Measuring Cultural Relatedness Using Multiple Seriation Ordering Algorithms

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Abstract Seriation is a long-standing archaeological method for relative dating that has proven effective in probing regional-scale patterns of inheritance, social networks, and cultural contact in their full spatiotemporal context. The orderings produced by seriation are produced by the continuity of class distributions and unimodality of class frequencies, properties that are related to social learning and transmission models studied by evolutionary archaeologists. Linking seriation to social learning and transmission enables one to consider ordering principles beyond the classic unimodal curve. Unimodality is a highly visible property that can be used to probe and measure the relationships between assemblages, and it was especially useful when seriation was accomplished with simple algorithms and manual effort. With modern algorithms and computing power, multiple ordering principles can be employed to better understand the spatiotemporal relations between assemblages. Ultimately, the expansion of seriation to additional ordering algorithms allows us an ability to more thoroughly explore underlying models of cultural contact, social networks, and modes of social learning. In this paper, we review our progress to date in extending seriation to multiple ordering algorithms, with examples from Eastern North America and Oceania.

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1 Introduction

Seriation is a set of methods which uses patterns in the occurrence or abundance of historical classes to construct an ordering among otherwise unordered assemblages or objects (Dunnell, 1970). Traditionally, the orders constructed by seriation were intended to be chronological, since seriation was intended for use as a relative dating method by its early 20th century developers (O'Brien and Lyman, 2000, 1998; Lyman and O'Brien, 2006; O'Brien and Lyman, 1999; Lyman et al., 1997). But seriation techniques also create orderings which incorporate the effects of spatial variation in addition to temporal change, as James Ford pointed out (Ford, 1938; Phillips et al., 1951; Ford, 1935).

Despite the success of seriation in understanding the large-scale structure of the archaeological record in the New World (Beals et al., 1945; Bluhm, 1951; Evans, 1955; Ford, 1949; Kidder, 1917; Mayer-Oakes, 1955; Meggers and Evans, 1957; Phillips et al., 1951; Rouse, 1939; Smith, 1950), the method has largely been ignored since the advent of radiocarbon dating given its primary association as a relative dating method. But seriation is only a dating method in the sense that chronology is one possible inference from mapping the spatiotemporal pattern of change in cultural variants. Other inferences are possible, and in particular, there is a growing understanding that seriation is one of several methods for inferring historical and heritable continuity and thus documenting the evolutionary history of past populations (e.g., O'Brien and Lyman, 1999, Ch. 3).

Similarity between classes of artifacts constitutes heritable continuity when it arises from information being passed between populations over time; that is, from cultural transmission processes. Although the fact that seriation, in some sense, measures cultural transmission has been implicit since the earliest discussions of the method, the connection remained a common sense generalization until the mid 1990's. Fraser Neiman, in his dissertation and later his seminal 1995 article, noted that the unimodal patterns that form the core of the traditional frequency seriation technique are regularly seen in the trajectories seen when simulating unbiased transmission (Neiman, 1995). In order to make this connection both rigorous and useful in empirical work, we began a research program aimed at exploring the connection between cultural transmission models and seriation methods (Lipo et al., 1997), which has resulted in numerous publications, new seriation software algorithms, and many conference papers (Hunt et al., 1995; Lipo et al., 1995; Lipo and Eerkens, 2008; Lipo and Madsen, 2001; Lipo, 2001, 2005; Lipo and Madsen, 1997; Lipo et al., 2015; Madsen and Lipo, 2014, 2015; Madsen et al., 2008; O'Brien et al., 2015).

The core of the all seriation techniques are a set of "ordering principles" which describe how the data points making up each assemblage or object are rearranged in order to achieve a valid seriation solution. Traditionally, there are two (Dunnell, 1970; Rouse, 1967; Whitlam, 1981). The "occurrence principle" states that a valid ordering leaves no temporal gaps in the distribution of the historical classes used, and thus that temporal orders are continuous (Dempsey and Baumhoff, 1963; Rowe, 1959). The "frequency principle" states that in a valid ordering, the frequencies making up the continuous distribution of each historical type will be unimodal, possessing a single peak of "popularity" (Nelson, 1916).

