A Theoretically-Sufficient And Computationally-Practical Technique For Deterministic Frequency Seriation

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Abstract

While Frequency seriation played a key role in the formation of archaeology as a discipline , its due to its ability to generate chronologies. Interest in its utility for exploring issues of contemporary interest beyond chronology, however, has been limited. This limitation is due in part partly due to a lack of a quantitative means for generating quantitative algorithms that can be used to build deterministic seriation solutions. Brute force approaches to solving seriation orders are impossible due to the numbers of possible combinations that need to be explored, a number that easily outstrips all When the number of assemblages becomes greater than just a handful, the resources required for evaluation of possible permutations easily outstrips available computing capacity. Similarity-based measures offer an On the other hand, probabilistic approaches to creating seriations offer a computationally manageable alternative but rely upon a compressed description of the data to order assemblages. This compression eliminates removes the ability to fit data using use all of the features of the seriation method, and thus offers little confidence in our data to fit to the seriation model, obscuring violations of the model, and thus lessens our ability to interpret the resulting orderunderstand the degree to which the resulting order is chronological, spatial, or a mixture. Recently, frequency seriation has been reconceived re-conceived as a general method for studying the structure of cultural transmission through time and across space. This The use of an evolution-based framework renews the potential for seriation but also calls for a computationally feasible algorithm that is capable of producing solutions under varying configurations, without manual trial and error fitsfitting. Here, we introduce the Iterative Deterministic Seriation Solution (IDSS) for constructing frequency seriation solutionsserations, an algorithm that dramatically constrains the search for potential valid orders of assemblages. Our initial implementation of IDSS does not solve all the problems of seriation, but begins to moves towards a resolution of a long-standing problem in archaeology while opening up new avenues of research into the study of cultural relatedness. We demonstrate the utility of IDSS using late prehistoric decorated ceramics from the Mississippi River Valley. The results compare favorably to

previous analyses but add new details into the structure of cultural transmission of these late prehistoric populations.

Introduction

As a means of Seriation is a set of methods which use historical classes to chronologically order otherwise unordered archaeological assemblages and/or objects [1]. Frequency seriation is a technique that produces chronological sequences by arranging descriptions of artifacts using patterns of relative artifact abundances to build chronologies, deterministic frequency seriation has assemblages so that the frequencies of artifact classes jointly form unimodal distributions. Developed in the early 20th century, frequency seriation played an integral part of role in the emergence of archaeology as a coherent discipline [2] . Developed almost 100 years ago, deterministic frequency seriation and enabled culture historians to construct regional chronologies and was paramount in generating much of our understanding of of prehistory throughout the New World [3–12]. Yet, for the last 50 years, frequency seriation has been largely ignored due to its association with relative chronology and the mistaken belief that radiometric dating techniques have replaced it. Now, saddled Saddled with a prevalent misunderstanding that seriation is simply a "dating method" [13] , that is useful only when radiocarbon dating is impossible [14], deterministic frequency seriation has never been developed into fully developed as a computational algorithmthat can take it beyond its original roots in culture history. While there has been some interest in seriation for disciplines outside of archaeology [15–18], to the extent that methodological development has occurred in archaeology over in the last 50 years, the focus has been largely on reducing frequency seriation to the method to probabilistic similarity-ordering problems that can be attacked via multivariate statistical methods [19–23].

The roots of frequency seriation, however, stem from a deterministic algorithm that identifies orders on the basis of occurrence and frequency criteria. [1]. Recently, deterministic frequency seriation has regained (hereafter, DFS) received some attention due to the demonstration that the method can be theoretically explained with rationalized using an evolutionary framework. While Dunnell [24, 25] hinted at this possibilitythe potential of this idea has been long recognized [24–26], the work of Neiman [27] firmly established an explanatory basis within cultural transmission models for the unimodal distributions that form the core of the frequency seriation algorithm. While the potential of this idea is has been long recognized [26], this Neiman's achievement has led to the reimagining of deterministic frequency seriation re-imagining of DFS as a general tool for studying patterns of cultural inheritance within populations through time and across space [28–40]. With these advances, there remains substantial promise for deterministic frequency seriation DFS to again become a primary tool for archaeological analyses as it enables researchers to quantitatively track patterns of interaction, define social communities, and trace lineages among past populations, in addition to informing upon chronology. In this way, frequency seriation could serve as a key method in the establishment of a fully evolution-based discipline.

