’s model combines social learning, in the form of random copying, a spatial structure to interaction, in the form of localized copying of neighbors on a lattice, and the tendency to interact most strongly with those to whom we are already culturally similar (homophily). The model displays a rich and interesting set of behaviors, and has been extensively studied by social scientists and physicists (Castellano et al. 2009). First we review the basic model, and in the following section our modified algorithm.

6.2.2.1 Axelrod’s Original Model

The original model locates N individuals on the nodes of a regular lattice or grid, but various network structures have also been studied. Each individual is endowed with F integer variables $(\sigma_1, \dots, \sigma_F)$, that can each assume q values. In the original model, each variable is a “cultural feature” each of which can assume q “traits.” In each step, a randomly chosen individual i and a random neighbor j are selected, and “interact” with probability equal to the overlap between their cultural repertoire. Overlap, in the basic model, is simply the fraction of features for which i and j possess the same trait value:

possible unlabelled rooted trees on 40 vertices (using Otter’s (1948) approximation).

$$p(i, j) = \frac{1}{F} \sum_{f=1}^F \delta_{\sigma_f(i)\sigma_f(j)} \quad (6.1)$$

where $\delta_{i,j}$ is Kronecker’s delta function, taking the value 1 when its two arguments are equal and 0 otherwise. When individuals interact, the focal individual i takes the trait value of its neighbor for one of the features where the two individuals differ.

Interaction has no effect when two individuals already possess identical cultural repertoires, and there is no probability of interaction if individuals have no traits in common. This eventually causes the model to reach an absorbing state where no further changes are possible. Instances of the model are initialized with a random distribution of traits among individuals, and left to update until the steady state is reached. The evolution of the population leads to two classes of absorbing states: (a) a “monocultural” state in which all individuals share the same set of variables, and (b) a “polycultural” state in which subpopulations exist which share the same set of variables within the group, and are completely different from their neighbors.

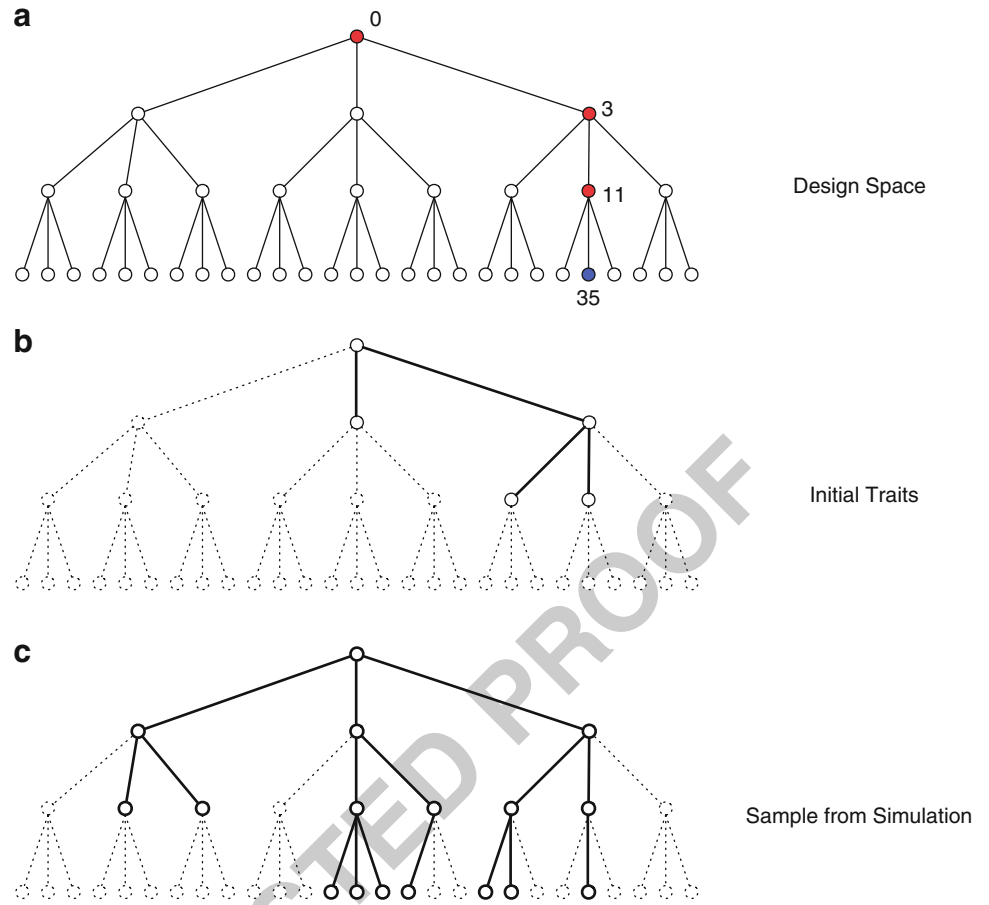
Which of the two results is reached, and the statistical character of “polycultural” states when they exist, depends mainly upon the number of traits possible q for each cultural feature. For small values of q , individuals share many traits with their neighbors, interactions are thus frequent, and one domain comprising a single set of traits will grow to become fixed within the entire population. In contrast, when the value of q is high, individuals start out sharing very few traits, with interactions that are correspondingly less frequent. Regions of uniform cultural variation do grow, but as they do, sets of individuals who share no traits at all (and thus do not interact) grow as well, and often prevent any single regional culture from expanding to fix within the population.

Many variants of the basic Axelrod model have been studied, including the addition of “drift” via the introduction of copying error, situating agents on different types of complex networks, the addition of an external “field” to simulate the effects of mass media, and copying that obeys a “conformist” or majoritarian rule by selecting the most common trait among the neighbor set (Castellano et al. 2000; De Sanctis and Galla 2009; Flache and Macy 2006; González-Avella et al. 2005, 2006, 2007a,b; Klemm et al. 2003a,b, 2005; Lanchier et al. 2010; Lanchier 2012). In general, modifications of the basic model can reduce the tendency of the model to produce polycultural solutions, or change the time scale or location of the critical point.