Both principles work, as demonstrated by the robustness and continued utility of the basic chronological frameworks erected by culture historians in the first half of the 20th century using seriation along with stratigraphy and marker types (Lyman et al., 1997). The frequency principle remains, however, an empirical generalization which is only suggested by the behavior of cultural transmission models, rather than being a necessary consequence. This suggests to us that seriation as a method requires further methodological development, especially if it is to be one of our major tools in tracing historical and heritable continuity in the archaeological record.[1]

INTRODUCTION INCOMPLETE UNTIL LATER SECTIONS DRAFTED

2 Seriation and the Frequency Principle

Seriation, in the Americanist sense, was initially developed by Alfred Kroeber (Kroeber, 1916) in the Southwest, on the basis of changes in ceramic decorations from Zuni Pueblo. The approach proposed by Kroeber was quickly amended by Leslie Spier, Alfred V. Kidder and Nels C. Nelson, all of whom were conducting stratigraphic excavations in the American Southwest (Kidder, 1917; Nelson, 1916; Spier, 1917). This group of researchers all noticed that when ceramics were described in a particular way – called "stylistic" by Kidder (1917) – the temporal distribution of the types took the form of "normal curves." Using such types, it was apparent that a series of assemblages collected from the surface or otherwise undated could be arranged in chronological orderings by rearranging them so that all type distributions approximated "normal curves" simultaneously. The orders constructed in this way could be tested by finding stratified deposits and were found to be correct.

As powerful as seriation proved to be, these early formulations were entirely intuitive and based on the generalization that greater temporal differences between assemblages caused larger differences between frequencies of decorated types, and that properly constructed historical types displayed a clear pattern of change (Phillips et al., 1951, p. 220):

> If our pottery types are successful measuring units for a continuous stream of changing cultural ideas, it follows that when the relative popularity of these types is graphed through time, a more or less long, single-peak curve will usually result. Put in another way, a type will first appear in very small percentages, will gradually increase to its maximum popularity, and then, as it is replaced by its succeeding type, will gradually decrease and disappear.

This compactly describes the "popularity principle," originally articulated by Nelson (1916) and Wissler (1916). A key word in the above is "usually," since not all

[1] Cladistics and phylogenetic methods, especially those which take into account temporal differences in the samples being studied (stratocladistics) and which are capable of yielding phylogenetic networks in addition to trees, are the other major tools by which we can measure heritable and historical continuity.

types display the unimodal distribution described, even when the attributes chosen are explicitly stylistic and decorative. Types suitable for frequency seriation were a subset of stylistic variation, comprising those which displayed spatial and temporal contiguity, a long enough duration that the types overlapped in their representation among sites and assemblages, and those whose distribution through time displayed the characteristic unimodal form which allowed the analyst to arrange them by eye. The process of constructing and testing such types became known, after Krieger (1944), as applying the "test of historical significance." Despite formalization of how seriation worked to produce chronologies, the core of the methods – unimodality and the popularity principle – remains an empirical generalization.

2.1 Unimodality and Cultural Transmission Processes

In most cases (such as the above quote from Phillips, Ford, and Griffin), the popularity principle is simply assumed to hold in culture-historical applications. It is clear that culture historians assumed that what generates heritable continuity, and what drives the unimodal pattern in type frequencies, is cultural transmission and the changing adoption of cultural variants over time. As Lyman (2008) documents in careful detail, early 20th century anthropology and archaeology understood and discussed a variety of transmission processes informally, as generating the patterns they studied, even if they used different terms and did not form quantitative models for it. Rouse (1939), for example, explicitly discussed the diffusion of cultural traits, in terms that we now recognize as a spatiotemporal model of transmission. Kroeber, the father of frequency seriation, clearly understood the connection between his previous work and trait diffusion (Kroeber, 1937). There are many more examples (Lyman, 2008).

It was not until archaeologists began working with stochastic models of cultural transmission, however, that we could easily visualize the sheer variety of patterns that cultural transmission processes can, and do, generate. This allows us to easily explore the precise conditions under which unimodal distributions occur in type frequencies, what classification methods tend to produce it, and what dimensions of variation combine to produce mostly unimodal behavior. Archaeologists have long worked with models of diffusion, with those models becoming increasingly quantitative, statistical, and even explicitly mathematical by the 1970's (e.g., Ammerman and Cavalli-Sforza, 1971). But deterministic models are not well suited for understanding the details of individual social learning events "add up" to produce a population level effect, and the latter is what we need to understand in order to solidly ground a seriation ordering algorithm in cultural transmission. Dunnell's (1978) exposition of style as neutral variation led to adoption of stochastic models of drift from population genetics as the main tool for exploring cultural transmission dynamics. Many previous models of diffusion tended to be deterministic, especially those stemming from the interdisciplinary literature on the diffusion of innovations (e.g., Rogers, 2003). Neiman (1995) simulated drift in cultural variants as an unbiased transmission process, as shown in Figure 1. Immediately apparent is the fact that some variants do display unimodal patterns, but most variants are multimodal or display violations of unimodality at small scales even if the macroscopic shape seems to conform to the popularity principle.

