

Modeling the genealogy of a cultural trait

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ABSTRACT

The mathematical study of genealogies has yielded important insights in population biology, such as the ability to estimate the time to the most recent common ancestor (MRCA) of a sample of genetic sequences or of a group of individuals. Here we introduce a model of cultural genealogies that is a step toward answering similar questions for cultural traits. In our model individuals can inherit from a variable, potentially large number of ancestors, rather than from a fixed, small number of ancestors (one or two) as is typical of genetic evolution. We first show that, given a sample of individuals, a cultural common ancestor does not necessarily exist. We then introduce a related concept: the most recent unique ancestor (MRUA), i.e., the most recent single individual who is the earliest cultural ancestor of the sample. We show that, under neutral evolution, the time to the MRUA can be staggeringly larger than the time to MRCA in a single ancestor model, except when the average number of learning opportunities per individuals is small. Our results point out that the properties of cultural genealogies may be very different from those of genetic genealogies, with potential implications for reconstructing the histories of cultural traits.

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1. Introduction

One of the most intriguing questions in the study of cultural evolution is to what extent cultural data can inform us about the past. Researchers have used cultural datasets to estimate the dates of important historical and evolutionary events, such as the age of human language (Perreault and Mathew, 2012), the spread of ethno-linguistic groups (Gray et al., 2009), and the origin of the capacities for cultural transmission (Lind et al., 2013). In particular, phylogenetic methods from molecular systematics have been applied to cultural datasets to infer the ages of cultural “taxa”, such as languages, and the relationships between them (Gray and Atkinson, 2003; Kitchen et al., 2010; Walker and Ribeiro, 2010; Reesink et al., 2009; Rogers et al., 2009).

These methods are a useful complement to archeological and historical evidence of cultural change, but rely on data from assemblages of many cultural traits typified at a population level, and thus investigate *macroevolutionary* cultural change. For example, these studies usually treat languages as characteristic sets of lex-

ical, phonemic, and grammatical features shared by all members of a population. Individual cultural traits – e.g. words, techniques for making hand axes, oral literature, folksongs, childrearing practices, etc. – may have unique histories that are lost when considering only the larger systems they constitute at the macroevolutionary level. While we acknowledge the difficulty inherent in defining a ‘single’ cultural trait – indeed, many traits can be thought of as combinations or systems of component traits – we assert that whatever the definition, single traits spread due to the *microevolutionary* process of individual to individual transmission. In this paper, we develop a model of the history of a single cultural trait transmitted between individuals based on population size, mode of trait transmission, and current prevalence of the trait.

In order to investigate the history of a cultural trait we require a model of the genealogical process for learned traits. In population biology, the mathematical study of genealogies has flourished since the introduction of Kingman’s “coalescent”, a retrospective model of how lineages of gene copies merge in common ancestors (Kingman, 1982a,b,c). The coalescent predicts the statistical properties of genealogies and thereby enables the estimation of other aspects of population history such as ancestral population size. A central concept in genetic genealogies is the most recent common ancestor (MRCA), i.e., the most recent individual in the past whose gene copy is ancestral to all those in the present. The coalescent estimates that, for a population of size N , the expected time to MRCA

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is of the order of N generations (Hudson, 1991). Might retrospective models from population genetics shed light on the behavior of cultural trait genealogies, just as molecular systematics has done for cultural taxa? We argue that fundamental differences in the nature of cultural transmission make genetic genealogical models unsuited for culture. While genes are inherited uniparentally (or, in the case of recombination, biparentally), cultural traits can be inherited from multiple ancestors. For example, an oral story may be learned in repeated episodes from a number of sources.

Here we introduce a simple, neutral model of cultural genealogies in order to investigate the relationship between the individual-to-individual nature of cultural transmission and historical inference based on cultural data. Specifically, we model the history of learning events pertaining to a single cultural trait possessed by a group of individuals. Each individual has a variable, potentially large number of cultural ancestors—in contrast to models of genetic genealogies in which each individual has one or two ancestors. Individuals form their traits based on information inherited from their multiple ancestors—thus, a learning event may represent the partial or complete transmission of a trait. We first show that, for a sample of individuals drawn from a population, a cultural MRCA does not always exist. That is, the genealogical lines of the sampled individuals may fall into two or more disjoint sets, without ever intersecting. Alternately, we define a concept related to the MRCA but that identifies an individual that is guaranteed to have existed. We call this individual the *most recent unique ancestor* (MRUA), defined as the most recent single individual who is a source of cultural information for individuals in the sample. For any random sample of a population of fixed size and undergoing neutral cultural evolution, we show that the expected time to the MRUA grows hyper-exponentially with population size, and thus, above certain parameter values, is much larger than the time to MRCA in a uniparental model. This result highlights the need for more theory on historical inference based on cultural data.