6.2.2.2 Semantic Extensions to the Axelrod Model

We begin each simulation with N (100, 225, or 400) agents, arranged on a square grid. A design space is created, with some number of trait trees (4 or 16), with uniform branching

Fig. 6.3 Illustration of a design space composed of a single trait tree, along with a random initial trait chosen from the design space, and a final sample from a simulation run, showing the evolution of traits within the design space. Also shown in the (a) are the “prerequisites” for a cultural trait (35), as an example



factors and depth factors (3 or 5). An example of such a tree is shown in panel A of Fig. 6.3. Initial traits (and their prerequisites) are chosen randomly across the configured number of trait trees, as follows. For each individual, we select a random number t between 1 and 4, and repeat the trait selection process t times for that individual. In each selection, we choose a random tree in the design space, and then select a depth in the tree for the trait, given by $d \sim \text{Poisson}(0.5)$. This biases trait selection towards the root of the tree, as one would expect in young or inexperienced individuals. We then walk d steps into the tree, making uniform random selections for the children of each vertex. The path of vertices thus constructed is added to the individual's trait set, giving them an initial trait and its necessary prerequisites. One such initial trait is shown in Panel B of Fig. 6.3. Given that individuals begin with a small number of initial traits (between 1 and 4, selected randomly), and their prerequisites, the initial trait endowment of an individual is between 1 and $4h$, where h is the maximum depth of the design space (either 3 or 5 in the experiments reported here).⁵

Once the population is initialized, the simulation runs a discrete approximation to a continuous-time model. In other words, only one agent changes at each elemental time step, as in the original Axelrod model and the Moran model of population genetics and its cultural version (Aoki et al. 2011; Moran et al. 1962; Moran 1958). At each step, an agent (A) is chosen at random, and a random neighbor of A is then selected (agent B). Their probability of interaction is given by the overlap of trait sets, which is most simply calculated as the Jaccard overlap between the set of tree vertices each possesses, thus replacing Eq. 6.1 with:

$$J(A, B) = \frac{|V(A) \cap V(B)|}{|V(A) \cup V(B)|} \quad (6.2)$$

where $V(i)$ represents the vertex list for trait trees held by individual i in the population.

If the agents end up interacting, agent A observes the traits currently possessed by B, and selects a trait (T) that it does not already possess to learn. If agent A has the necessary prerequisite traits for the selected trait, it can learn

⁵At maximum, this yields some individuals who begin the simulation with up to 20 traits. The median number of traits in samples taken after 6–10 million time steps is considerably higher – 259 traits per cultural

configuration or region. Thus, cultural repertoires in the simulation grow through copying and innovation, as expected.

trait T . If not, there is a probability $\mathbb{P}(I)$ that B can teach A a necessary prerequisite for T instead. This simulates the process of agent B structuring the learning environment of A through formal instruction or apprenticeship, for example. If such a prerequisite learning event occurs given $\mathbb{P}(I)$, agent A learns the most fundamental of T 's prerequisites that it does not already possess. For example, agent A might require the trait closest to T (e.g., trait 11 in Fig. 6.3, if the original trait targeted was 35).

Additionally, at each time step, there is a probability $\mathbb{P}(m)$ that one random individual in the population will learn a new trait (and necessary prerequisites) that it does not already possess. For example, if an innovation event occurs and an agent discovers trait 35 by individual trial and error learning, we assume that the agent also discovered traits 0, 3, and 11. Thus innovation can introduce one trait to the population, or a linked set depending upon its prerequisites and what the innovating individual already "knows." This model of innovation simulates an ongoing process of individual learning unconnected to social learning or teaching within the population. Because this functions much like "infinite-alleles mutation" in the classical Wright-Fisher neutral models (Ewens 2004), or like noise terms in Axelrod, Ising, or Potts models (Castellano et al. 2009), we will refer to this as the "global innovation rate" in this chapter.

One of the editors noted that this model of innovation may not be as realistic as an alternative, where random innovations would be "discoverable" only with the correct prerequisites in place. We believe that innovation in the face of skill or knowledge prerequisites is continuous between these two models. Occasionally one will discover a new piece of knowledge or develop a skill, having learned surrounding and related knowledge. In other situations, individuals may learn sequences and sets of information or skills by trial and error and "tinkering." The "size" of innovations that can be learned purely by individual trial and error should thus vary between these extremes, biased towards the "small" end of the range. Our selection of an innovation model where individuals discover a trait and its prerequisites thus potentially overestimates the effect of individual learning, but it made certain graph operations easier, and can be relaxed in future models.

Each simulation run lasts 10^7 steps, which yields between 10^4 and 10^5 copying events per individual, depending upon population size.⁶ Since we do not explicitly model the interaction between cultural transmission and biological

reproduction here, we can interpret the model as representing either fine-grained learning within individuals over the course of their lifetimes, or long-term cultural evolution within a fixed size population where we are not modeling fitness. We felt this simplification was appropriate in a pilot study exploring structured information models, but a more detailed study would include dynamics on two time scales: developmental learning and evolutionary dynamics given birth and death. Samples are taken beginning at 6 million steps, and sampling at an interval of 1 million steps, and record the trait trees seen in the population. An example of such a sampled tree is shown in Panel C of Fig. 6.3. For reference, the full algorithm for each copying step is given in the Appendix as Algorithm 1.

6.3 Measuring Cultural Diversity and the Results of Structured Learning

Each sample from a simulation run is composed of the distinct sets of trait trees possessed by individuals in the population, along with summary statistics. If a simulation run converges to a monocultural solution, the sample will have one set of trait trees, which are shared across the entire population. In other cases, there will be clusters of cultural configurations which might be unique to a single individual, or shared by some number of agents. Each cluster will be composed of some number of trait trees (typically, the number configured for the simulation run: 4 or 16, but perhaps a subset), and each trait tree will be the result of many agents learning traits and their prerequisites socially, and for runs with a non-zero mutation rate, by individual learning or innovation. Each cluster will thus have some number of traits, typically higher (often much higher) than the initial endowment given to the population.