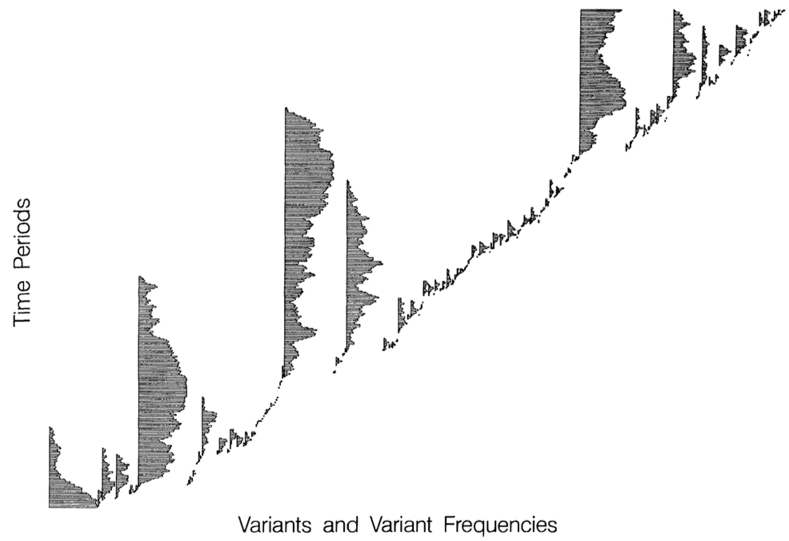

Fig. 1 Neiman's simulation of drift in cultural variant frequencies under unbiased cultural transmission (reproduction of Figure 2a from Neiman 1995.)

The lesson of Figure 1 is that there is nothing necessary about unimodality given cultural transmission, but that it can occur. But culture historical types used in seriation were **constructed** to yield unimodal distributions, and a key element in such construction is ensuring that types are composed of multiple dimensions of variation which co-occur on artifacts identified to that type. We can imagine selecting the traits shown in Figure 1 and intersecting combinations of them to form multidimensional classes. In doing so, it is likely that unique combinations of those variants would not recur and might show unimodal distributions more often. It is also likely that time averaging (ubiquitous in the archaeological record) will smooth out some of the minor variation in variant frequencies, as will the vagaries of sampling archaeological deposits.

Taken together, these factors seem to explain why the intuitive construction of historical types, from the continuous flow of the products of cultural transmission processes, worked to produce chronology through application of the common-sense popularity principle, and why not all artifact classes constructed from otherwise "stylistic" dimensions of variation, are suitable for frequency seriation using unimodality as the ordering criterion.

2.2 *Continuity: An Alternative to Unimodality*

Despite being able to understand unimodality as the probable consequence of carefully selecting some dimensions of variation over others, the smoothing effects of time averaging, and the smoothing effects of sampling by archaeologists, there are still several reasons why we might wish to find alternatives to unimodality as an ordering principle for seriations. First, from a performance perspective, searching for unimodal orders is computationally expensive, even for relatively small data sets (Madsen and Lipo, 2014). Even with the iterative, agglomerative method that we introduced recently (Lipo et al., 2015), the computation time can diverge for data sets as small as 30. This is a large number of assemblages by most archaeological standards, but with good techniques and ordering principles seriation may scale to much larger problems, and even be applicable to the flood of data seen in modern day life.

Second, and more importantly from a theoretical perspective, it is important to be able to trace heritable continuity even if does not display a particular type of temporal frequency distribution. Using traditional type construction methods and the test of historical significance, culture historians were able to find **enough** conforming types and classes to construct regional chronologies. But there is a strong relationship between the number of classes in a seriation, and our ability to map differences across space and time. Later in this paper, we introduce formal models of regional interaction in the form of interval temporal networks. One of us (Madsen) is presently working on classifying regional interaction models by the structural properties they leave behind when cultural transmission is simulated on such regional models and then seriated. Doing this kind of detailed analysis requires many types and frequently, many assemblages to be successful. Even if unimodality suffices for rough chronology, additional ordering principles will be highly useful for studying regional interaction and the evolutionary history of technology.

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A theoretically sound ordering principle for seriation should be derivable from characteristics of the underlying cultural transmission processes that we believe drive the spatiotemporal variation seriation measures. Formal models of cultural transmission, such as those formulated by Boyd and Richerson, Cavalli-Sforza and Feldman, and borrowed from population genetics (Boyd and Richerson, 1985; Cavalli-Sforza and Feldman, 1981; Neiman, 1995) are stochastic autoregressive processes, in the sense that the probability distribution of outcomes at a given time are dependent upon the outcomes from the immediate past. Mathematically, we usually formulate cultural transmission models as Markov processes, usually of first order (i.e., without dependencies on states previous to the immediate past state). Such models are certainly capable of making large changes in state over short time intervals, but large jumps are rare compared to small changes in state, especially in large populations.This is the reason why we (and culture historians) often have an expectation that cultural transmission has a "gradual" character to it.

