

Empirical Sufficiency and Neutral Theory: Building Seriation and Classification Into Archaeological Models of Cultural Transmission☆

Mark E. Madsen

Department of Anthropology, Box 353100, University of Washington, Seattle WA, 98195 USA

Abstract

Despite growing application of formal cultural transmission models in archaeology, the common approach is synchronic and reconstructionist, yielding few testable conclusions about the archaeological record. Culture-historical methods, especially seriation, are natural observational tools for fitting cultural transmission models to archaeological data, given that seriation is inherently diachronic and treats change as evolutionary and continuous. Continuing previous research, I construct and evaluate statistical models linking neutral theory, models of regional interaction, and seriation solutions. To do so, I employ a computational model of unbiased transmission within a regional metapopulation which explicitly embeds paradigmatic classification as the bridge between trait transmission and culture-historical method. I assess the utility of the methods developed using a case study from Carl Lipo's study of Late Prehistoric ceramics from the Phillips, Ford, and Griffin study area.

☆Revision: 7617653 (2012-11-09)

Email address: mark@madsenlab.org (Mark E. Madsen)

URL: <http://madsenlab.org> (Mark E. Madsen)

1. Introduction

A key result of an evolutionary approach to archaeology is the realization that cultural transmission theory provides a grounding explanation for the success of culture-historical methods—and the seriation method in particular—in constructing chronologies and understanding regional-scale patterns in the archaeological record. Many of the early applications of formal transmission models in archaeology drew upon, and sought to enhance, traditional methods with the quantitative insights gained from theory.

Neiman (1995) introduced formal transmission models to archaeology in the form of the classic Wright-Fisher neutral theory, and used this model to study spatiotemporal patterns of interaction using ceramic types, given Dunnell's (1978) linkage of stylistic classes to homology and neutrality. Neiman further suggested that drift was sufficient to create the characteristic form of seriation solutions. Lipo, Hunt, Dunnell and this author (1997) employed seriation not to construct chronology but to map regional-scale patterns of interaction, by partitioning solutions into subsets of assemblages that seriate together successfully. Lipo (2001) extended this line of reasoning and deepened our understanding of the methods required to produce such analyses with real artifact assemblages.

In addition to grounding culture-historical methods in a mechanistic scientific theory, this line of research strongly suggests that *culture-historical methods are the natural observational tools for testing hypotheses that arise when considering cultural transmission processes as archaeological explanations*. The advantage of using seriation of analytic classes as the observational method for linking cultural transmission theory to archaeological data is that seriation treats change through time as continuous. Change is monitored through the frequencies of analytic artifact classes chosen to respond to variation over particular temporal and spatial scales. If we construct transmission models in such a way that their observable consequences are measured through seriations, then we avoid synchronic reconstructionism in applying cultural transmission theory to the archaeological record. A seriation *solution*, comprising a set of assemblages measured with a set of archaeological classes which fully meet the requirements of the seriation method, is therefore the basic observational unit I intend to study in my dissertation research.

Development of seriation as a tool requires methodological research. Even with innovations by Lipo and colleagues (Lipo et al. 1997; Lipo and Madsen 2000; Lipo 2001), three challenges remain. The first is “rewriting” neutral models to include observational units separate from the “trait” information which flows within the population; observational units which represent the multidimensional nature of archaeological classes and types. The second challenge is matching the level of modeling to the scale at which we have measured variability (not just central tendencies) in a given empirical case. In many cases, assemblages are characterized by a single set of artifact class frequencies, which means that descriptions of variability can only be obtained at the scale of multiple assemblages. This requires models of cultural transmission within multiple populations, with the model structured in a manner appropriate to the settlement and land-use patterns involved. The third need is development of statistical models which link the structure and parameters of cultural transmission models to variation in the quantitative properties of seriation solutions, when variation is measured using archaeological classes and seriated using Lipo's “iterative pairwise frequency seriation” method.

I propose to address these methodological and theoretical challenges in my dissertation research through numerical simulation in two phases of modeling and analysis. The first phase of research focuses upon understanding the dynamical and statistical behavior of cultural transmission models augmented with archaeological classifications. The second phase of my research will consider the

methodological and practical issues involved in applying the result of Phase I to real archaeological data. Carl Lipo's (2001) dissertation research greatly expanded our initial foray into using seriation to measure interaction between populations. In that work, he identified several clusters of ceramics assemblages in the St. Francis and Memphis portions of the Phillips et al. (1951) study area that appear to represent strongly interacting populations, outside of which interaction was much less intense. Given multiple seriation solutions (which display different average assemblage richness, and evenness of classes represented), I ask *what model of information flow within a cultural metapopulation best accounts for the observed pattern of seriation solution groups, and intra-seriation patterns of richness and evenness?* Furthermore, I consider how we can perform statistical inference to select the model which represents the best fit to specific seriations obtained in the course of an archaeological study.

2. Case Study: Regional Interaction from Mississippian Ceramic Seriations

From 1940 through 1948, Philip Phillips, James A. Ford, and James B. Griffin made systematic collections of ceramics across the Lower Mississippi River Valley (Figure 1).¹ The PFG study made collections from 383 different locations, producing over 346,000 ceramic samples Phillips et al. (1951). This monumental study firmly established the basic chronology of later prehistoric occupation in the Valley, demonstrated the utility of Ford's particular approach to ceramic seriation and chronology building, and gave rise to the basic culture-historical concept of "phase" as a space-time unit (Dunnell 1985; Lyman et al. 1997; O'Brien and Lyman 1998; Lipo et al. 1997; Lipo 2001).

For 46 assemblages collected by PFG in the St. Francis and Memphis areas, Lipo (2001) performed new seriations using a modification of Ford's deterministic frequency seriation technique. The original PFG seriations presented solutions for each analytical subdivision of the study area, and had departures from the unimodal expectation of the method Dunnell (1970). To yield solutions which meet the assumptions of the method, it is clear that not all assemblages will fit in the same seriation solution. Using error estimates for frequencies given binomial error terms to test whether differences in frequencies were significant, Lipo used an iterative approach to construct the largest seriation groupings possible from the original PFG solution. This type of seriation result I term a "*seriation solution group*," and this class of solutions are, I claim, the best archaeological observable for measuring the differences between differing models of cultural transmission within and between a set of archaeological assemblages, given diachronic and time-transgressive data. The resulting seriation groups for the St. Francis and Memphis study areas are shown in Figure 2.

Lipo's study area, given new fieldwork, comprised a portion of the original St. Francis and Memphis areas from the PFG study, but he also created seriation solution groups for the full set of assemblages in both PFG analytical areas (which met sample size requirements). These solutions, which are the result also of pairwise significance testing, are shown in Figure 3. The spatial extent of each solution group is mapped in Figure 4. Not only do these seriations yield a temporal order for assemblages in each spatial area, but immediately we can see that seriation groups as a whole differ in ways which can be related quantitatively to the statistical properties of an unbiased cultural transmission model. Seriation groups shown here differ in average class richness, and the evenness of frequencies. For example, Group 1 and Group 5, for example, have greater richness and a flatter diversity profile than Group 2b or Group 7.

¹Hereafter, the study and its authors are referred to as "PFG" for brevity.

Such differences arise in neutral theory principally through differences in the amount of new variation introduced into a population, either through endogenous innovation or the flow of information from outside a population (loosely, “migration”).² Richness and evenness are measured in seriation with respect to a specific classification. These variables are thus always relative to a “design space” (O’Brien et al. 2010), and we need to understand the degree to which different instances of a neutral model (e.g., innovation rates and migration patterns) yield distinguishable values in that design space. Conversely, we need to understand the degree to which different instances of neutral models are equifinal when observed through a particular design space.

Therefore, the goal of my case study is to understand what *classes* of neutral models can best account for the histories seen in seriation solution groups both from Lipo’s study area and for the remainder of the full PFG collection. Of the 383 assemblages PFG collected, only 220 assemblages have decorated sherds (the remainder being representing by Bell Plain, Neely’s Ferry Plain, or both. Of the assemblages with decorated sherds, only 63 assemblages have more than 50 decorated sherds. I intend to use as many of these assemblages as possible (given consideration of sample size effects) to expand the seriation solutions created by Lipo (2001) and widen the area over which we understand the nature of interaction patterns in the Lower Mississippi River Valley.

3. Research Problems

My dissertation research comprises five specific research questions:

Research Question 1 (Adequacy of Unbiased Cultural Transmission).