From the sampled trait trees, we calculate summary statistics as follows. The ratio of the number of traits in the sample to the full design space size (or "remaining density" of traits) is one measure of trait richness. The radius of a rooted tree is the number of edges in the path from root to the furthest edge. The average radius of trees in a sample (or its ratio to the depth of the design space) is another richness measure, aimed at measuring whether knowledge with multiple prerequisites is being learned within the simulated population. Similarly, in the original design space, the branching factor describes how many children each node in the tree started with, so measuring the average vertex degree gives us a rough measure of how broad a cultural repertoire is. Each of these measures is illustrated in Fig. 6.4 for an example tree selected from our data.

⁶One hundred thousand was chosen as a compromise for running large batches of simulations in parallel. Some simulation runs, especially in small design spaces with very high prerequisite learning rates, can converge to a monocultural solution and quasi-stable equilibrium quite quickly; in the largest design spaces and low learning rates, convergence may never occur even though the process is well-mixed. However, the processes have reached a quasi-stable equilibrium, verified by

examining samples at different times for secular trends in median and mean values, which were not found.

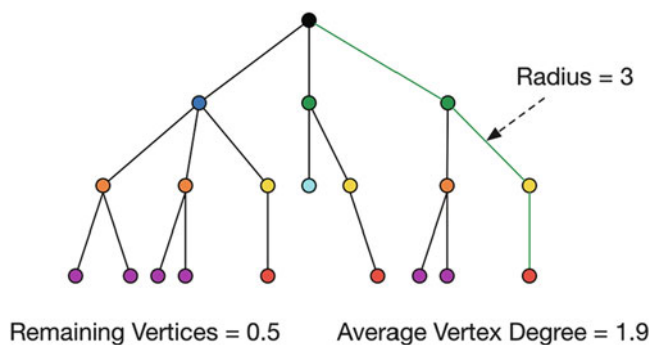


Fig. 6.4 An example set of traits at the conclusion of a simulation run, extracted from a simulation with branching factor 3 and depth factor 3, and a single trait tree as the trait space. The remaining density of vertices, mean vertex degree, and radius of the tree are noted. Vertex colors denote “structural equivalence” classes or “orbit structure,” as measured by adjacency patterns, and is one measure of the symmetries present in the tree

In addition to these simple numerical measures comparing final trees to the original design space, it is useful to measure something about the overall “shape” of the trees themselves. One way of formalizing this notion is to examine the *symmetries* of the final trait trees. Examining Fig. 6.4, if we ignore the exact identities of traits for the moment, it is apparent that there are repeating patterns. For example, the left-most branches each terminate in a pair of leaves. This pattern is repeated on the second right-most branch. These types of repeating patterns are computationally expensive to search for in large sets of trees, but we can summarize them by considering trait trees as algebraic objects and examining their *automorphisms*.

An automorphism is a function which maps an object to itself, in such a way that the structure of the object is preserved (Rotman 1995). Graph automorphisms map vertices in a graph to each other, preserving properties such as the adjacency pattern of edges. The six vertices which mark the repeating pattern of leaf-pairs in Fig. 6.4 are an automorphism of the tree, and thus are symmetries we can measure. An overall measure of “how symmetrical” (or “how many interchangeable patterns”) there are in a graph possesses given by the total number of automorphisms found, called the size of the automorphism group or $|Aut(G)|$ (Godsil and Royle 2001). A tree with no repeating patterns will thus have an automorphism group size of 1, indicating that the only symmetry is the entire tree itself. A balanced tree with branching and depth factors of 3, as depicted in Fig. 6.2, has approximately 1.3×10^{10} automorphisms. The more repeating patterns there are in trait trees, the more automorphisms they will possess.

Because group sizes grow quickly and the accuracy of performing calculations with truly astronomical numbers is low, another possible measure of the symmetries present is to count the *classes* of equivalences into which vertices fall.

The *orbits* of the automorphism group are the sets of vertices which are interchangeable by some permutation that preserves structure. For example, the graph in Fig. 6.2 has five orbits, with each vertex at a given level interchangeable (in a structural sense). Similarly, the six leaf vertices that are part of pairs in Fig. 6.4 are part of the same orbit; in this illustration, each orbit is given a different color to highlight their equivalence. For each cultural region found when sampling a simulation, we calculate the size of the automorphism group and the number and multiplicity (frequency) of orbits. For this analysis, we employ the *nauty* + *Traces* software by Brendan McKay and Adolfo Piperno (McKay and Piperno 2014).⁷

6.4 Experiments

Given a modified Axelrod model on a tree-structured trait space, we expect to see greater cultural diversity, differentiation among groups of individuals, and larger sets of traits as the “learning environment” is tuned from a low to high probability of teaching and learning among individuals. We also expect that individual innovation, independent of the social learning context, will increase the amount of the technological design space that a population explores, which leads to enhanced opportunities for differentiation even through simple random copying. Here we measure cultural differentiation by the number of clusters of individuals who share the same trait trees when we sample the population.

Second, we looked at whether highly structured learning environments, represented here by higher probabilities of naive individuals gaining the prerequisites for the skills and information they encounter with peers, led to deeper and richer cultural repertoires. We explore a number of ways to measure the richness of a cultural repertoire in a model with structured relations between traits, through the use of graph properties and symmetry measures. The measures used are those described above: the tree radius (or depth), mean vertex degree, the fraction of remaining vertices, and the size of the automorphism group of sampled trait forests. Finally, we began to examine how the structured learning environment might interact with demography, by simulating the same parameters across two sizes of population.

For this chapter, we examined populations of size 100, 225 and 400, to begin to examine the effects of population size. For these populations, we examined design spaces that were small (4 trait trees) and large (16 trait trees). Within each size, we further examined combinations of branching factor and depth factor with values of 3 and 5, thus yielding 8 total sizes of design space (Table 6.1).

⁷Nauty+Traces can be downloaded at <http://pallini.di.uniroma1.it/>. We employed version 2.5r7 for this research.