The probabilistic gradualism of change over small time periods in our cultural transmission processes suggests a "continuity" principle, strongly related to notions of continuous functions in mathematics: samples which originate close together in time, space, or both will be close in type frequency and the presence/absence of types, especially compared to samples which are further apart. This continuity principle immediately leads to considering ordering algorithms based upon minimizing a suitable distance metric, with assemblages represented by points in a multidimensional space of type frequencies or counts.

2.3 Statistical Seriation Methods

The earliest statistical techniques for seriation were also built upon using interassemblage distance metrics. Brainerd and Robinson (Brainerd, 1951; Robinson, 1951) pioneered a method for seriation based upon the similarity between assemblages, measured as a scaled version of the Manhattan (or city-block) distance between assemblage frequencies. When these scaled distances (which became known as Brainerd-Robinson coefficients) are arranged in a matrix with the largest values nearest the diagonal and the lowest values in the corners and away from the diagonal, the order of assemblages by row or column provides the seriation solution. In practice, most real data matrices cannot be put in perfect Robinson form without violations.

What followed Brainerd and Robinson's pioneering work was a minor industry in methods for matrix ordering, in the face of the practical difficulties in coercing most data sets into a perfect linear ordering (e.g., Dempsey and Baumhoff, 1963; Kendall, 1963; Matthews, 1963; Bordaz and Bordaz, 1970; Gardin, 1970; Kendall, 1970, 1971). As access to computers by researchers in the social sciences increased, computerized algorithms for examining permutations quickly proliferated (Ascher and Ascher, 1963; Craytor and Johnson, 1968; Kuzara et al., 1966). Kendall (1969) and others attacked the ordering problem through the use of multidimensional scaling, and later correspondence analysis would be used with success in determining probabilistic seriation orders, and just as importantly, quantifying the degree of departure from the ideal seriation model (Smith and Neiman, 2005). For a detailed review of the many variants on this type of probabilistic seriation solution, see (Marquardt, 1978).

Not all of the similarity measures used in this literature are true distance metrics, but many are, and there were calls to simplify the problem by directly minimizing inter-assemblage distance, and thus the total "path length" of a candidate seriation solution. Kadane (1971) describes this approach, and it was adopted later by Shepardson (2006) in his construction of the "Optipath" seriation algorithm, which has distance minimization at its core.

Where existing distance/similarity methods encounter a problem is the assumption that a seriation solution must be a single linear order. In an earlier paper, we describe a seriation algorithm (iterative deterministic seriation solutions, or IDSS) that finds all of the possible orders in a set of data that conform to an ordering principle, and where those orders have overlap in assemblages, IDSS constructs a graph with branches that recognizes that the best solutions may not be linear (Lipo et al., 2015). Departures from linear seriation solutions have always been treated as "stress" or "error," especially when statistical methods such as MDS or correspondence analysis are employed. Practitioners usually recognize that such departures arise from coercing data which naturally sit in a larger number of dimensions – because of spatial variation and other factors – into a one-dimensional order. In essence, methods which attempt to coerce a complex spatiotemporal pattern into a linear ordering tend to treat departures from linearity as noise, which is then ignored.

But the departure from linearity is not "noise," in the statistical sense. Especially if one accounts for sampling error in constructing seriation orders (as we do in IDSS by using the bootstrap to construct confidence intervals around the empirical frequencies), then departures from a linear ordering are **signal**, not noise. Such solutions reflect the fact that an assemblage at time T_1, for example, may be the closest match to two different assemblages at later times T_2 and T_3 for example, given slightly different areas of overlap in their type frequencies. This can occur because the seriation method is inherently spatiotemporal, instead of simply measuring time (as culture historians have always known), and it can also reflect the splitting of populations into separate lineages (or their merger).

2.4 Exact Distance Minimization Ordering: "Continuity" Seriation

Instead of the "approximate" distance minimization algorithms employed in multidimensional scaling and Shepardson's OptiPath seriation software, we explore exact solutions using our IDSS software. For simplicity in the configuration of the software, we summarize our approach by calling it "continuity" seriation, to emphasize that we want solutions that have the smoothest, most continous transition of type frequencies when we consider pairs of assemblages. We achieve this by locally minimizing the inter-assemblage distance within the solution graph, which automatically yields the minimum total "path length" for a seriation solution.