Even though individual copying behavior is heterogeneous, with individuals displaying biases of different strength and “direction,” these biases may cancel out when observed at the level of whole populations, particularly when averaged over time. To what extent can archaeologists ignore models of bias from “dual-inheritance” theory and simply use unbiased transmission models to explain archaeological phenomena? This question is important because although models of copying bias are psychologically realistic compared to unbiased transmission, the results of such bias may be undetectable when averaged over time and over a heterogeneous population.

Research Question 2 (Behavior of Unbiased Transmission in Design Space).

How do the quantitative descriptions of expected richness and evenness change as we observe trait transmission through the analytic filter of paradigmatic classifications with the same characteristics we observe in real artifact typologies?

Research Question 3 (What Metapopulation Dynamics Cause Multiple Seriation Solutions?).

In a metapopulation model of unbiased transmission, with variable innovation rates, variable “migration” rates between communities, and demic colonization and extinction, what models lead to multiple seriation solutions within a regional population?

²I use the term “migration” and “migration rate” throughout given its prevalence in the theoretical literature, and am not implying residential relocation of people. Migration here denotes non-local information flow: individuals do move around a landscape, and have opportunities to spread information outside their own immediate social groups or local populations.

Research Question 4 (What Drives Richness and Evenness Patterns in Seriation Solutions?).

Seriation solution groups seem to vary in overall richness (the number of classes represented across all assemblages in a solution group) and average evenness (calculated for each assemblage and then averaged). What statistical model best relates the characteristics of the generating metapopulation model with the richness, evenness, and size distribution of seriation solutions?

Research Question 5 (Accounting for Differences in PFG Seriation Solutions).

Given modeled relationships between seriation solution groups and interaction structure, which specific models of unbiased transmission in a regional metapopulation best account for each solution group in the PFG case study?

4. Research Methods

4.1. Model Construction

In this research, I employ a “forward-time” approach to computational modeling of unbiased cultural transmission, by contrast to most modeling in theoretical population genetics today, which employs the coalescent or “backward-time” approach (Kingman 1977; Durrett 2008; Wakeley 2008). In archaeological research, we are interested in the entire distribution of variants which transmitted through the population, samples of which may be deposited and become part of the archaeological record regardless of which variants ultimately leave descendants in later generations.

In this research, I employ a framework written by the author specifically for cultural transmission simulations. This project calls for integrating computation models of archaeological classification and seriation, which require code beyond that supplied by population genetics frameworks. My simulation codebase is called **TransmissionFramework**, and is available as open-source software.³ **TransmissionFramework** runs on any platform capable of supporting a Java 1.6+ runtime, with optional scripts requiring Ruby 1.9+.

4.2. Simulating Archaeological Classification

Currently, **TransmissionFramework** like most cultural transmission simulations has a single representation of cultural variants, and all counts and frequencies tracked have “traits” as the unit of both transmission and observation. The framework is flexible enough, however, to “observe” other units which are functions of traits. I will implement paradigmatic classification (with multiple hierarchical levels) given this capability.

In the abstract, a paradigmatic classification is a set of dimensions along which variation can occur, split into modes or attributes which describe discrete portions of the variability in that dimension (Dunnell 1971). The classification itself is constructed by intersecting each dimension, to form their combinations (Figure 7). Formally, the set of classes is the discrete product space of the dimensions. In a real classification used by archaeologists, each dimension and all of the modes would possess detailed definitions called *significata*, with each class thus possessing a necessary and sufficient definition for membership. In the abstract formal version described here, since I want to understand the quantitative effects of observing trait transmission through a classificatory filter of given dimensionality and granularity, definitions with archaeological content for classes are omitted from the simulation model.

³**TransmissionFramework** can be downloaded or the code examined at <http://github.com/mmadsen/TransmissionFramework>.

A classification model comprises (a) A set of traits which form the actual transmitted information, and where copying and innovation occurs. (b) Some number of observational dimensions, each specified by some number of attributes, and (c) A mapping which describes how traits are assigned to dimensions and modes for observation. These elements will be implemented in **TransmissionFramework** in such a way that dimensionality and granularity of classes is adjustable for each simulation run.

4.2.1. *Implementing Metapopulation Cultural Transmission*

Implementing multiple population or metapopulation models in **TransmissionFramework** is mostly complete. Individual agents in the framework may be tagged with identifiers which allow any statistic to be measured for the subset of agents holding that identifier. An example might be "Deme 2" as a tag, in which case trait counts are calculated not only for the entire population, but separately for Deme 2. Agents can have any number of tags, and tags can be changed. The latter feature allows easy implementation of permanent or temporary migration, by switching "Deme 2" for "Deme 6" and, possibly, back again.

What remains to be implemented is the modeling of a process for creating new demes and having existing demes go extinct. There are two requirements. First, it should be possible to specify a probability distribution governing deme lifetime and deme birth rate, and allow random configurations to unfold across many simulation runs. This allows the study and statistical analysis of transmission in evolving metapopulations in the abstract. Second, it should also be possible to provide a *configuration* for a metapopulation, with a specific number of demes, and an order of occupation and deme durations. This will allow representing particular empirical cases, such as assemblages from the PFG case study, so that we can analyze the properties of transmission across a specific region.

Finally, new demes should be populated by colonization from existing demes, and it should be possible to specify different models for this colonization. Slatkin (1977) distinguished between two extremes: a "migrant-pool" model whereby colonists for a new deme are drawn randomly from the whole metapopulation, and a "propagule pool" model, where colonists are chosen from a single extant deme in the population. The migrant-pool model will allow creation of island model scenarios useful for testing, while the propagule-pool model allows the modeling of more realistic empirical scenarios where settlements are derived from known sources, given historical continuity of artifact classes.

4.3. *Model Verification*

Verification answers the question, "how accurately does a computational model solve the underlying equations of a theory for the observable quantities of interest." In a more general sense, verification addresses how well a computational system reflects the conceptual model an investigator has in mind, but in this research I employ the NRC's mathematically-oriented definition since it provides a clear way to determine whether a model has been verified for the purposes at hand. A key recommendation from the NRC report is to employ a layered strategy to verify complex, multi-scale computational models. In this research, I address verification at two scales: verification of the dynamics of unbiased transmission within a single population, and verification of the dynamics within and between demes in a metapopulation.

TransmissionFramework is constructed to be easily testable, in order to verify its functionality as new models are constructed or features added. Unit tests (or code verification) are a "best practice" from software engineering that bundle integral software tests with the actual simulation code, to verify that code acts as expected. An example from the current version of **TransmissionFramework** is a test which automates the following sequence: (a) Construct a dimension with eight traits or modes;

(b) Construct 88 agents, and have each agent adopt one of the traits in different proportions; (c) Verify that the total of trait counts across all traits at the end of all adoption events is 88. Other tests verify different aspects of the code base, and taken together, unit tests provide a means of ensuring that the low-level operations which compose a computational model are performing as specified.

Solution verification begins where unit tests end, and are often called “functional tests” in software engineering, since they verify the proper functioning of a system from end to end: given known inputs, does the system yield known good outputs? For unbiased transmission in a single population, I verified a key observable quantity in the well-mixed Wright-Fisher infinite-alleles model within **TransmissionFramework**.

The number of variants expected K_n in a sample of size n is a good test of the proper functioning of a copying model because for a computational model to report a correct distribution of values for K_n , both the copying rules and innovation rules in the model must be functioning correctly, and be called in the correct proportions per unit time.

Using the frequency spectrum of the WF-IA, [Ewens \(2004, Eq. 3.94\)](#) gives the expected value of K_n for a specific θ value:

$$\mathbb{E}(K_n) = \int_0^1 (1 - (1 - x)^n) \frac{\theta}{x} (1 - x)^{\theta-1} dx \quad (1)$$

I performed multiple simulation runs at θ values ranging from 2 to 40, for 5000 generations in a simulated population of 2000 individuals. Each parameter combination was represented by 3 simulation runs. The initial transient behavior of the model is discarded from data analysis by skipping the first 750 generations, given the mixing time analysis by [Watkins \(2010\)](#). At each time step in a simulation run, the simulator took a sample of 30 individuals and tabulated the traits held by those individuals, and recorded the value of K_n . This yielded 408,478 samples of K_n across across validation runs. For each value of θ , I calculated the mean and standard deviation of K_n values.

Table 1 compares the expected values with the distribution of simulated values. In all cases, the analytical results are extremely close to the observed mean K_n values from simulation, and certainly well within 1 standard deviation. At least from the perspective of K_n as a model observable, **TransmissionFramework** properly implements the well-mixed Wright-Fisher infinite-alleles model. Additional observable quantities may require verification during my dissertation research, and I will follow the same approach outlined here.