Table 6.1 Size of design space for different trait tree configurations

Branching factor	Depth factor	Number of trait trees	Size of design space
3	3	4	160
5	3	4	624
3	5	4	1,456
5	5	4	15,624
3	3	16	640
5	3	16	2,496
3	5	16	5,824
5	5	16	62,496

t2.1
t2.2
t2.3
t2.4
t2.5
t2.6
t2.7
t2.8
t2.9

Table 6.2 Parameter space for simulations described in this chapter

Simulation parameter	Value or values
Population rate at which new traits arise by individual learning	0.0, 5e−05, 0.0001
Maximum number of initial traits (not including their prerequisite sites) each individual is endowed with	4
Number of distinct trees of traits and prerequisites	4, 16
Population sizes	100, 225, 400
Replicate simulation runs at each parameter combination	25
Maximum time after which a simulation is sampled and terminated	10,000,000
Individual probability for being taught a missing prerequisite	0.05, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9
Number of branches at each level of a trait tree	3, 5
Depth of traits in each trait tree	3, 5

t4.1
t4.2
t4.3
t4.4
t4.5
t4.6
t4.7
t4.8
t4.9

Further, we examined three levels of global mutation or innovation rate: zero, or no mutation, and 0.00005 and 0.0001. Such rates created a constant supply of new innovations, but several orders of magnitude less frequent than copying and prerequisite learning events. The full set of parameters are given in Table 6.2. In this pilot study, for each combination of all of the above parameters, we performed 25 replications. With 5 samples per simulation run, this yielded 10,963,691 samples of cultural regions.

6.5 Results

We begin by noting that compared to the original Axelrod model, or neutral and biased copying models, the dynamics of our semantic Axelrod model are highly variable. A very wide range of outcomes is possible for each parameter combination, especially when the size of the design space is large. Some variables, such as the average vertex degree of sampled trait trees, are strongly overlapping across all learning rates and do not appear diagnostic of different learning environments, at least in these initial experiments. Given the large amount of variability in the dynamics, larger numbers of replications would be useful, although this is computationally quite expensive at present.⁸ That said, several features of the data are strongly suggestive that hierarchical trait

models have potential in modeling cumulative technological evolution, making the computational expense worthwhile.

6.5.1 Cultural Diversity

Variation among individuals is foundational to evolutionary processes, and is the raw material from which differentiation between regions and cultural groups is constructed. Figure 6.5 depicts the number of cultural configurations (i.e., trait trees) in a population of size 100, for the smallest trait space with only 160 total traits, and relatively high levels of individual innovation. For example, in the leftmost panel the large peak just above zero indicates that most simulated populations are characterized by one or a few sets of trait trees. Five learning rates are depicted, increasing from left to right across the panels. At the very lowest rate of learning fidelity, with only a 10 % chance of being taught a needed prerequisite for knowledge being copied, most of the populations simulated share a single set of traits, and even individual innovation does not drive significant exploration of the space of structured traits. With increased fidelity in teaching needed prerequisites, however, simulated populations begin exhibiting marked differentiation, with individuals possessing more unique configurations of traits from the overall design space.

⁸The simulations reported here ran on a cluster of 6 compute-optimized “extra large” Linux instances on Amazon’s EC2 computing cloud, for a total of 17 days of wall clock time and 2,075 CPU hours. We plan

further optimizations to the simulation code to make larger samples economically feasible.

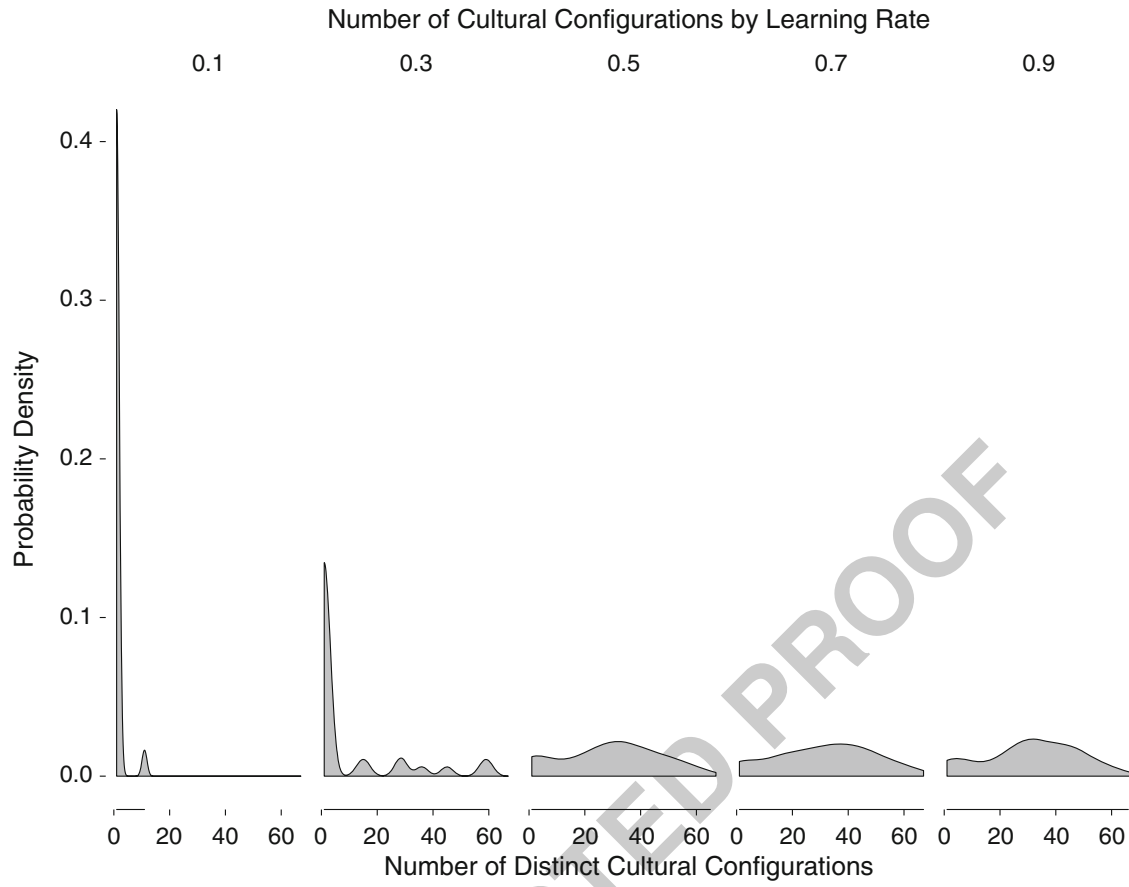


Fig. 6.5 Number of cultural configurations in simulations with the smallest trait space (160 total traits in 4 trees), and a high individual innovation rate (10^{-4})