Our algorithm makes no use of the unimodality criterion, and produces equivalent results in almost all cases, as we show in the next section. The algorithm currently employs the Euclidean distance between assemblage counts or frequencies, although it can use any distance metric. Given a table of inter-assemblage distance metrics, we first construct pairs of two-vertex graphs which represent the "closest" assemblage for each assemblage in the data set (mirrored pairs are filtered out since they are isomorphic). The edge weight given to each edge is the Euclidean distance between the assemblages represented by vertices. For each of the minimal graphs in this initial set, we then find the assemblage with the shortest distance to each of the two ends, and continue iterating. Crucially, if there are equal-distance options, both possible solutions are retained. The result of this iteration is a collection of graphs which represent partial minimum-distance paths through the set of assemblages. This collection of partial graphs are then overlaid to form a single solution using a “minmax” approach as described in our paper on the IDSS algorithm in general (Lipo et al., 2015).

The general approach is the same one we take to frequency seriation; what differs here with “continuity” seriation is how we form the set of candidate partial solutions. Instead of enforcing unimodality within each partial solution, we minimize Euclidean inter-assemblage distance. The resulting minmax graph is linear only if all of the candidate partial solutions perfectly overlay themselves into a linear solution, and otherwise will have a tree structure with branches. The possibility of branching is what allows a seriation solution to express both spatial and temporal structure simultaneously. The ability to inform on both allows investigation of social network structure, and interaction and social learning patterns in past populations, at scales more detailed than entire cultural manifestations or phases. We believe that seriation, augmented in this way, sits between the microevolutionary level where we investigate evolution in single populations, and the macroevolutionary level, best explored using the tools of phylogenetic analysis and cladistic techniques.

3 Comparing Frequency and Continuity Seriation

In this section we compare the results of our IDSS frequency seriation algorithm, described in a recent paper (Lipo et al., 2015), and our exact distance-minimization or “continuity” algorithm. It is difficult to compare the algorithms on a very large set of empirical data sets, so we begin by examining a large sample of data sets generated by sampling simulated cultural transmission, within a regional metapopulation model of multiple communities. We described the overall model, called “SeriationCT,” in a conference paper last year, but we review the essentials here.[2]

Seriation of artifact assemblages is inherently a regional-scale problem, whether for chronology or tracking interaction and social learning processes. Thus, the fundamental abstraction for modeling is a graph or network which (a) represents the intensity of contact, migration, and interaction between communities of people at any given point in time, (b) allows the set of communities to evolve, with some communities going away and others originating over time, and (c) representing how both the pattern and intensity of inter-community contacts evolves over time. Social network or graph models, especially weighted graphs, form an essential ingredient for this type of modeling, but need to be extended to the temporal dimension.

Extending networks for modeling time-transgressive change employs so-called “temporal network models,” which record the changing structure a network or graph over a series of time points (Holme and Saramäki, 2012). For our purposes, “interval” temporal networks are the right abstraction. Such graphs represent interactions that occur and persist over a measurable duration as edges that carry time indices. Interval graphs can be modeled mathematically in a number of ways, but in an al-

[2] The SeriationCT software is open source, and is located at Github. Experiments using it to generate the data analyzed here, and more network models, are described and linked on Madsen’s website and lab notebook.

gorithmic setting the most convenient is to define a sequence of separate graphs, where each graph G_t in the sequence represents one or more change events within the network between times t and $t+\delta t$ (where $\delta t = t+1-t$). In a fully continuous temporal representation, each graph in the sequence specifies a single change event, and thus is equivalent to the way that a continuous-time stochastic process represents events. In situations where our observations are coarse grained due to time averaging or recovery methods (or both), each graph in the sequence may represent a number of change events which occur over the duration assigned to that graph in the sequence.

Change events encompass anything that modifies the graph. Vertices may be added or removed, and edges may be added or removed. In addition to addition and removal, if the graphs in the sequence are weighted, slices may record events where the strength of an edge changes, without other topological changes to the graph. If other attributes are present on vertices or edges (e.g., labeling edges for a type of interaction), changes to those labelled attributes would also constitute a change event and would be recorded by a graph in the sequence with changed attribute values. An interval temporal network is thus defined as an ordered set of graph "slices," each slice associated with a time index. The changes themselves can be found by "subtracting" two graph slices and obtaining lists of vertex and edge changes.