Despite its potential, the use of deterministic frequency seriation DFS as a productive tool for archaeological research remains difficult, and methods for constructing and evaluating solutions are incomplete. While a handful of assemblages can be seriated using hand manipulation, sorting through all possible orderings for a set of assemblages is neither feasible nor systematic. When the numbers of assemblages gets larger than 10, the number of possible orders to be evaluated yields grows, a combinatorial explosion sets in, first visible once 10 or more assemblages are analyzed.

The order of magnitude of numbers involved makes brute force approaches impossible   48
even using modern computing power. This limitation was recognized early in the   49
discipline. When archaeologists became concerned with the quantitative basis of their   50
methods, statistical probabilistic approaches were developed that could construct orders   51
on the basis of similarity scores [41–49].   52

Advances in matrix reordering techniques such as such as multidimensional   53
scaling [50–53], spectral algorithms [54] and Bayesian analyses [55–57] offer increasing   54
degrees of sophistication but follow the same basic principle of using similarity as a   55
basis for constructing orders. All of these approaches guarantee solutions but also   56
eliminate much of the information that is available in the violations of the underlying   57
model, a limitation that results in the inability to distinguish different causal influences   58
upon seriation orders. Techniques using correspondence analysis [**?**,39,58–60] ameliorate   59
this issue to some degree but at the risk of equifinality.   60

With similarity-based With probability-based seriation techniques one is guaranteed   61
to find a solution, but the order produced in the order reflects sources of variability   62
beyond time including the effects of sample size, biased transmission processes and   63
spatial variation   [**?**] [1]. While one may suspect that the final order is largely   64
chronological, whether it is not possible to ascertain the degree to which the order   65
represents time or other possible factors. The order of any particular subset of   66
assemblages can be explained to have their orders represent chronology, their might be   67
explained as a consequence of several factors: chronological order, layout in space, a   68
function of differences in the relative degree of interaction – contact between   69
populations —or some combination of these factors– is not clear. . Allowing a   70
computational method to obscure the causal influence of these factors destroys the value   71
that seriation can have in helping disentagle such factors in real data sets.   72
Here, we introduce a new quantitative seriation algorithm that addresses the   73
computational barrier inherent in deterministic frequency seriation DFS while also   74
building upon the logical structure of the original method. The algorithm succeeds by   75
iteratively constructing small seriation solutions and then using the successful solutions   76
as the basis for creating larger ones. Significantly, the proposed algorithm produces the   77
entire set of unique valid seriation solutions. , and does not stop when a single valid   78
solution has been located. This is important because there are typically a number of   79
valid orderings. Some are suboptimal solutions because they are subsets of larger, more   80
complete ones. Others are simply valid alternative solutions, which point to the   81
influence of multiple causal factors. By including all valid orders, one can use the   82
patterning distribution of solutions as data regarding the structure of transmission. By   83
aggregating multiple sets of valid solutions, orderings that incorporate space and time   84
are possible, moving seriation beyond simple ordinal "dating" of assemblages and   85
allowing its use in measuring relatedness and cultural transmissionat regional scales.   86
The approach interaction between localities, and thus evidence about past cultural   87
transmission. Our algorithm also enables statistical assessment of the significance of   88
solutions, given the sample sizes employed. Using an example from the Mississippi River   89
valleyValley, we demonstrate how the new algorithm provides detailed insight into the   90
temporal and spatial structure of inheritance. Suitably extended in this way, we argue   91
that deterministic frequency seriation DFS has the potential to inspire new innovative   92
approaches to the archaeological record as much as it did in the 1930s as a critical tool   93
for building chronology.   94

Materials and Methods

~~The Method~~ A Short History of Seriation in Archaeology

~~It is not~~ While not in common usage, seriate and seriation are English words that refer to arranging or occurring in one or more series [61]. The terms describe an archaeological method without defining it —there are many ways to order or arrange items in a series. The origins of the method are a bit opaque since variants were in used before it was given the name. Identifying its history and understanding the scope of the method, therefore, requires tracing the components involved in seriation that emerge over time and under which contemporary seriation now exists.