Looking at the data from another perspective, we can hold the fidelity of learning constant (say, at a 40 % chance of being taught a needed prerequisite), with the same global innovation rate (10^{-4}) as Fig. 6.5, and examine the effect of different size design spaces (Fig. 6.6). In general, populations exhibit greater differentiation between individuals as the design space gets larger, as prerequisite learning helps individuals acquire adjacent traits, and individual innovation randomly explores more distant portions of the design space.

Given the structure of the Axelrod model, with the strong tendency towards cultural uniformity given homophily, all simulated populations converged to a single cultural configuration in the absence of a global innovation rate. This highlights the importance of various “innovation” and “invention” processes in the creation and maintenance of cultural differentiation and diversity (Eerkens and Lipo 2005; O’Brien and Shennan 2010), and suggest that highly conservative cultural repertoires, such as those posited to precede behavioral modernity in hominin populations, occur whenever individuals engage in social learning in small technological design spaces, in the absence of strong and regular individual innovation.

6.5.2 Trait Richness and Knowledge Depth

Cumulative evolution of technology is represented in our model by the population learning its way down the trees which compose the design space. Possession of traits deeper in the trees represents skills or information which is more specific, possessing more prerequisites. Thus, we expect that the depth (or “radius,” see Fig. 6.4) of trees would increase with the prerequisite learning rate, representing a learning environment which is structured to ensure such acquisition.

Figure 6.7 gives the *normalized* mean radius of cultural regions, broken out by the prerequisite learning rate along the horizontal axis, and each group of 3 boxplots displays the differing global innovation rates studied. Radii are normalized to the depth of their design space, to facilitate comparison. The results indicate that essentially two regimes exist: shorter trees, which do not grow much beyond their initialized size, and larger trees. The mean radius has an asymptote just above 0.75, achieved with the prerequisite learning rate is approximately 0.4 or higher. Further increases do not seem to matter. Additionally, the difference between the two global innovation rates is small – what matters most in terms of

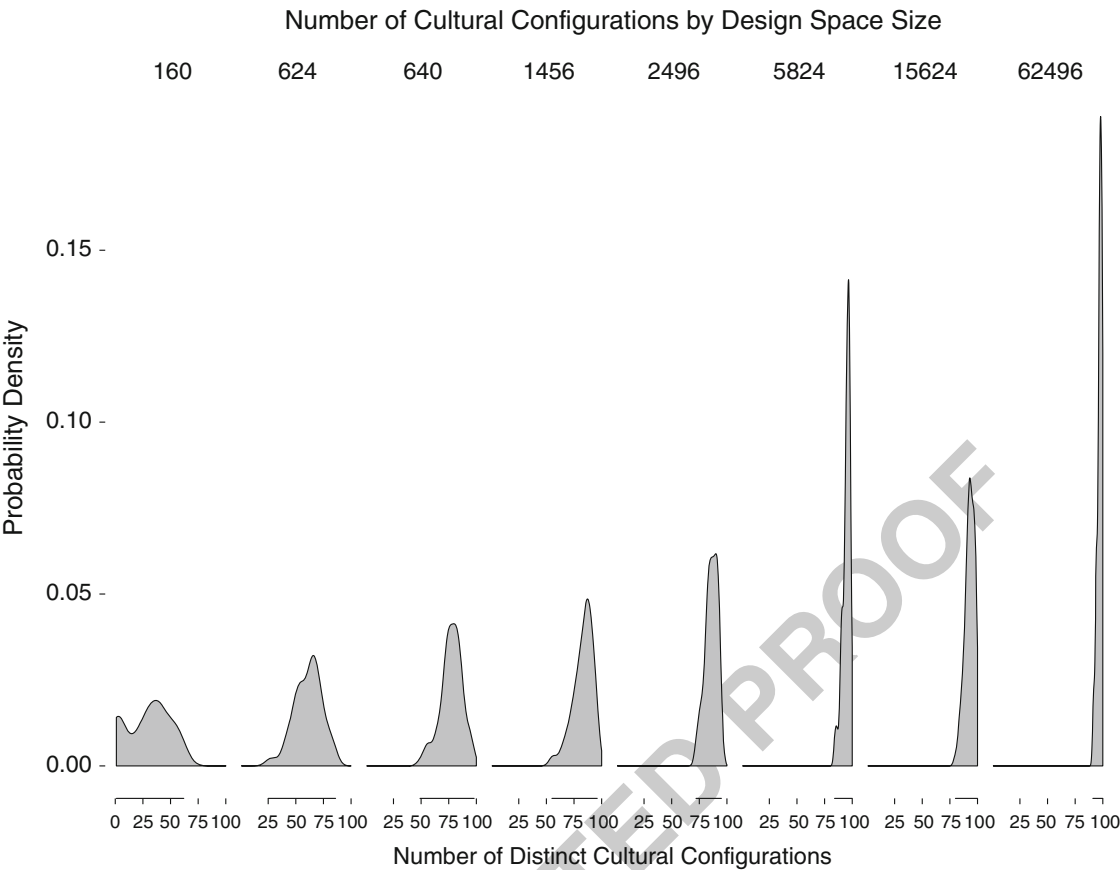


Fig. 6.6 Number of cultural configurations in simulations with an intermediate learning rate (0.4), across different sizes of trait space