Constructing a time-transgressive regional metapopulation from an interval temporal network occurs by giving interpretations to vertices, edges, and other attributes of the graph. In our research, vertices represent communities of individuals, with population sizes which may change or not over time. Edges represent the presence of interaction between two communities, which could represent learning between individuals, or migration of individuals bringing portions of a cultural repertoire between communities. The weight given to an edge is typically a relative measure of interaction betweeh communities, normalized by the rest of the communities, since there is no good way in a simple structure like this to model the absolute intensity of such interaction. When communities come into existence, by members of an existing community founding a new settlement, a vertex is added to the network and it acquires connections to other communities (according to the class of model we are constructing). Similarly, communities may go away over time, and the vertex is then removed. Interaction patterns may change as well, resulting in the addition or removal of edges over time, or change in the edge weights.

For example, we can create a model whereby two clusters of communities are tightly interconnected internally, and have some sparser relationship between the clusters, and slowly lose that interconnection to become separate, non communicating lineages, using a model similar to that shown in Figure 2.
The third and fourth columns in the figure describe the change events. The third describes changes to the network structure in each time slice, and the fourth describes the interpretation of those structural changes in terms of a regional metapopulation model.

Interval temporal networks, interpreted as regional metapopulation models, thus form a basic tool for modeling many classes of regional histories and interaction patterns. For purposes of comparing frequency and our continuity seriation algorithms,

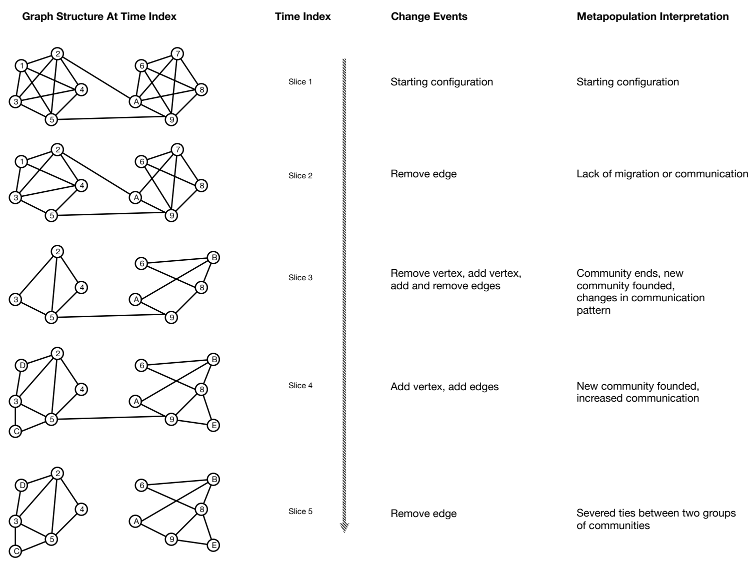

Fig. 2 Example of an interval temporal network interpreted as a regional metapopulation model, with vertices representing communities, weighted edges representing intensity of interaction and migration, and changes in each representing their respective evolution over time.

we focus on a regional model of the type depicted in Figure 2, but with a larger number of communities than shown. In that model, four clusters of communities start out at the beginning of the time period under consideration being tightly interconnected within each cluster, and more loosely connected among the four clusters. At any given time, each cluster has 8 communities spread over a geographic area, so with four clusters, there are 32 communities in the region under consideration. At a late point in the time interval under consideration, the connections between pairs of clusters is removed, creating two non-interacting sets of community clusters, to model the origin of separate "lineages" of cultural transmission in a region.[3]

Given this model of interaction between communities, we then simulate the standard unbiased cultural transmission model across this network. The changes specified by the temporal network guide the addition of new subpopulations or their demise in the model, and the edge weight pattern defines migration of individuals between communities, and thus the possibility of cultural variants flowing between communities. Simulation of transmission occurs for 12,000 time steps, with

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[3] This model is available for inspection as a set of GML network files in experiment "sc-2" in the experiment-seriation-classification repository maintained by Madsen. That experiment focused on differentiating different classes of lineage-splitting or coalescence models through their seriation solutions, and here I focus only on the data resulting the "early lineage splitting" model.

the change events occurring regularly over that interval, creating change in interaction over time as social learning proceeds.

During the evolution of the model, we record the frequencies of individual variants, and their co-occurrence to mimic archaeological classes or types which are defined by multiple dimensions of variation. Recording of frequencies occurs within each of the 32 communities present at any given point in time, so we can measure spatial and temporal variation in cultural variants. For purposes of the experiments reported here, we sample innovation rates from a prior distribution which allows any given simulation run to have a very low innovation rate, through relatively high innovation rates.[4]

Following simulation and data recording, the raw data are processed in ways that mimic the time averaging that occurs in archaeological deposits, and the sampling that archaeologists do when taking surface collections from such aggregated deposits. This chain of processing is depicted in Figure 3. First, recorded cultural variants are aggregated for each community across the simulated time that community existed, so that all variant frequencies are time averaged in the manner described and modeled by Premo (2014) and Madsen (2012). Then, from the time averaged data for each community, an assemblage of 500 simulated artifacts is drawn from the raw data. This has a tendency to represent common variants well, and capture some but not all rare variants. From this sampled data, we then take a sample of the available communities, since seriations are always performed on a sample of archaeological deposits selected by the archaeologist (whether in rigorous or ad hoc ways). Finally, we filter the types present in each group of assemblages, to remove those types which are present only in one assemblage (as one would do in a manually constructed seriation), since those types do not contribute to ordering.