Sir Flinders Petrie [62] is generally credited with inventing seriation. Working with predynastic Egyptian materials, Petrie used ceramics found in graves to develop a chronology. Petrie's break with archaeological tradition was to treat each grave lot as a sample of a continuous sequence of changing forms instead of as an exemplar of a period or stage. Since the history of Egyptian ceramics must have followed some particular course and thus presented an unique sequence of ceramic type replacements, the combinations of ceramic types found in grave lots allowed him to reconstruct both the history of ceramics and arrange the grave lots in chronological order. As in all seriation, the product was just an order; one had to determine independently (usually through superposition) which end of the order was most recent.

Alfred L. Kroeber [63] is credited with stimulating the American development. Kroeber did not cite Petrie's work, and likely developed his version of seriation independently. The form and context of Kroeber's proposal are dramatically different from Petrie's and points strongly for an independent origin. Indeed, even in his seminal "Zuni Potsherds" (1916) paper Kroeber describes how the idea of extracting chronology from type composition occurred to him as he observed variability in pottery decoration among Southwestern pueblo deposits. The primitive seriation 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 [7, 61, 63–65]. This group of researchers all noticed that when ceramics were described in a particular way —called "stylistic" by Kidder [7] —the temporal distribution of the types took the form of "normal curves." Coupled with Kroeber's initial insight, it was apparent that a series of assemblages collected from the surface or otherwise undated could be arranged in chronological order by rearranging them so that all type distributions approximated "normal curves" simultaneously.

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. The shape of the curves that led to the ability to order assemblages were not justified and even the terms used were *ad hoc*: the distributions were not "normal" in a statistical sense. Since knowledge of rates of change was impossible, all that one could say about the characteristic distributions were that they were unimodal in that they had a single peak frequency and decreased in value away from the peak in both directions. Furthermore, there was little interest in figuring out why the characteristic distributions occurred. It was enough that they did and could be used to order assemblages. Rationalization was limited to rephrasing the frequency observations as "popularity," and an answer to the question why did stylistic types display "normal distributions" was that styles simply increased in popularity until they reached a peak and then declined. Such statements are, of course, just descriptions of the observed frequencies and represent, moreover, the selection of simply one type of distribution that the popularity of styles can take. Seriation thus was based on an empirical generalization about the distribution of

stylistic classes through time. [145]

Almost all of the early work involved frequencies of stylistic (historical) pottery [146] classes used as attributes of assemblages, the assemblages being groups of artifacts, [147] usually but not always, pottery. But as Petrie's work showed, the groups ordered might [148] be objects, i.e., groups of attributes. Descriptions used for assemblages were frequencies [149] of historical classes; those for objects were presence/absence tabulations. By the 1930s, [150] use of the method had spread from the Southwest to include the Eastern United States [151] and the Arctic and by the 1940s even Peru and Amazonia had chronologies based on [152] seriation [9,66]. James A. Ford [67,68] played a critical role in disseminating the [153] method so widely and was the only scholar to take an interest in the theoretical aspects [154] of seriation until the 1970s [69–71]. Although Kroeber had been aware of potential [155] problems derived from sample size effects, Ford brought these considerations to the fore, [156] albeit in a highly intuitive, non-quantitative, and ultimately incorrect way. More [157] importantly, he deduced a series of conditions under which the empirical generalization [158] driving seriation might be expected to hold: (1) assemblages seriated must represent [159] brief intervals of time; (2) assemblages seriated must come from the same cultural [160] tradition; and (3) assemblages seriated must come from the same local area. The [161] meaning of key terms like "brief interval," "cultural tradition," and "local area" were [162] left undefined. [163]