5. Simulation Experiments: Research Questions 1-4

5.1. Question 1: *Adequacy of Unbiased Cultural Transmission*

The first research question is wholly theoretical, and addresses whether archaeologists need to employ detailed models of individual-scale transmission rules in order to explain archaeological data, particularly at and above the assemblage scale. The alternative hypothesis, which I propose here, is that although we know individual humans display various transmission biases (e.g., [Boyd and Richerson 1985](#); [Henrich and Gil-White 2001](#); [Henrich 2001](#); [Henrich and Boyd 1998](#)), in a population heterogeneous for these rules, the statistical properties of social learning will converge at a population level to appear unbiased. This hypothesis is also a possible explanation for why Bentley’s recent work on contemporary data sets (some of which I have collaborated upon), fit some of the expectations of random copying, even though we know modern individuals often display various transmission biases ([Hahn and Bentley 2003](#); [Herzog et al. 2004](#); [Bentley 2005, 2007](#); [Bentley et al. 2007, 2009](#)).

I propose a simple experiment. **TransmissionFramework** already has implementations of conformist and pro-novelty bias, and agents can have heterogeneous copying (and innovation) rules. If the alternative hypothesis is correct, then heterogeneous populations which are mixtures of conformism and pro-novelty bias will display population-level outcomes for trait richness and evenness that fit the expectations of a comparable neutral model. The degree to which this is true will likely depend upon the relative strengths of conformist and pro-novelty bias, and the relative proportion of each strategy in the population. Thus, the desired outcome of this analysis is a “phase diagram” displaying the region of parameter space in which heterogeneous populations have unbiased population-level outcomes.

5.2. Question 2: *Behavior of Unbiased Transmission in Design Space*

The second research question asks how the statistical properties of unbiased cultural transmission, and specifically the WF-IA neutral model, can be measured when trait evolution is observed through analytic classifications of the kind used in archaeology. Since the analyst controls the construction of a classification independent of the information which was transmitted, the statistical measures we typically examine for transmission models, will necessarily be transformed into functions of the dimensionality and granularity of the classification.

I propose to address research question 2 by the following simulation protocol:

1. Construct a set of dimensions for observation, with at least five nested hierarchical levels. Few archaeological studies have employed more than two, or three at the extreme, but if our goal is to understand how the mean and variance of quantitative variables, such as class richness, scale with the dimensionality of a classification, a larger number of dimensions is necessary to understand whether scaling is linear or nonlinear, for example.
2. Construct several alternative sets of modes or attributes for each dimension, as arbitrary partitions of the unit interval. Each dimension should be cut into 2, 4, 8, and 16 modes, and for each level of mode granularity, at least eight different partition sets will be generated.
3. Each set of underlying parameters for the WF-IA model (population size, innovation rate) will be replicated 100 times for each configuration of the observational classification.
4. For each run, after the simulation reaches equilibrium (i.e., the number of “generations” specified by the mixing time analysis by [Watkins 2010](#)), samples of both traits and observational classes of size 50, 100, 500, and 1000 will be taken at intervals using the time-averaging protocol described in [Madsen \(2012\)](#).
5. Given the analysis in [Madsen \(2012\)](#), there seems to be two regions of behavior for the neutral WF-IA model: very small innovation rates, with $\theta < 1.0$ where copying dominates the dynamics of trait frequencies, and intermediate to high innovation rates, with $\theta > 1.0$ where innovation pressure dominates trait frequencies. A set of innovation rates will be chosen to cover these regions, but fewer values than employed in my recent analysis, where many of the θ levels showed little difference in dynamics.

Samples will be post-processed to describe the distribution of richness K_n and evenness values (using a normalized version of the t_f measure employed by [Neiman \(1995\)](#), called the “index of qualitative variation” or IQV ([Wilcox 1973](#))).

Given these data, I will formulate a candidate set of statistical models with richness and evenness as measured by the simulated classifications, as response variables, and predictor variables including the size of the design space (i.e., number of classes, or simply dimensionality of the classification), and the parameters which drove the neutral WF-IA model (i.e., innovation rate).

5.3. Question 3: *What Metapopulation Dynamics Cause Multiple Seriation Solutions?*

The third research question asks how regional variation in population structure and information flow within a transmission process results in seriation solutions which are partitioned into sets, as occurs in the case study. The first step in analyzing this question is to constrain the notion of “population structure” and migration matrices to be studied, since there are an infinite set of possible structures one could study.

Several disciplines have studied “spreading” or diffusion processes on structures which approximate Figure 5, Model B. Epidemiology and studies of information spreading on social networks have yielded a large body of literature on the effects of spatial structure on diffusion processes. For my purposes, the results suggest that several factors matter in changing the ease with which information flows within a structured population:

1. The presence or absence of long-distance dispersal or connections;
2. The number of strong connections between subpopulations; alternatively, the “average degree” in a social network graph;
3. The presence of clustering among subpopulations, both spatially and in connections and migration flows.

Simple models of these factors are shown in Figure 9, where “connections” indicate regular information flow and copying between at least some individuals in those demes. In Model 1, demes are connected to their spatial neighbors, but also possess long-distance links to demes which might not be neighbors. Model 2 is the opposite, with demes are connected only to spatial neighbors. Model 3 is the same as Model 2, but with much sparser connections among spatial neighbors. Model 4 introduces clustering of migration connections, such that there is constrained information flow among demes.

I propose to use these four models the basis for constructing simulated metapopulations, and performing seriations of the simulation output measured through analytic classification. The patterns of connections shown in these four models actually correspond to migration rates defined between demes in the metapopulation. The classification will be chosen to have the same dimensionality and structure as the PFG types which compose the case study. Additionally, although Figure 9 displays a static snapshot of connections, simulations will employ a model where demes have durations and exit the model, with new demes being added with random links corresponding to the population structure model being tested. The diachronic aspect to population structure models is crucial for creating transmission simulations which will seriate like real archaeological data.

With respect to the four models, their structure leads to the following predictions. The first model, with long-distance connections, will not easily split into multiple seriation solutions without extremely high levels of endogenous innovation to “drift out” information flowing in from all parts of the metapopulation. In contrast, the fourth model with clustering should yield seriation solution groups for each of the densely connected structures, and the “boundaries” between seriation groups will correspond to the areas of sparser linkage. This will occur at intermediate and even low innovation rates.

At a given level of endogenous innovation, Model 2 should always yield larger seriation solution groups than Model 3, since lower migration and nearest-neighbor migration patterns should yield a classic “isolation by distance” dynamic. I propose to examine a range of endogenous innovation rates relative a fixed intensity of migration across populations configured as Model 2 and 3 to determine if a “critical ratio” of migration rate to endogenous innovation yields partitioning into seriation solutions, relative to the density of connections.

5.4. *Question 4: What Drives Richness and Evenness Patterns in Seriation Solutions?*

The fourth research question assumes the results of Question 3, and asks what factors of the transmission process in a metapopulation drive the differences in class richness and evenness seen in different seriation solution groups. Recall from Figures 2 and 3 that solution groups vary in the number of classes represented, and the degree to which a seriation solution is dominated by one or a few classes, or whether many classes have intermediate frequencies.

In the single-population neutral model, both richness and evenness are determined by the innovation rate. In a metapopulation, these variables will be driven both by innovation, but also the pattern and rates of migration between demes. For example, the larger a seriation solution group, the greater mean richness ought to be, at a constant rate of innovation. Since more demes are strongly connected, there are more demes for a rare trait or class to occupy and persist within the population, so larger seriation solution groups should have “reservoir effect,” with higher richness overall.

I propose to monitor richness and evenness patterns during the simulation runs executed to address Question 3, and examine the relationship between migration models and these variables. No additional simulation runs will need to be done, and these appear as separate research questions because they represent different aspects of examining the behavior of unbiased cultural transmission through seriation methods. The same analysis strategy will be used, with a set of candidate statistical models, with richness and evenness distributions across and within seriation solution groups as response variables, and the same predictor variables as described in the previous section. In publication, these results will be combined with the results from Question 3.

6. Model Inference for PFG Ceramic Assemblages

From 1940 through 1948, Philip Phillips, James A. Ford, and James B. Griffin made systematic collections of ceramics across the Lower Mississippi River Valley (Figure 1).⁴ The PFG study made collections from 383 different locations, producing over 346,000 ceramic samples Phillips et al. (1951). This monumental study firmly established the basic chronology of later prehistoric occupation in the Valley, demonstrated the utility of Ford’s particular approach to ceramic seriation and chronology building, and gave rise to the basic culture-historical concept of “phase” as a space-time unit (Dunnell 1985; Lyman et al. 1997; O’Brien and Lyman 1998; Lipo et al. 1997; Lipo 2001).