The resulting set of assemblage-level type frequencies were then fed into our IDSS seriation program, asking it to produce both a frequency seriation using unimodality as the ordering criterion, and a continuity seriation, using exact distance minimization as the ordering criterion. We did this for 50 simulation runs with different parameters across the "lineage splitting" regional model described above, and compared the resulting seriation solutions. We measure whether frequency and continuity solutions are identical by testing whether the solution graphs are isomorphic, which means that the same vertices are connected to the same neighbors by the same edges. Of the 50 simulation runs examined here, in 80% of cases the continuity and frequency seriations give an exactly identical solution. Of the remaining non-identical solutions, we find that the differences nearly always involve the repositioning of a single assemblage. In the next section, we examine such a case in detail to understand what drives such differences when they occur.

[4] The details of the prior parameter distributions are relatively unimportant for purposes of comparing seriation algorithms, but are found in the experiment-seriation-classification repository under experiment SC-2 in the file "seriationct-priors.json".

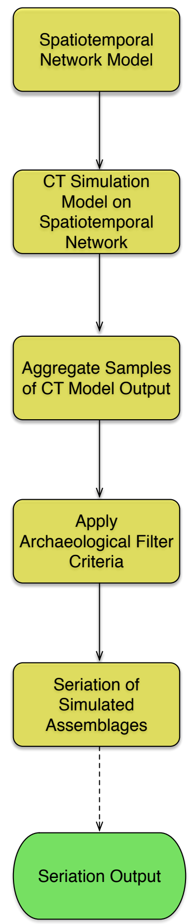

Fig. 3 Processing steps in simulating cultural transmission on a regional metapopulation model of lineage splitting, to compare seriation ordering algorithms.

3.1 Examining a Solution Which Differs

Of the differing solutions, we selected one (f8a6f378) at random to show the details of how frequency and continuity solutions differ. Figures 4 and 5 depict the frequency and continuity seriations, respectively, in the form of graphs which connect assemblages which are "adjacent" in the seriation solution. This makes it easier to see where an assemblage is really part of several solutions, which can indicate lineage splitting or differentiation occurring over space. We introduced this format for seriation solutions in our recent article on IDSS seriation (Lipo et al., 2015).

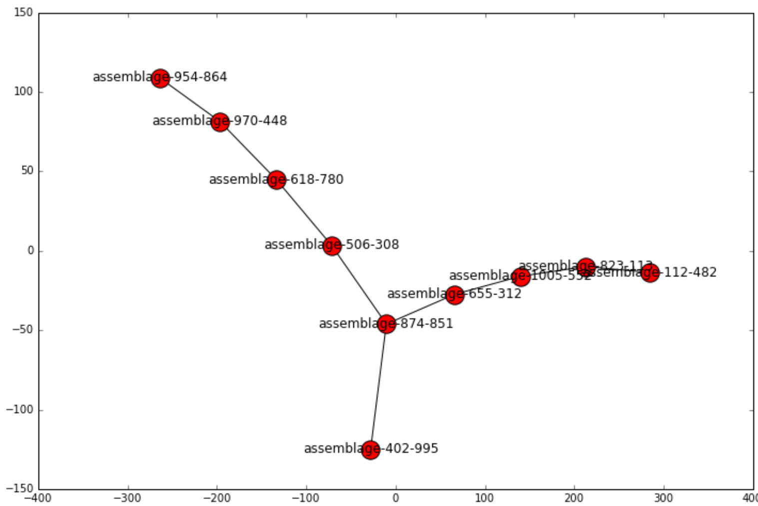

Fig. 4 Frequency seriation solution for simulation run f8a6f378 on the "lineage splitting" regional interaction model.

Although the graphs are laid out slightly differently (as a function of an automated graph layout algorithm), it is apparent that most of the seriation ordering is the same. Simulated assemblage 954-864 anchors one end of the ordering, while assemblage 112-482 anchors the other.[5] Both solutions also show a branch for assemblage 402-995, which belongs to one of the two lineages after the connections between two sets of communities is lost. It is a single assemblage branch because of the vagaries of sampling assemblages out of the total set of communities in this example. The main difference between the solutions comes in assemblage 618-780 and where it connects. In the frequency solution it occurs "inline" while in the continuity solution, interassemblage distance is minimized by removing it to a small branch of its own.