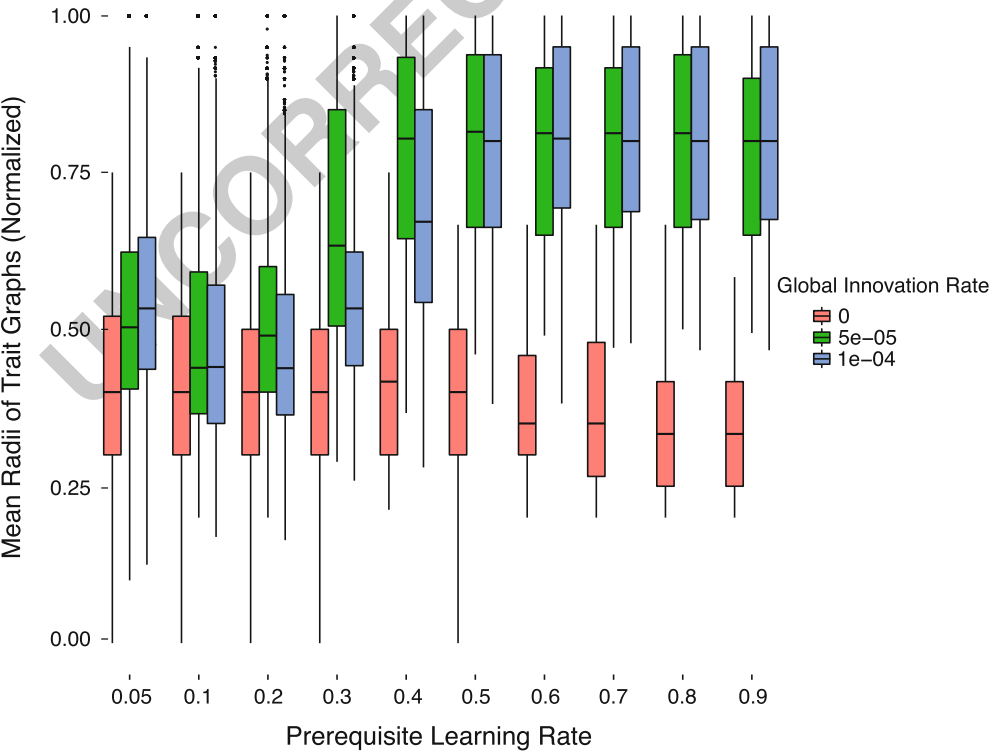
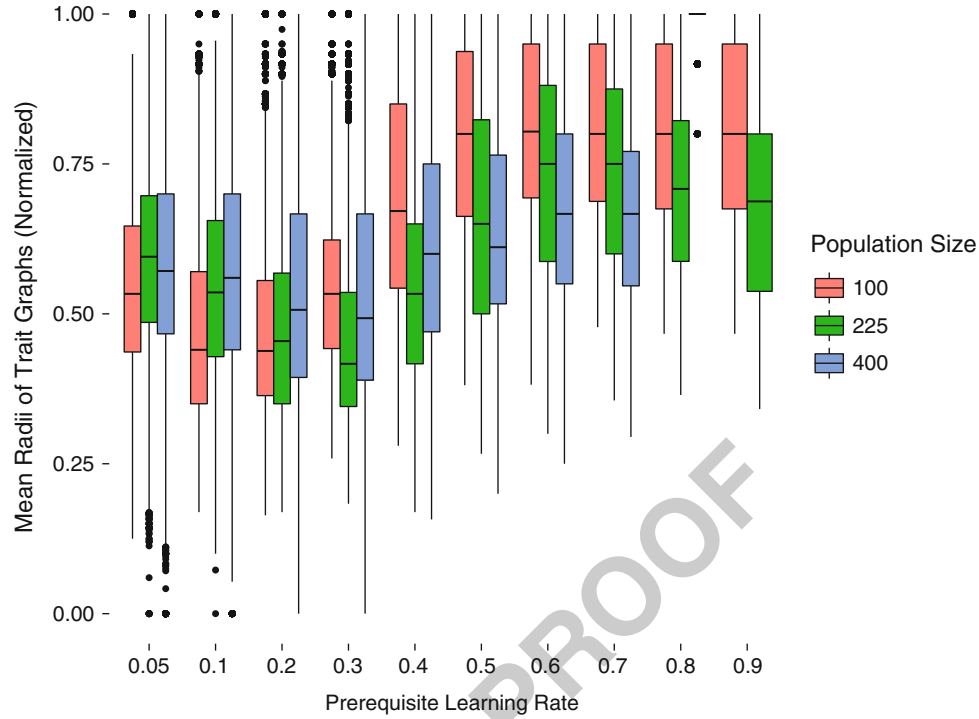


Fig. 6.7 Mean depth of trait sets, by prerequisite learning rate and global innovation rate, for population size 100

Fig. 6.8 Mean depth of trait sets, by prerequisite learning rate and population sizes of 100, 225 and 400



qualitative behavior is the presence of global innovation outside the teaching or learning of prerequisites themselves.

6.5.3 Population Size

Earlier, we mentioned that population size does not seem to be a primary factor in explaining the measured diversity in cultural transmission models, except perhaps in bottleneck situations like the one Henrich analyzes in Tasmania (2004). Instead, population size may have an interaction effect with other factors, yielding smaller second-order effects. We examined the effect of population size in the research reported here, repeating the entire set of simulation runs for populations of 100, 225, and 400.⁹

Figure 6.8 displays the relationship between mean radius (or depth) of the cultural traits in each cultural sample, as in Fig. 6.7 above, but the boxplots are instead colored by population size. At least over a range of group or deme sizes likely to be relevant to Paleolithic archaeology, population size makes no difference to the qualitative behavior of the model. There is, however, a very slight decrease in mean radius of trait sets with larger population size, which is likely a consequence of a larger population spreading out over the trait space.

⁹We should note that learning rates of 0.8 and 0.9 for population size 400 were cut short due to budget constraints, but this does not appear to affect the pattern in our dataset.

6.5.4 Trait Tree Symmetries

Finally, we examined the algebraic properties of the trait trees composing cultural regions, examining both the number of vertex equivalence classes (orbits) and the size of the automorphism group of the trait forests. We examined the raw metrics, and versions normalized by the size of the maximally symmetric forest with the same number of traits, branching factor, and depth factor. The latter proved difficult and led to serious overflow problems even with 64 bit arithmetic, so we focus here on the raw automorphism group size.