Of the 383 assemblages collected in the original Phillips et al. (1951) survey, only 220 assemblages have decorated sherds. Of the assemblages with decorated sherds, only 63 assemblages have more than 50 decorated sherds (Table 2). Six of these assemblages were also recollected by Lipo (2001) for his dissertation work, increasing the sample sizes at those localities, and verifying the quality of the original data collection done by Phillips et al.

⁴Hereafter, the study and its authors are referred to as “PFG” for brevity.

The goal of my case study is to apply the results of examining the four theoretical and methodological questions to explaining the quantitative characteristics of seriation solution groups from the Phillips, Ford and Griffin survey. Not only do seriation solutions, such as those depicted in Figure 2 and 3 indicate potential chronological relationships, but as proposed here, they are an observable, empirically sufficient window into the dynamics of cultural transmission in each geographic area during the Late Prehistoric period in the Mississippi River valley.

Given a set of seriation solutions from the selected PFG assemblages, I propose to test which of the population structure models (e.g., Figure 9) best account for the groupings of assemblages across the study area. The variables used to describe seriation solutions are those studied above: class richness, evenness, and the “size” or scope of seriation groups in a relative sense across the region. These variables are measured relative to the modified PFG classification used by Lipo (2001) to conduct seriations (and employed here as well).

There is no simple way to determine a “fit” between population structure models and these quantitative descriptions of a seriation solution. I propose to use simulation once again to understand the likelihood that a specific interaction structure leads to seriation solutions with the specified combination of descriptors, in the context of a given classification “design space.” The approach is an application of the model selection and multimodel inference approach described by (Burnham and Anderson 2002).

Although my main interest in this analysis is constructing and testing methods for making cultural transmission models empirically sufficient using seriation methods, a concrete outcome of this analysis should be a “map” of regional differences in interaction models and relative differences in innovation rates, over the duration of seriation solutions for the Late Prehistoric period in the PFG study area, enhancing and extending the analysis done by Lipo (2001) for the northern section of the study area.

7. Summary

This research proposes to address the empirical sufficiency of cultural transmission models employed in archaeology, building methods for studying transmission at regional scales, using assemblage-level artifact class frequencies (from published or newly collected data), and with strong methods for evaluating the relative support the data provide for alternative models. I propose to do so not by increasing the psychological realism of the models themselves, but by constructing archaeologically appropriate measurement tools to bridge model and observation.

I propose construction and analysis of a computational model incorporating solutions to both problems, and demonstrate the utility of the results by an expansion of the analysis begun by myself and colleagues in Lipo et al. (1997), and greatly expanded by Lipo (2001). I break this analysis into five research questions. The first four address specific theoretical and methodological questions, the results of which will be submitted to journals for publication. My dissertation draft will include the four manuscripts (or publications), a review of the theoretical models, a discussion of the state of cultural transmission modeling in archaeology, documentation of the computational model and tests of its validity, and the results of my case study of Late Prehistoric ceramic assemblages in the Lower Mississippi River Valley.

References

Bentley, R. 2007. Fashion versus reason-then and now. *Antiquity*, 81(314):1071–1073.

- Bentley, R., Lipo, C., Herzog, H., and Hahn, M. 2007. Regular rates of popular culture change reflect random copying. *Evolution and Human Behavior*, 28(3):151–158.
- Bentley, R., Madsen, M., and Ormerod, P. 2009. Physical space and long-tail markets. *Physica A: Statistical Mechanics and its Applications*, 388(5):691–696.
- Bentley, R. A. 2005. Academic copying, archaeology and the english language. *Antiquity*, 80(307):196–201.
- Boyd, R. and Richerson, P. 1985. *Culture and the Evolutionary Process*. University of Chicago Press, Chicago.
- Burnham, K. and Anderson, D. 2002. *Model selection and multimodel inference: a practical information-theoretic approach*. Springer Verlag.
- Dunnell, R. 1970. Seriation method and its evaluation. *American Antiquity*, 35(3):305–319.
- Dunnell, R. 1985. Archaeological survey in the lower mississippi alluvial valley, 1940-1947: A landmark study in american archaeology. *American Antiquity*, 50(2):297–300.
- Dunnell, R. C. 1971. *Systematics in prehistory*. Free Press, New York.
- Dunnell, R. C. 1978. Style and function: A fundamental dichotomy. *American Antiquity*, 43(2):192–202.
- Durrett, R. 2008. *Probability models for DNA Sequence Evolution*. New York, Springer, 2nd edition edition.
- Ewens, W. J. 2004. *Mathematical Population Genetics, Volume 1: Theoretical Introduction*. New York, Springer, 2nd edition.
- Hahn, M. W. and Bentley, R. A. 2003. Drift as a mechanism for cultural change: an example from baby names. *Proceedings of the Royal Society Biology Letters B*, 270:S120–S123.
- Henrich, J. 2001. Cultural transmission and the diffusion of innovations: Adoption dynamics indicate that biased cultural transmission is the predominate force in behavioral change. *American Anthropologist*, 103(4):992–1013.
- Henrich, J. and Boyd, R. 1998. The evolution of conformist transmission and between-group differences. *Evolution and Human Behavior*, 19:215–242.
- Henrich, J. and Gil-White, F. 2001. The evolution of prestige: freely conferred deference as a mechanism for enhancing the benefits of cultural transmission. *Evolution and Human Behavior*, 22:165–196.
- Herzog, H. A., Bentley, R. A., and Hahn, M. W. 2004. Random drift and large shifts in popularity of dog breeds. *Proceedings of the Royal Society of London Series B-Biological Sciences*, 271:S353–S356.
- Kingman, J. 1977. The population structure associated with the ewens sampling formula. *Theoretical Population Biology*, 11(2):274–283.

- Lipo, C. and Madsen, M. 2000. Neutrality, "style," and drift: Building methods for studying cultural transmission in the archaeological record. In Hurt, T. D. and Rakita, G. F. M., editors, *Style and Function: Conceptual Issues in Evolutionary Archaeology*, pages 91–118. Bergin and Garvey, Westport, Connecticut.
- Lipo, C., Madsen, M., Dunnell, R., and Hunt, T. 1997. Population structure, cultural transmission, and frequency seriation. *Journal of Anthropological Archaeology*, 16(4):33.
- Lipo, C. P. 2001. *Science, Style and the Study of Community Structure: An Example from the Central Mississippi River Valley*. British Archaeological Reports, International Series, no. 918, Oxford.
- Lyman, R., O'Brien, M., and Dunnell, R. 1997. *The rise and fall of culture history*. Springer.
- Madsen, M. E. 2012. Unbiased cultural transmission in time-averaged archaeological assemblages. *ArXiv e-prints*, 1204.2043.
- Neiman, F. D. 1995. Stylistic variation in evolutionary perspective: Inferences from decorative diversity and interassemblage distance in illinois woodland ceramic assemblages. *American Antiquity*, 60(1):7–36.
- O'Brien, M. and Lyman, R. 1998. *James A. Ford and the growth of Americanist archaeology*. Univ of Missouri Pr.
- O'Brien, M., Lyman, R., Mesoudi, A., and VanPool, T. 2010. Cultural traits as units of analysis. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 365(1559):3797–3806.
- Phillips, P., Ford, J., and Griffin, J. 1951. *Archaeological Survey in the Lower Mississippi Alluvial Valley, 1940-1947*. Papers of the Peabody Museum of American Archaeology and Ethnology 25. Harvard University, Cambridge.
- Slatkin, M. 1977. Gene flow and genetic drift in a species subject to frequent local extinctions. *Theoretical population biology*, 12(3):253–262.
- Wakeley, J. 2008. *Coalescent Theory*. Cambridge, Harvard University Press.
- Watkins, J. 2010. Convergence time to the ewens sampling formula. *Journal of Mathematical Biology*, 60:189–206.
- Wilcox, A. 1973. Indices of qualitative variation and political measurement. *The Western Political Quarterly*, 26(2):325–343.