Ford, like his predecessor, arrived at the final arrangement by eyeballing trial and [164] error orderings for conformance to the unimodal distribution model. Entirely a manual [165] process, Ford's technique requires arranging strips of paper representing assemblages [166] and with type frequencies graphically depicted as bars. One would move the strips [167] around until the pattern of the bars in each type would match "battleship-shaped" [168] curves. For many workers, this crude process was a critical failure of Ford's technique. [169] In 1951, George Brainerd and Eugene Robinson proposed an entirely new technique for [170] arriving at the order of groups [43,72]. They devised a measure of similarity, since [171] termed the Brainerd and Robinson Index of Agreement or simply the Brainerd and [172] Robinson Coefficient, with which pairs of assemblages could be compared in terms of [173] type composition. Thus described, they noted that in correct solutions the most similar [174] assemblages were adjacent to one another; since this order was unique, groups could be [175] chronologically ordered simply by arranging them so that the most similar units were [176] adjacent. Brainerd and Robinson did this by rearranging rows and columns in a square [177] matrix (each group is compared with every other group) of similarity coefficients; in a [178] perfect solution, the magnitude of the similarity coefficients would decrease uniformly [179] (monotonically) away from the diagonal of the matrix (the groups compared with [180] themselves). Cowgill [51] developed a similarity-based approach for occurrence [181] descriptions paralleling the techniques developed by Brainerd and Robinson for [182] frequency descriptions. [183]

Thus, two kinds of seriation approaches emerged. Occurrence seriation uses [184] presence/absence data for each historical class from each assemblage [62,63]. Frequency [185] seriation uses ratio level abundance information for historical classes [65,67,68]. Like [186] Ford, one could insist on an exact match with the unimodal model before regarding an [187] order as chronological, a deterministic solution. Alternatively one could accept the [188] "best fit" to the unimodal model as chronological, a probabilistic solution [73]. Each of [189] these approaches to seriation can subsequently be built to utilize raw data (identity [190] information whether frequency or occurrence values) or similarity coefficient (e.g., [191] Brainerd Robinson, squared Euclidean distance) to form the basis for ordering. Thus, as [192] shown in Fig 1 with two kinds of description (frequency/occurrence), two approaches to [193] ordering (identity/similarity), and two possible solutions (deterministic/probabilistic), [194] there are eight different families of seriation techniques available to archaeologists [1,73] [195]

Since Brainerd and Robinson [43,72], the majority of efforts have focused on [196]

Figure 1. Classification of seriation techniques. Dunnell [73] defines seriation to be a set of methods which use historical classes to chronologically order otherwise unordered archaeological assemblages and/or objects. Historical classes are those which display more variability through time than through space. Occurrence seriation uses presence/absence data for each historical class from each assemblage [62,63]. Frequency seriation uses ratio level abundance information (in percentage for) for historical classes [65,68,74]. Frequency and occurrence seriation techniques can take the form of deterministic algorithms that require an exact match with the unimodal model or probabilistic algorithms that accept departures from an exact fit. Identity approaches employ raw data (whether frequency or occurrence) to perform the ordering. Similarity approaches transform the raw data into a non-unique coefficient (e.g., Brainerd Robinson, squared Euclidean distance); the coefficients then form the basis for ordering.

probabilistic approaches and researchers have brought increasingly sophisticated numerical approaches to bear on seriation [46,54–57,75–82]. These probabilistic approaches generally seek to find approximate solutions by reducing the dimensionality of the data set. They will find a solution even when joint unimodality is not possible and most measure the departure from a perfect solution by calculating stress (residuals) or by examining variability within higher dimensions. As a whole, these techniques treat seriation as an empirical generalization about the way "data change" through time rather than a set of theoretical rules used for explanation. Variability in the frequencies of classes beyond the generalization is treated as noise rather than information about violations to the model and much of the utility of deterministic solutions that can be created by hand ordering is lost. Consequently, most of these quantitative approaches remain in the programmatic literature. Most practical work continues to be done pretty much as Ford did it in the 1950s, hand creating orders using graphical representations of relative frequencies in order to establish deterministic solutions.

Explaining Seriation

To understand how to build an automated algorithm that is true to the seriation method, one must look in detail at its requirements. In his 1970 paper, Dunnell evaluated Ford's criteria [1,67,68]. Ford's conditions 1 and 2 were found to be sound and conditions that groups to be seriated (objects or assemblages of objects) had to meet for the generalization warranting the method to apply. Groups did not have to be of short duration (time between the addition of the first and last element to the group) in some absolute sense as Ford supposed, but group duration did have to be comparable among the included cases. Groups did have to belong to the same tradition (ancestor-descendant relationships). While there was no way to assess whether these conditions were met *a priori* by a given set of assemblages, Dunnell showed that when deterministic-identity approaches were used, seriation could not be made to yield incorrect answers on these grounds, thus securing the chronological warrant for arrangements derived by those techniques. The other techniques are not robust in this regard and the orders arrived by those means may or may not be chronological.