2. Model

2.1. Defining the MRUA concept

The distinction between MRUA and MRCA exists because of differences between cultural and genetic inheritance. A single gene copy is inherited uniparentally, and has its origin in a single individual. This means that as we move backwards in time lineages of copies of a gene will eventually converge in the common ancestor. Even in the event of recombination, the gene copy has at most two parents and those lineages too will eventually merge in a common ancestor. By contrast, a person's cultural trait may have inputs from many sources. The original trait could have arisen in a single individual or among a group of individuals. In the latter case it is clear that no single MRCA exists. However, even if a trait has a single origin it may still be modified by subsequent inputs of information. The individuals who contribute this additional information may be “dead ends” in the genealogy, since their own learning lineages may never merge with the others in the sample. Fig. 1 depicts an example of a cultural genealogy as a directed graph. The nodes represent individuals in the genealogy, and arrows show ancestor–descendant relationships (arrows point from ancestor to descendant). At the top of the figure we have individual A, who possesses a cultural trait, let us say knowledge of a specific folksong. At some point in the past, A learned her song from B, C, and D. Prior to that, B and C learned it from E, thus E is their common ancestor. However, Individual D served as a learning model for A – perhaps contributing a new verse – without having learned anything from E. Thus, E is not a *common ancestor* for everyone in the genealogy, but she is still the earliest single individual who contributes to the song learned by A. For this reason, we refer to E as the *most recent unique ancestor*, or MRUA.

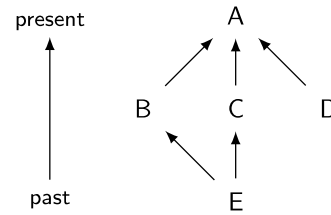


Fig. 1. Sample learning genealogy for a cultural trait (e.g. a folksong). While B, C, D, and E are all ancestral to A, only B and C share a common ancestor in E. D has no learning lineages that intersect with the other individuals in the genealogy.

In genetic evolution, origin and common ancestry coincide. As we have seen, in cultural evolution there may be no common ancestor, since: (1) individuals may independently invent a trait that already exists (e.g. Leibniz's and Newton's independent inventions of the calculus), and go on to serve as learning models; and (2) individuals may independently invent some information that gets incorporated into a trait even without possessing it themselves, as in the example of D above. Therefore, the origin of a trait for some group of individuals is represented by the MRUA, which plays a role analogous to the that of the MRCA in the neutral coalescent.

2.2. Learning model

To investigate the properties of cultural genealogies, we begin with a simple model of cultural transmission. We consider a fixed population of N individuals that evolves according to a continuous-time Markov process in which only two events can occur:

Replacement: A randomly selected individual is removed from the population and is replaced by a naive individual.

Learning: A randomly selected individual learns from another randomly selected individual.

The time between successive replacement events is exponentially distributed with rate r per individual, and the time between successive learning events is exponentially distributed with rate a per individual. Equivalently, we can say that replacement and learning events occur according to a Poisson process with rate $(a+r)N$. A given event is a replacement with probability $r/(a+r)$, and a learning event with probability $a/(a+r)$. The expected lifetime of individuals is $1/r$, and the expected number of learning events per lifetime is a/r .

This model allows individuals to acquire multiple cultural ancestors via multiple learning events in the course of a lifetime. We define a learning event as the transmission of some amount of information about a trait from one individual to another. We do not assume that the event causes the exact replication of a cultural trait, and we leave unspecified exactly how an individual forms her cultural trait from multiple inputs. While cultural transmission can be conceptualized in many ways (Henrich and Boyd, 2002), here we are concerned only with tracking genealogies of a single trait. In other words, regardless of the details of how cultural transmission occurs, we can consider anyone from whom an individual has learned as the individual's cultural ancestor. Note that in a multiple-ancestry model it is important to distinguish learning events from ancestors. Any number of learning events with the same ancestor, in fact, results in a single lineage in the genealogy (see Section 2.3).

2.3. Genealogical model

The aim of a theory of cultural genealogies is to infer the statistical properties of genealogies from knowledge of the process that generates them, which, in the present case, is the simple cultural transmission process introduced above. We are not tracking

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