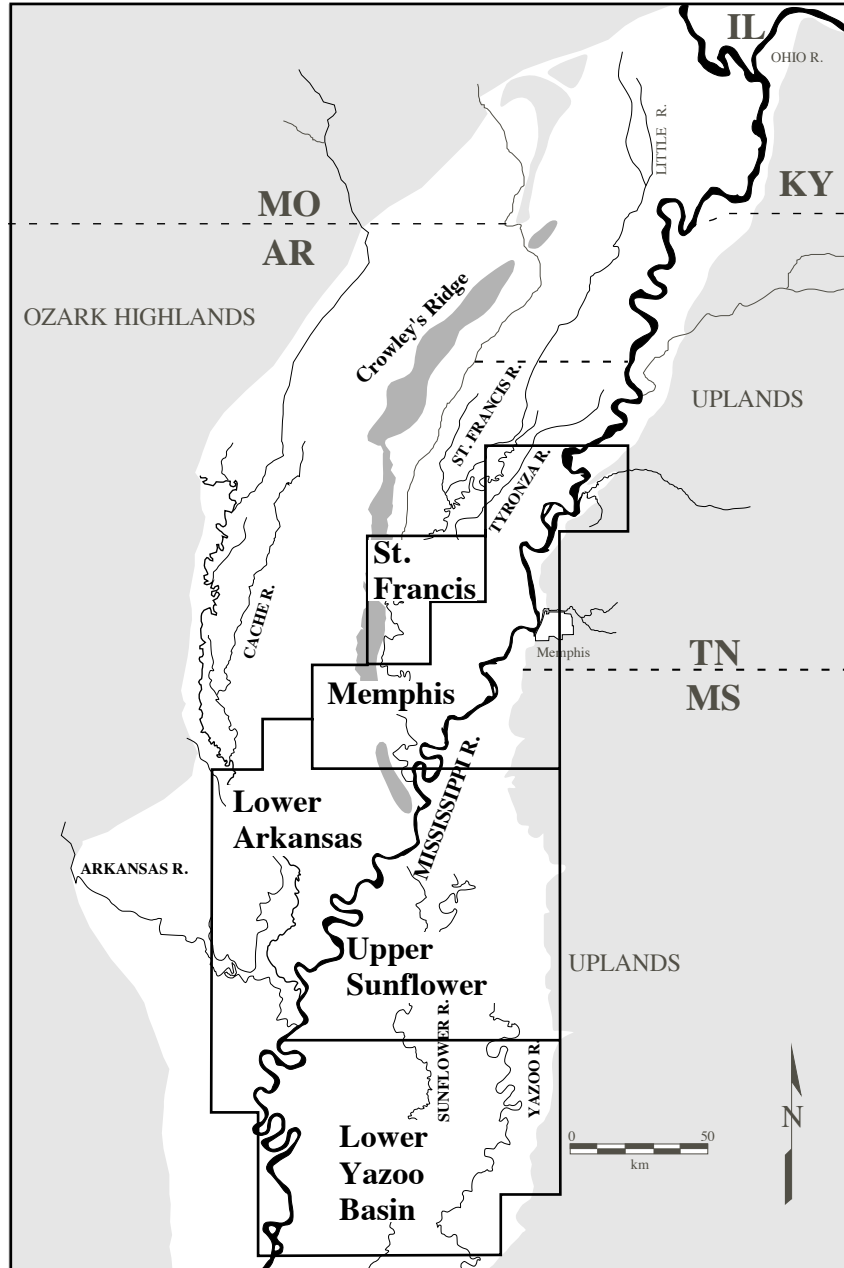


Figure 1: Subdivision of the [Phillips et al. \(1951\)](#) study area into arbitrary analytic units by James Ford. Reproduced with permission from [Lipo \(2001, Figure 2.3\)](#).

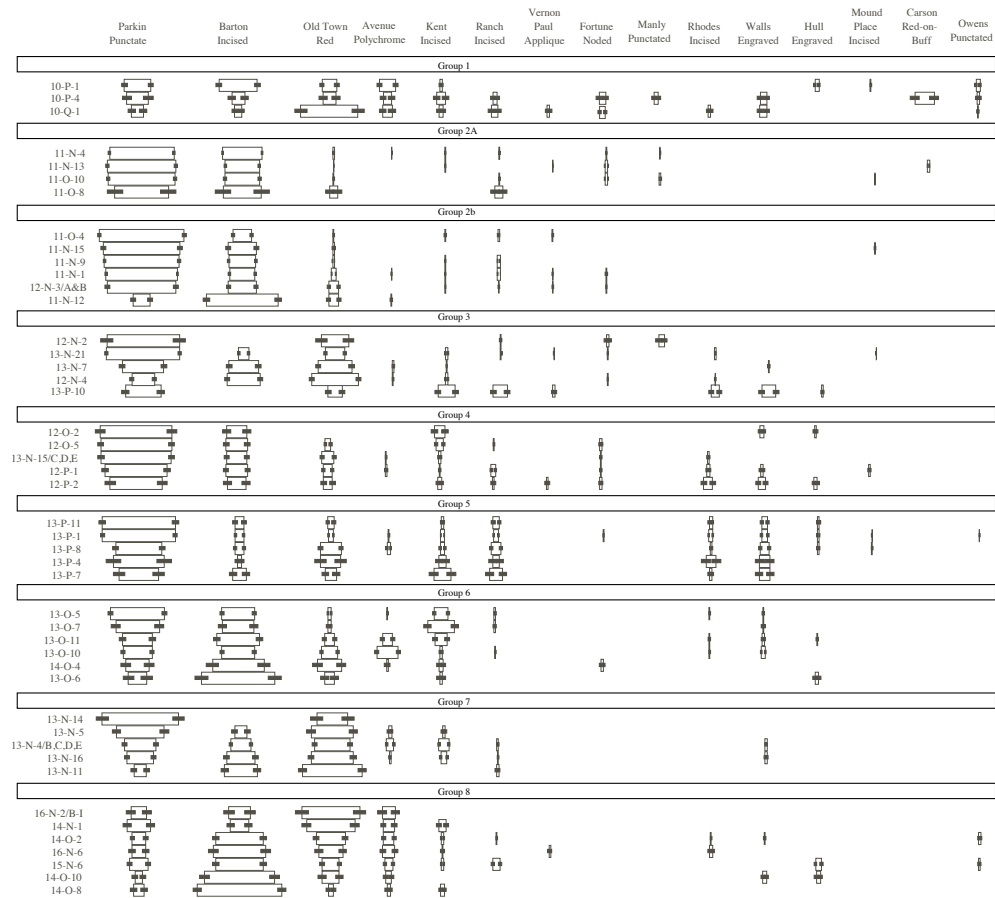


Figure 2: Results of iterative deterministic seriation by Carl Lipo for PFG assemblages in the combined Memphis and St. Francis area. The eight solution groups are the largest seriations that could be formed using the assemblages without violating the requirement of unimodality within binomial error limits. Reproduced with permission from [Lipo \(2001, Figure 4.4\)](#).