The "local area" criterion proved to be another matter. Dunnell [1] showed that this condition did not apply to the groups to be seriated as Ford had assumed. Rather it was a deficiency in the warranting generalization; the method was under determined. The generalization only spoke to temporal distributions of types, not their spatial distributions. As Ford intuitively appreciated and others showed empirically in the 1960s, frequencies of types varied in space and that variation could be mistaken for difference in age. Ford's solution was to limit the amount of space in a seriation, but

this was a heuristic and did not address the underlying issue. To get rid of spatial variations would limit a seriation to a simple point in space; one would simply be doing superposition under a different name. Using the different properties of space and time, Dunnell showed that the effect of spatial variation could be eliminated by multiple seriations of the same events using different materials (e.g., pottery types, point types, grave types, etc.) and extracting the common order as chronological. Seriation thus became a more complicated and demanding dating method. Archaeological reaction to this was mixed. Many simply abandoned the method relying on other methods like radiocarbon dating wherever possible; others simply ignored the limitations of seriation and continued in the manner of Ford.

Limits of Current Seriation Approaches

Thus, it is not accidental that most practical approaches to creating deterministic seriation solutions have remained largely hand-built despite the availability of computer processing tools. Seriation, whether employing class frequencies or simple occurrence information to order assemblages, yields solutions that are located identified from the permutations of the set of assemblages. The set of possible permutations that must be examined are is vast in numbers. Moreover, seriation has been related to the "traveling salesman problem"(TSP) in which one is given a list of cities and their pairwise distances, and tasked to find the shortest possible route that visits each city exactly once and returns to the origin city [82–84]. If one tries to solve the TSP by examining all possible routes, it quickly becomes impossible as the number of solutions increases exponentially with the as the factorial of the number of cities in the list. Given the number of solutions that must be searched, even parallel clusters of the fastest available computers are insufficient when the number of assemblages gets larger than 14 (Figure ??). 14. As described in more detail by Madsen and Lipo [85], the problem is confounded to an even greater degree since the single best even worse than factorial, in that the best seriation solution may be some a combination of sub-solutions of the entire set of assemblages .

which break the available assemblages into sets. When this possibility is included, the growth of possible solutions is even greater than factorial (Table 1).

The TSP problem
The combinatorial challenge with DFS has generally led many to use approximate approaches, based upon reduced similarity descriptions of type frequencies. Deterministic algorithms for frequency seriation, however, have advantages over similarity approaches since they make use of all of the type abundance information for each assemblage to build orders, thus allowing orders to be rejected and the search space thus reduced. Currently, only hand-built approaches have been the only feasible way of creating deterministic seriation solutions [32,33,86]. In addition to integrating pairwise statistical evaluation for comparison of assemblages [32], manual solutions have the advantage of a general pattern recognition strategy that is inherent in our cognition. While unquantifiable and imperfect, researchers have had to accept that The disadvantage of hand-built solutions are effectively a "best guess" or suffer from the limitations of similarity-based techniques. solutions, even augmented by pairwise significance tests and bootstrap confidence intervals [32], is that investigators tend to stop when they find a valid solution given the effort involved. But a solution may be one of many possible, each representing potential information about change in cultural traits and their spatiotemporal histories. If what we seek is not merely a rough chronological order but information about cultural transmission, then we need to study all of the solutions.

N	Total Solutions	Seconds	Years
4	15	0.00012	3.7e-12
6	4.7e+02	0.0037	1.2e-10
8	5.2e+04	0.4	1.3e-08
10	1.5e+07	1.1e+02	3.6e-06
12	8.5e+09	6.6e+04	0.0021
13	2.6e+11	2e+06	0.064
14	8.9e+12	7e+07	2.2
15	3.5e+14	2.8e+09	87
16	1.6e+16	1.2e+11	3.9e+03
20	1.7e+23	1.3e+18	4.2e+10
40	9e+65	7e+60	2.2e+53
60	5.1e+116	4e+111	1.3e+104
80	5.1e+172	4e+167	1.3e+160
100	4.4e+232	3.4e+227	1.1e+220

Table 1. Number of total solutions with multiple seriation groups and processing time for sets of assemblages $4 < N < 100$, testing solutions across a computing cluster with 64 cores, $5\mu s$ per evaluation. Once the number of assemblages is greater than 14, brute force methods requiring one to search all possible options clearly becomes impossible even with the fastest available computers working in parallel.