The logarithm of the automorphism group size does hint at interesting structure (Fig. 6.9). In the presence of mutation, the learning of prerequisites narrows the range of variability for the automorphism group size, and at higher learning rates renders the distribution multimodal. The modality arises because of the different combinations of branching factor and depth factor we employed for design spaces – i.e., some design spaces are “wide” and some are “narrow,” while also being “shallow” or “deep.” This gives rise to different modes in the measured symmetries, but overall the reduction in variability in symmetry is the most important qualitative effect seen in our data.

We do not fully understand the “shapes” of cultural regions to which the model appears to converge, but it appears that there is a tendency for trait graphs to converge towards shapes which have moderate numbers of symmetries. This graph is on a logarithmic scale, so a peak at 50

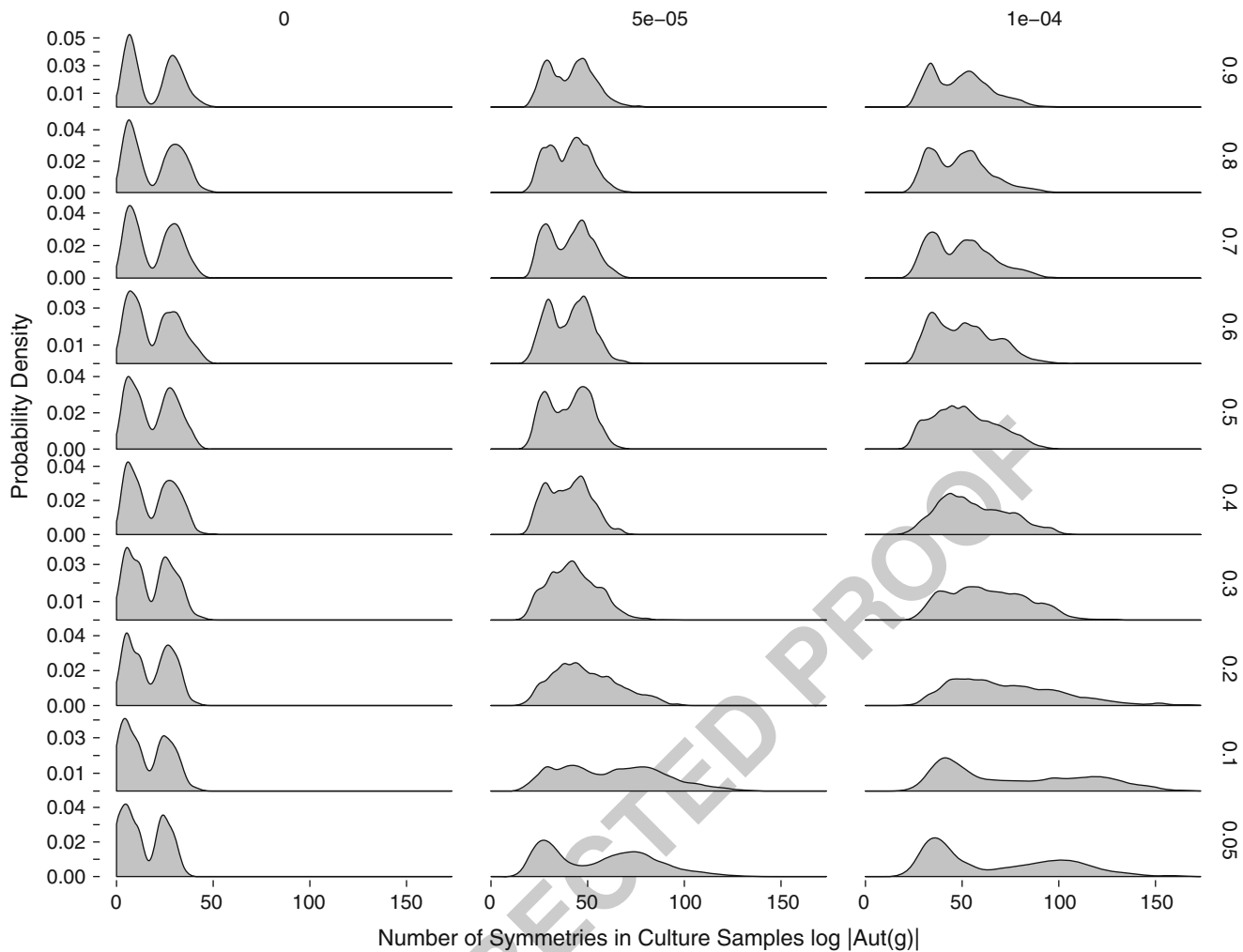


Fig. 6.9 Number of symmetries in trait tree samples, measured as the log of the order of the automorphism group of the trait graphs, broken down by prerequisite learning rate (*rows*) and global innovation rate (*columns*)

along the horizontal axis corresponds to a trait graph with approximately 5×10^{21} symmetries. This is a fairly small number, compared to the original design spaces, which have symmetries ranging from approximately 10^{41} – $10^{6,496}$. Thus, the geometry of cultural traits in our hierarchical design spaces are fairly asymmetric and represent small and very specific segments of the total design space.

Further analysis of trait graph “shapes” is needed to tell whether there are repeating patterns or graph “motifs” which characterize a social learning model in a graph-structured trait space. The results here are suggestive of such a phenomenon, but inconclusive given just the bulk algebraic properties of cultural regions, since the size of the automorphism group (or the number of orbits) tells only *how many* symmetries there are, not what types of symmetries exist. The next step in our analysis of shape is to pursue a geometric decomposition of the graph following Ben MacArthur and Rubén Sánchez – García’s (2008) work on the symmetries of complex networks.