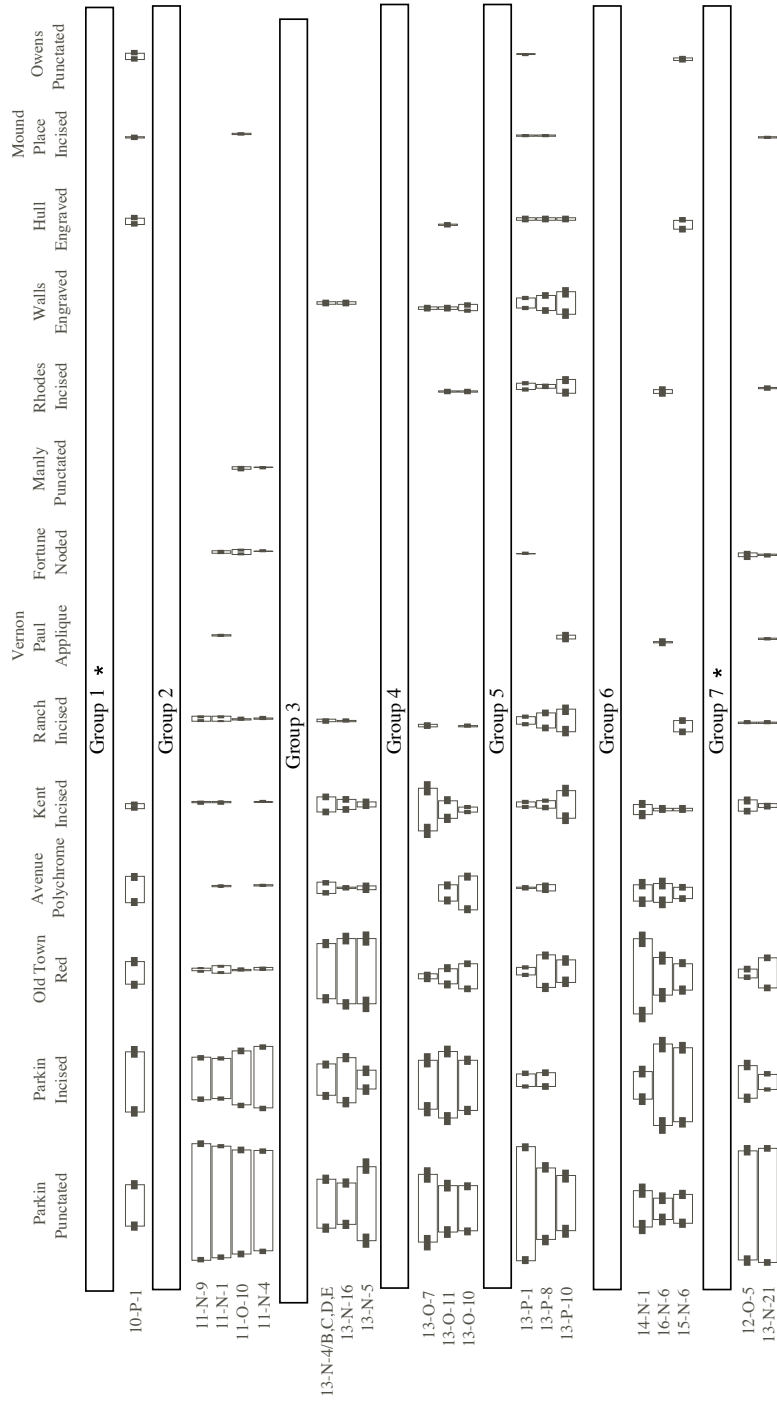


Figure 3: Results of iterative seriation with pairwise significance testing. Groups 1 and 7 have no implied order given < 3 assemblages. Reproduced with permission from Lipo (2001, Figure 4.11).

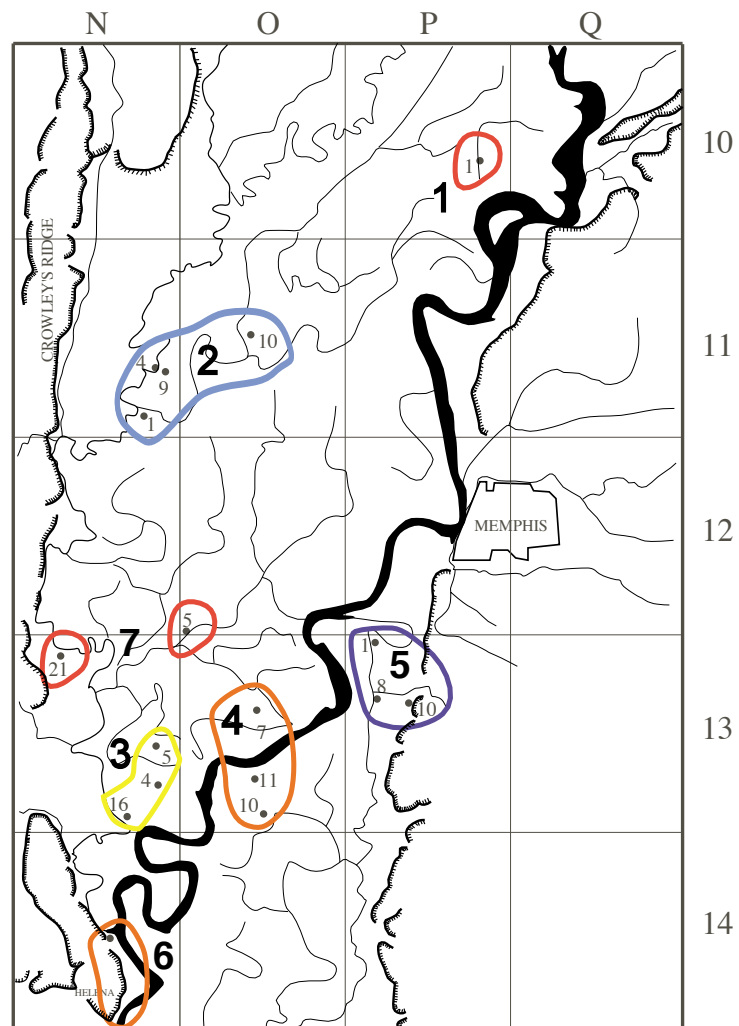
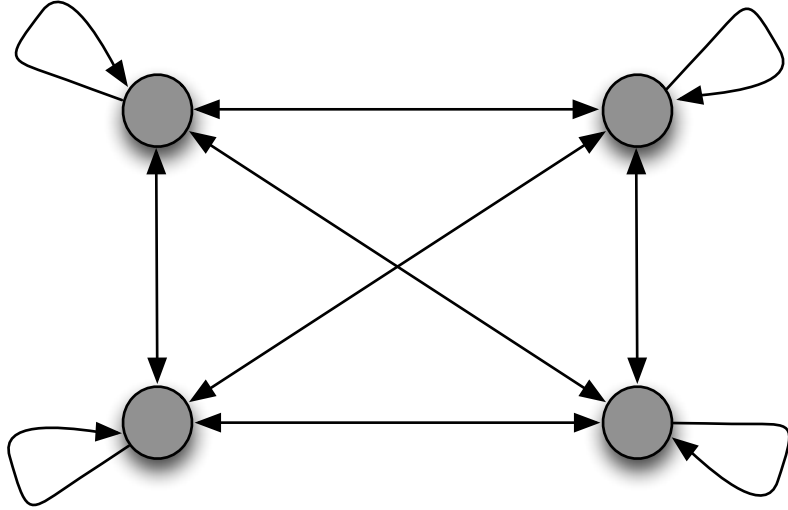


Figure 4: Spatial pattern of assemblages from seriation solutions in Figure 3. Reproduced with permission from Lipo (2001, Figure 4.10).

(a)



(b)

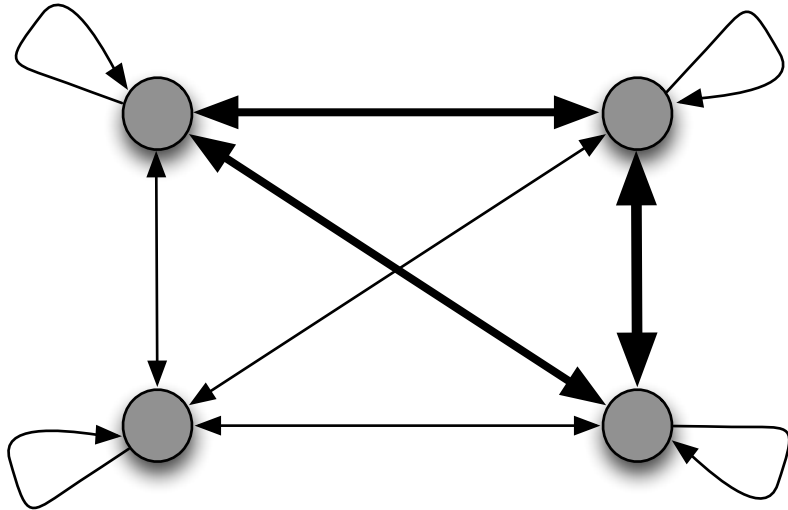


Figure 5: Examples of simple metapopulation models. Each circle represents a deme or local population, and arrows are unbiased transmission flows, either within the deme itself (represented by the looped arrow), or between demes. Model (a) depicts the well-mixed version of a metapopulation model, with homogeneous flows between all demes; this model is equivalent to Wright's classical "island" model in population genetics. Model (b) depicts a metapopulation model with variable flows between demes, with arrow thickness indicating the rate of information flow.