Ultimately, however, neither choice is neither manual sorting nor probabilistic methods are satisfactory since the strength of seriation as a method rests on statistical assessment of the solutions, a requirement that ultimately requires us to deterministically finding all the all solutions that match the dual requirements of continuity and unimodality. Full Thus, an exhaustive characterization of the search space to find all of the valid orders is integral to the methods. method. In addition, we need to know how sets of assemblages fail to produce a valid seriation order. Since we explain variability in frequencies as a function of transmission through time and space, finding the points at which assemblages cannot be fit fitted together is as important as finding those assemblages that do can be seriated [32, 86]. In contrast, approximate similarity orderings sharply limit the degree to which seriation can "find" the points at which probabilistic orderings force all data points into a single solution, and thus are limited in their ability to locate the boundaries at which seriation solutions cannot be constructed, and thus renders the method . As a consequence, probabilistic seriation methods are generally unsuitable for disentangling the contributions of space, intensity of contact, and time.

Figure 1Fig 2, for example, demonstrates the kind of results that occur using with even correspondence analysis, which is the best available similarity-based seriation techniques such as correspondence analysis [?, 39, 59, 87] on large probability-based seriation technique [39, 59, 77, 87]. The example is a set of assemblages of well-described ceramics from the lower Mississippi River Valley [10, 32, 88]. As shown in Panel B of Figure 1Fig 2, the results generally meet the expectation of unimodality, but there are many deviations in the distribution. When we examine the distribution of the assemblages that comprise the solution (Figure 1Fig 2, Panel C and Figure 2Fig 3), we can see that the type frequencies show substantial spatial patterning. The problem, however, is that given any order, how does one distinguish the varying effects of space from those of time? How does one trace the population structure separately from both time and space?

Figure 2. The results of a probabilistic seriation analysis for a set of late prehistoric ceramics assemblages from the Memphis and St. Francis areas as described by Lipo [89] and Phillips and colleagues [10] Here, the figures show the the results of correspondence analysis (CA) for the dataset in Table 2 following [90]. (A) Symmetric map of the CA, showing the first 2 dimensions. (B) The seriation order produced from the CA shown in standard centered bar format. (C) CA results shown with clusters as determined by hierarchical cluster analysis on the principle components. One can see that the change in the frequencies of types roughly follows a unimodal distribution, but there are numerous violations of unimodality as well. Data and R code for the correspondence analysis are available at `https://github.com/mmadsen/lipomadsen2015-idss-seriation-paper`.

Figure 3. Spatial groups of assemblages as determined by the hierarchical cluster analysis on of the principle components generated through the CA analysis as shown in Figure 1Fig 2.

A Model-based Approach To Solving The Seriation Conundrum: IDSS

We argue that at least some progress can be made towards these answers
We argue above that seriation would be greatly improved by returning to deterministic methods. Significantly, while probabilistic approaches produce approximate answers, they do so by throwing away unique frequency pattern information. The pattern of frequency changes between assemblages, with some classes increasing in frequency, while others hold steady or decline, not only uniquely identifies how assemblages "fit" together as cultural traits flow through the larger population in different directions, this detail is useful in reducing the seriation methods that use identity data. We further contend that basing seriation algorithms on the behavior of cultural transmission models derived from evolutionary theory will reduce the scope of the seriation problem, helping to winnow possible solutions and thus reduce the task of assessing potential orders. In a theoretical sense, we contend that model-driven seriation may alleviate the combinatorial nightmare. The combinatorial issue is partially a function of having reduced the description of the problem to one that has the same computational complexity as other "intractable" problems, such as the "traveling salesman" problem or finding Hamiltonian paths in a graph. By using the concepts embedded cultural transmission theory, we can achieve a description that has better performance properties, though any such method will still be computationally expensive.