6.6 Discussion

The “semantic Axelrod” model described here specifically addresses social learning of knowledge with “prerequisite” structure, and a learning environment which is tunable from low to high fidelity, simulating the intensity with which “teaching” occurs in addition to imitative copying. The model displays a characteristic increase in the cultural repertoires of individuals, as they learn in environments of higher fidelity. At the individual level, an increase in higher fidelity learning within structured information environments both creates path-dependency in what is learned, and increases the chances for specialization among individuals. Hominin populations in which complex knowledge is taught systematically along with prerequisites will accumulate and retain skills and technology faster and to a greater extent than those groups which rely upon natural pedagogy and imitation for social learning.

Previous research had established the importance of teaching and learning environments for cumulative cultural evolution and cultural diversity (Aoki 2013; Castro and Toro 2014; Creanza et al. 2013; Nakahashi 2013). Our contribution in this paper is a model capable of connecting the fact of teaching with the actual structure and content of cultural knowledge. Such models, we believe, are important in explaining the explosion of cumulative material culture that accompanies behavioral modernity. The model described here only makes a start on modeling the additive and recombinative complexity of real technologies, but it does display accumulated depth of “knowledge” or “skills,” as represented by the radius or depth of trait trees. In combination with realistic models of technology – such as the production sequences studied by experts on stone tools – we believe that empirically sufficient models of the evolution of specific technologies are possible and within reach.

Several areas suggest themselves for future research in structured information or “semantic” cultural transmission models. Some we are pursuing, others remain open questions and we invite collaboration towards their solution.

- Regional scale cultural differentiation given a metapopulation embedding of the basic model.
- Additional trait relations (e.g., class subsumption, functional equivalencies).
- Realistic technology models for key artifact classes (e.g., bifaces, scrapers, pottery).
- Incorporation of trait fitness in order to study directional change.

Models of the class introduced here are “thicker” descriptions of how humans acquire skills and information in real learning environments, and thus complement existing models which describe the conditions under which teaching and structured learning might evolve and spread. We believe models of this type make a needed “downpayment” on cultural transmission models which can substantively incorporate specialties such as archaeometry, the technological analysis of lithics and pottery (Tostevin 2012), and studies of how innovation occurs in various tool classes (e.g., O’Brien and Shennan 2010). Bringing cultural transmission modeling together with the details of technologies will be a crucial component in multifactor evolutionary explanations for the complex of changes seen in modern *Homo sapiens* and some Neanderthal populations in the later Paleolithic.

Acknowledgements The authors wish to thank Briggs Buchanan and Mark Collard for the invitation to participate in the symposium “Current Research in Evolutionary Archaeology,” at the 79th Annual Meeting of the Society for American Archaeology in Austin, TX. A summary of this research was presented in that session, and Alex Mesoudi provided valuable comments on an early post-conference draft. Kenichi Aoki and an anonymous reviewer provided feedback prior to publication, and although we did not take all of their suggestions, the comments

led to a number of improvements. Madsen wishes to thank Frédéric Chapoton of the Institut Camille Jordan for answering a question about the maximal automorphism group of trees.

Appendices

Algorithm Description

Algorithm 1 describes the “semantic” Axelrod model variant studied in this chapter. Within the algorithm, there are several functions which find traits with particular properties. Some, like **GetTraitUniquetoFocal()**, are fairly simple set operations but were abbreviated to clarify the notation.

Algorithm 1

Require: *innovrate* is the population rate at which individuals randomly learn a trait
Require: *learningrate* is the probability of learning a missing prerequisite during a learning interaction

```

1: focal ← GetRandomAgent()
2: neighbor ← GetRandomNeighbor(focal)
3: if focal = neighbor ∨ focal ∩ neighbor = ∅ ∨ neighbor ⊂ focal
   then
4:   exit { No interaction is possible, move on to next agent }
5: end if
6: prob ← (focal ∪ neighbor − focal ∩ neighbor) / focal ∪ neighbor
7: if RandomUniform() < prob then
8:   differing ← neighbor \ focal
9:   newtrait ← GetRandomChoice(differing)
10:  if hasPrerequisiteForTrait(focal, newtrait) = True then
11:    replace ← GetTraitUniquetoFocal(focal, neighbor)
12:    focal ← focal \ replace
13:    focal ← focal ∪ newtrait
14:  else
15:    if RandomUniform() < learningrate then
16:      prereq ← GetDeepestMissingPrerequisite(newtrait, focal)
17:      focal ← focal ∪ prereq
18:    end if
19:  end if
20: end if
21: if RandomUniform() < innovrate then
22:   focal3 ← GetRandomAgent()
23:   innovation ← GetRandomTraitNotInFocal(focal3)
24:   focal3 ← focal3 ∪ innovation
25: end if
```

GetDeepestMissingPrerequisite() is a procedure which takes the trait set of an individual, and a trait for which the individual is known to be missing necessary prerequisites, and returns the “most basic” missing prerequisite for that trait (i.e., closest to the root). This is done by finding the path which connects the root and desired trait, and walking its vertices from the root downward, checking to see if each vertex is part of the individual’s trait set. The first trait not found in the individual’s repertoire is returned.

Availability of Software and Analysis Code

The simulation software used in this chapter is available under an open-source license at Mark Madsen's GitHub repository <https://github.com/mmadsen/axelrod-ct>. Required libraries and software are listed in the source archive itself, and include Python 2.7 and the open-source MongoDB database engine to store simulation output.

The codebase consists of a set of library modules which implement the shared and unique aspects of each model, unit tests to verify the basic functionality of the code, and scripts which execute each model. The **axelrod-ct** repository contains three models:

- An implementation of the original Axelrod model using the **axelrod-ct** libraries.
- A basic model with an "extensible" trait space but no relations between traits.
- A "semantic" Axelrod model with tree-structured trait space representing prerequisite relationships between traits.

Stepwise extension from the original Axelrod to the semantic models on the same code library allowed a degree of verification, which is difficult in a situation where there is no existing mathematical theory against which to compare the code implementation (Committee on Mathematical Foundations of Verification Validation and Uncertainty Quantification, National Research Council 2012).

The analysis and final dataset reported here are available, along with the source of this paper and associated presentations, in an associated GitHub repository: <https://github.com/mmadsen/madsenlipo2014>. Statistical analyses of the final dataset were performed in R, rendering our results reproducible given simulated data from the "axelrod-ct" software linked above.

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