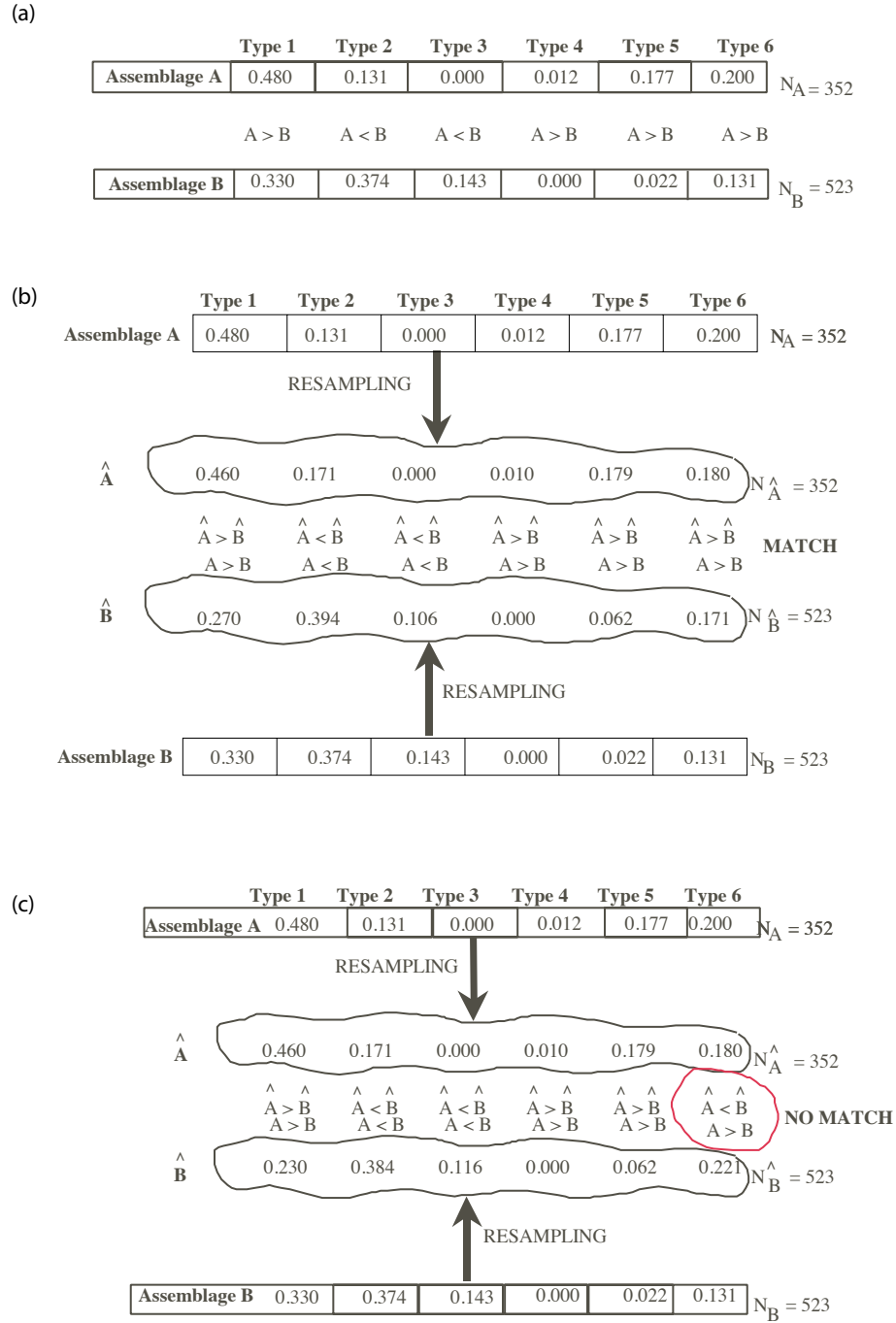


Figure 6: Iterative pairwise significance testing for frequency seriation (Lipo 2001). (a) Counts are converted to frequencies, and the “directionality” of frequency comparisons is calculated for each type. Given the frequencies of types, bootstrap sampling is used to draw a set of random assemblages. For each random assemblage draw, the directionality of each type frequency is evaluated. If all types in a random assemblage have the same directionality, a match is scored, as in (b). If a resampled assemblage has different directionality for one or more types, no match is scored. The proportion of matches in bootstrapped assemblages constitutes the p value for the test. Redrawn with permission from Figures 3.9 - 3.11 in Lipo (2001).

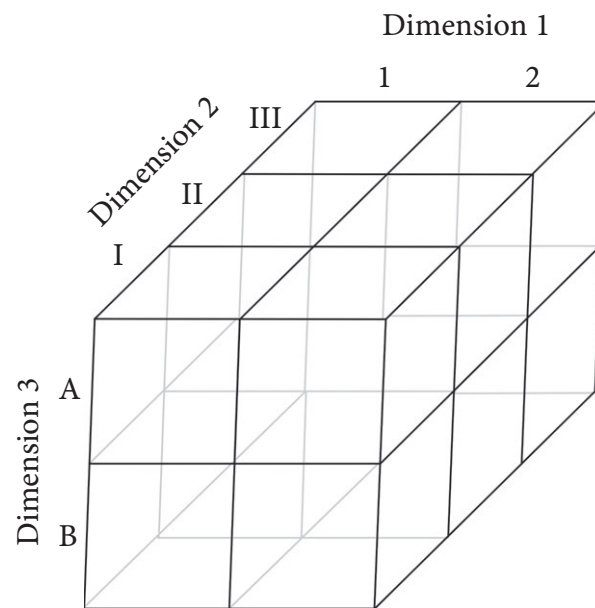


Figure 7: Schematic example of a paradigmatic classification. This classification employs three dimensions, two of which are described by two modes apiece, the third being described by three modes. The result is a design space composed of twelve mutually-exclusive classes.

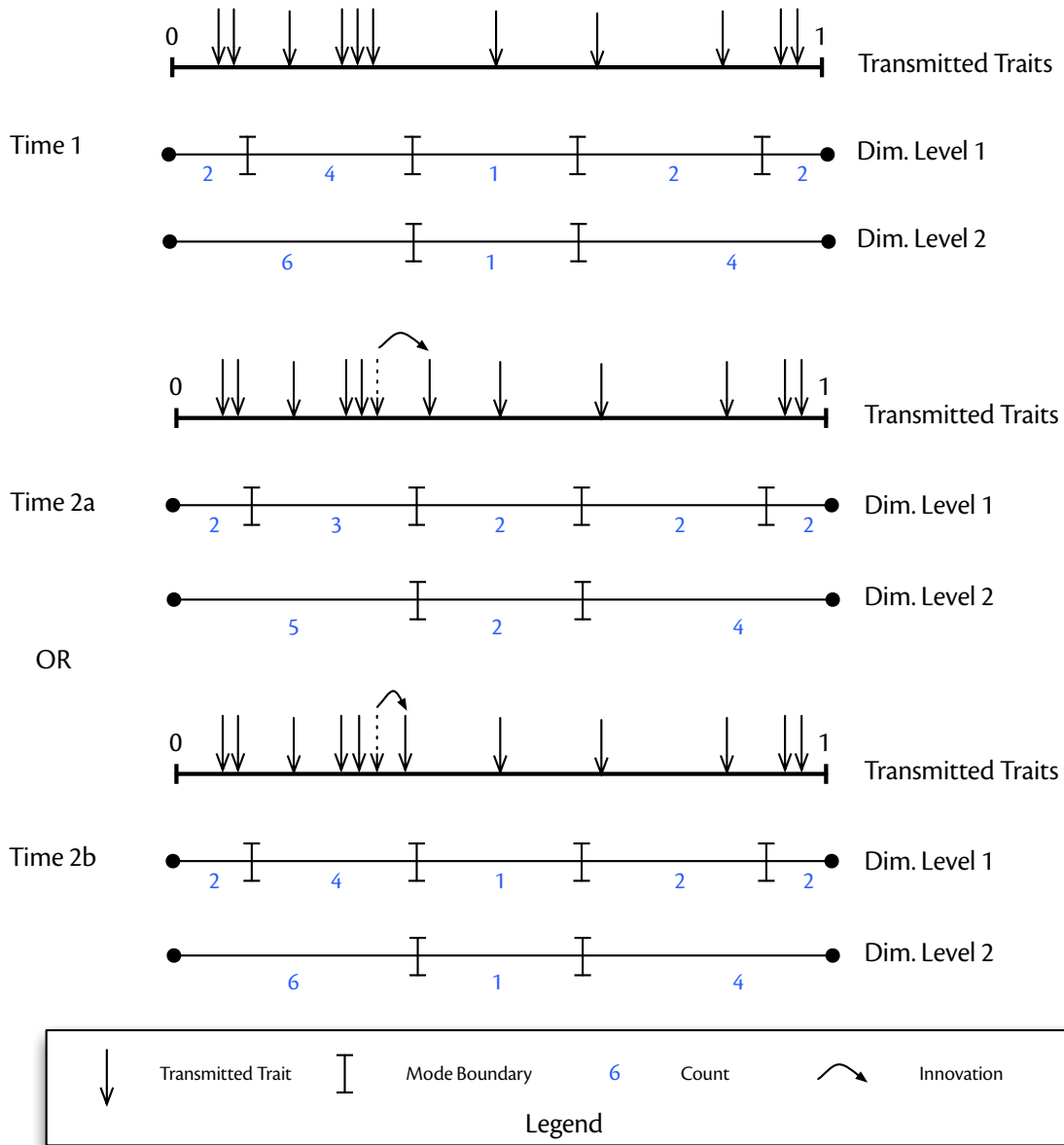


Figure 8: Schematic view of observing transmission outcomes through analytic classes. Only one dimension of a paradigmatic class is shown for visual clarity, but normally more dimensions would be modeled. Transmitted traits are shown as points on the unit interval $[0, 1]$, with innovation creating a new unoccupied point on the interval, a random distance away from the trait being “mutated.” The outcome of this process is being monitored by two hierarchical levels of analytic class, labeled 1 and 2, with 1 nested inside the definitions of 2. The vertical lines with bars indicate the boundaries between modes and schematically indicate mode “definitions.” Mode definitions are chosen at arbitrary distances and are not equal in length. Counts are shown below each dimension of the traits which map to each mode. See Section 4.2 for discussion of the two innovaton scenarios.