Switching to a more traditional tabular view of the type counts in Tables 1 and 2, several features are apparent. First, there are apparent violations of unimodality in the frequency seriation. But given our IDSS algorithm, we calculate a 95% confidence interval around each type count given the total sample size, and thus there are small differences (compared to the larger values) which are not statistically significant. Second, we can see that continuity solutions allow violations of unimodality (e.g., assemblage 823-113) but come up with the same overall structure. To us, this

[5] Simulated assemblage names here reflect geographic coordinates, since regional interaction models often bias interaction and migration by location or neighborhood.

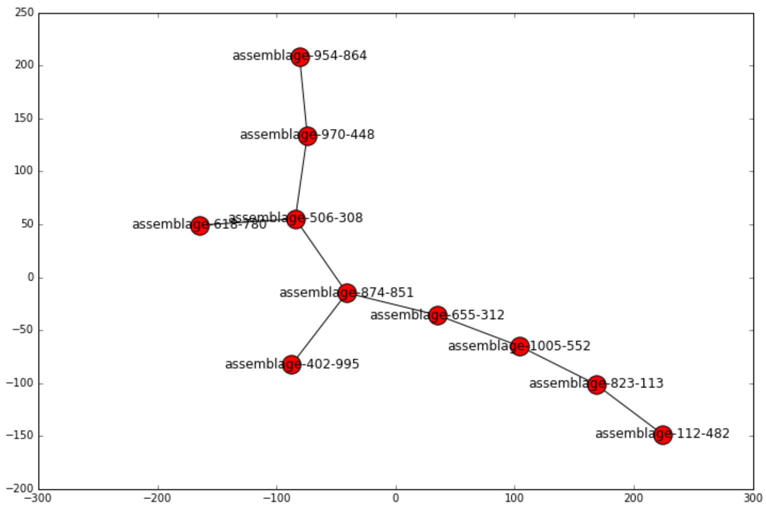

Fig. 5 Continuity seriation solution for simulation run f8a6f378 on the "lineage splitting" regional interaction model.

Assemblage Name	6022-0-1767	36526	36557	7005-0-1767	7628-0-1767	0-9222-3	1-0-1767	3771	6996-4-3
assemblage-954-864	10	160	0	49	92	0	0	0	9
assemblage-970-448	0	155	0	74	128	0	0	0	14
assemblage-618-780	123	50	0	164	121	0	13	0	14
assemblage-506-308	107	58	0	199	114	0	9	0	13
assemblage-874-851	81	66	0	165	0	0	162	6	17
assemblage-874-851	81	66	0	165	0	0	162	6	17
assemblage-655-312	0	52	16	111	0	20	269	6	26
assemblage-1005-552	0	53	32	72	0	61	182	41	8
assemblage-823-113	0	145	81	0	0	64	132	10	14
assemblage-112-482	0	24	151	0	0	157	81	49	9
assemblage-874-851	81	66	0	165	0	0	162	6	17
assemblage-402-995	106	65	0	29	0	0	192	0	7

Table 1 Raw data for frequency seriation for simulation run f8a6f378, grouped into blocks corresponding to the branches of the solution graph

shows that unimodality is sufficient but not necessary for using a seriation method to track the spatiotemporal structure of cultural transmission.

Assemblage Name	6022-0-1767	36526	36557	7005-0-1767	7628-0-1767	0-9222-3	1-0-1767	3771	6996-4-3
assemblage-954-864	10	160	0	49	92	0	0	0	9
assemblage-970-448	0	155	0	74	128	0	0	0	14
assemblage-506-308	107	58	0	199	114	0	9	0	13
assemblage-874-851	81	66	0	165	0	0	162	6	17
assemblage-655-312	0	52	16	111	0	20	269	6	26
assemblage-1005-552	0	53	32	72	0	61	182	41	8
assemblage-823-113	0	145	81	0	0	64	132	10	14
assemblage-112-482	0	24	151	0	0	157	81	49	9
assemblage-874-851	81	66	0	165	0	0	162	6	17
assemblage-402-995	106	65	0	29	0	0	192	0	7
assemblage-506-308	107	58	0	199	114	0	9	0	13
assemblage-618-780	123	50	0	164	121	0	13	0	14

Table 2 Raw data for continuity seriation for simulation run f8a6f378, grouped into blocks corresponding to the branches of the solution graph

3.2 Multiple Seriations for Phillips, Ford and Griffin (1951) data

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4 Discussion

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