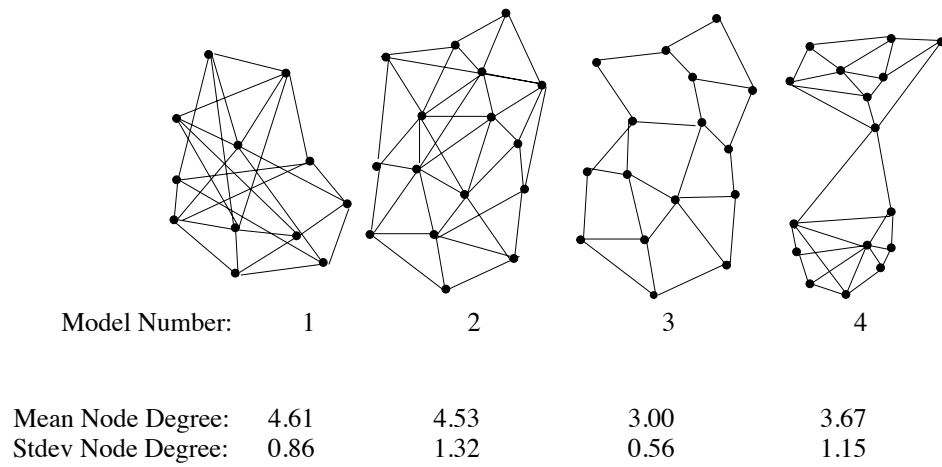


Figure 9: Four simple models of transmission flow between demes in a metapopulation. The first model depicts long-distance connections and dispersal of information, and relatively high and even flow between demes, with no isolated or “hot” spots. The second model possesses no long-distance connections, but still relatively high and even flow between demes at short distances. The third model has “nearest-neighbor” connectivity, as is typically modelled in lattice or island models of population structure. The fourth model introduces variability in linkage between clusters of demes, creating what graph and network theorists call “community structure.” Reproduced with permission from [Lipo \(2001, Figure 4.10\)](#).

Theta	$\mathbb{E}(K_n)$	Simulated \bar{K}_n	Sim. Stdev K_n
2	6.054	6.511	1.838
4	9.022	8.991	2.269
8	12.869	12.616	2.464
12	15.397	15.306	2.571
16	17.228	17.187	2.569
20	18.629	18.737	2.486
40	22.601	22.693	2.253

Table 1: Comparison of expected K_n from Equation (1) with simulated values from WF-IA model, for θ values from 2 to 40. Total sample size across θ values is 408,478 samples of size 30.

Table 2: 63 assemblages from [Phillips et al. \(1951\)](#) with more than 50 decorated sherds, tabulated with the number of decorated culture-historical types (richness). Total assemblage size and richness noted for comparison.

Site Name	Site Number	Total Sherds	Tot. Richness	Decorated Richness	Total Dec. Sherds
Parkin	11-N-1	6851	10	8	1303
Neeley's Ferry	11-N-4	7263	11	9	1269
Vernon Paul	11-N-9	2567	7	5	758
Williamson	11-N-13	4919	9	7	670
Leland	19-M-1	8394	12	10	647
Barton Ranch	11-O-10	4702	9	7	638
Silver City	20-O-5	2653	11	9	430
Castile	13-N-21	1999	11	9	394
Walls	13-P-1	3793	14	12	361
Powell Bayou	17-O-9	2230	17	15	351
Kinlock	19-N-1	5610	10	8	336
Arcola	20-M-1	2754	10	8	326
Cummins	11-O-4	713	8	6	261
Belle Meade	13-O-5	798	10	8	254
Rose Mound	12-N-3/A&B	1400	9	7	242
Kent Place	13-N-4/B,C,D,E	1026	9	7	241
Big Eddy	12-N-4	721	9	7	229
Hollywood	13-O-10	1486	13	11	226
Bush	17-M-11	4358	15	13	225
Stokes Bayou	16-M-6	2764	17	15	217
Fortune	11-N-15	685	5	4	200
Myer	16-N-10	1245	17	15	198
Jaketown	20-O-1	1157	9	7	197
L. Cormorant	13-P-8	930	12	10	192
Merigold	17-N-1	1903	18	16	183
Clay Hill	13-N-7	654	8	6	181
Wallace	17-K3	1507	9	8	176
Starkley	13-N-16	918	9	7	171
Mound Place	12-P-1	3178	12	10	168
Nickle	13-N-15/C,D,E	737	10	8	163
Carson Lake	10-P-1	3489	10	8	159
Montgomery	15-N-6	945	14	12	153
Owens	14-O-2	657	11	9	144
Deer Creek	20-M-2	1289	8	6	138
Cramor Place	12-O-5	1008	8	6	138
Turnbow	11-N-12	3052	9	7	129
Commerce	13-O-11	1097	10	8	128
Lipe	18-M-4	903	6	4	117
Parchman	15-N-5	998	13	11	114

Dupree	16-L-6	819	9	8	111
Woodlyn	13-P-11	847	10	8	107
Menard	17-K-1	1043	13	11	102
Grant Place	13-N-11	515	6	4	93
Irby	13-P-10	758	10	8	91
Salomon	15-O-1	1164	11	9	84
Alligator	16-N-2	1175	10	8	83
Marlow	18-N-1	486	8	6	81
Beck	13-O-7	257	8	6	79
Davis	13-N-5	456	7	5	79
Moore	14-N-1	296	7	5	78
Oliver	16-N-6	553	14	12	75
Oliver	16-N-6	552	11	9	74
Alma Brown	17-K-7/E/B	488	7	5	73
Old Town	15-N-3	506	8	6	66
Shelby Place	12-P-2	481	12	10	62
Dundee	14-O-8	621	7	5	61
Pouncey	12-O-2	439	7	5	60
West	14-O-10	258	8	6	57
Spendthrift	16-O-2	901	8	6	55
Vance	17-N-9	391	6	4	51
Notgrass	10-P-4	3182	13	11	50
Perry	14-O-4	321	8	6	50
Stoneville	19-M-3	229	8	6	50

Appendix A. Software Development Plan

The following tasks are necessary in order to use **TransmissionFramework** to address the research questions proposed here. The status of each task is current as of 2012-11-09.

Separate transmission traits and observational units

Traits and trait dimensions that comprise the information flowing within a population should be separate from a set of observational units, which can be mapped onto traits and trait dimensions in arbitrary ways. Traits should continue to be trackable by count or frequency, to allow us to understand the effect of observing trait dynamics through observational classes. [STATUS: *partial* TIMELINE: *In progress, requires 3 weeks solid effort*]

Paradigmatic classification

Simulation models should be configurable with one or more paradigmatic classifications, each of which specifies a number of dimensions and for each dimension, a number of modes. Dimensions are attached to Trait Dimensions, and it should be possible to manually specify the mapping of modes to segments of a Trait Dimension, or to generate random partitions of a Trait Dimension into modes. [STATUS: *partial* TIMELINE: *In progress, requires 1 week of solid effort on top of observational units infrastructure*]

Individuals assignable to deme or local sub-population [STATUS: *complete* TIMELINE: *complete*]

Deme-level frequency counting

Count/frequencies of observational units must be tracked for the metapopulation as a whole and for demes. [STATUS: *partial* TIMELINE: *On hold, mainly needs testing after classification features are done, possibly 3-4 days of work*]

Deme creation and destruction

Because archaeological samples are not fully contemporaneous and may not overlap in time, the model should allow new demes to enter the simulation, and for demes to go extinct. Since this uses the existing tagging mechanism, mostly this is wiring and testing. [STATUS: *unimplemented* TIMELINE: *Winter 2013*]

Population of demes

New demes should be populated either by colonization from a single “parent” deme, or by sampling individuals from the entire population (giving the classic island model). [STATUS: *unimplemented* TIMELINE: *Winter 2013*]

Configuration of population and deme profiles

Simulation models need a “profile” of what demes and population to create at run start, how demes and population evolve over time. This needs to be configurable to test randomized profiles, as well as generate data in configurations that match the parameters of empirical examples. [STATUS: *unimplemented* TIMELINE: *Winter 2013*]