by giving us specific patterns to search for and thus winnowing candidate solutions more strongly than do methods which employ similarity data. Dunnell [25] showed that evolutionary theory can explain why the empirical generalizations driving seriation are true (to the extent they areand why they fail) and when they fail. Taking historical classes to represent neutral traits (i.e., traits that have no measurable differences in terms of functional impactperformance and/or cost), the forces that primarily act on their temporal and spatial distribution are stochastic (drift). This is what produced both the unique, historically non-repetitive sequence of forms on which the seriation method depended and also accounted for unimodal distributions of relative abundances. Other workers [27, 32, 34, 40, 86, 88] Others have extended this work considerably [27, 32, 34, 40, 86, 88].

The problem remains, however, as to how to turn this theoretical knowledge into a

viable quantitative technique that can systematically generate seriation solution but that can also be statistically evaluated. Moving forward requires us to construct a technique that meets the demands of the deterministic frequency seriation method, as we now understand it. We see four major requirements for an algorithmic approach to deterministic frequency seriation.

While Neiman [27] has shown that cultural transmission of neutral traits does not always produce unimodal distributions, those distributions of class frequencies that are unimodal have a significant chance of being the product of cultural transmission. Further exploration of the relation of unimodality and culture historical practice is warranted but beyond the scope of this paper. When it occurs, however, joint unimodality across several classes is a unique marker which is exceedingly unlikely to occur by chance and definitely occurs through the spatiotemporal diffusion of traits within an interacting population. Thus, where it occurs, unimodality and especially the joint unimodality of multiple classes is a much stricter criterion to use in constructing seriation solutions than monotonic ordering of similarity indices. Many fewer candidate solutions will display joint unimodality than do monotonic similarity, and thus the use of joint unimodality helps avoid the need for brute force enumeration of possible solutions, given an appropriate search method.

In addition, cultural transmission models describe the flow of traits as having continuity within the limits of sampling and population size. In other words, we do not expect large jumps or discontinuities, and can use this criterion as a way of ranking possible solutions and even eliminating candidates that display large gaps in frequencies but otherwise are unimodal. Employing both continuity and unimodality as patterns or criteria places very strong constraints on possible solutions, potentially reducing the number of candidates that must be checked by many orders of magnitude. In the following sections, we develop this intuition into an algorithm. That algorithm must meet several requirements in order to be useful.

First, the algorithm must allow the analyst to address all of the requirements of the seriation method including unimodality and continuity. Unimodality is Consistent with the practice of culture history in archaeology, we treat unimodality as a construct that serves with continuity to help ensure that patterns observed are identify patterns that are potentially the product of cultural transmission. While [27] has shown that cultural transmission of neutral traits does not always produce unimodal distributions, those distributions of class frequencies that are unimodal have a have a significant chance of being the result of cultural transmission. In this way, unimodality provides a powerful heuristic for isolating patterns due to inheritance. Seriation is not a claim that transmission always creates unimodal patterns, so much as it is a selection of those data series which are unimodal, to serve as a measuring tool for prehistoric cultural contact and transmission.

Second, generation of candidate solutions should be automated, so that seriation can be used as part of larger analyses (e.g., spatial analysis, simulation studies of migration, trade, or cultural transmission). Third, the algorithm should provide error estimates and confidence bands where possible, to allow evaluation of the quality of a solution given the input data, and diagnosis of any violations of the method's assumptionsunimodality or continuity. Finally, the technique must be able to find all viable deterministic solutions given bounded and reasonable processing time for even relatively large sets of assemblage (e.g., 20 or 50), allowing replicate analysis such that resampling or the bootstrap can be used to calculate error terms and evaluate the effects of sample size.

These are not easy requirements to meet. In the space created by all the possible orderings of assemblages, the vast majority of orders are invalid, as the combinations

violate the conditions of the deterministic frequency seriation DFS method due to deviations from unimodality and/or continuity. Thus, the way to avoid the combinatorial explosion inherent in the seriation problem is to devise a meaningful "pruning" heuristic that can shrink the effective search space by excluding possible orderings that cannot lead to full solutions given violations of the seriation modelEven with stricter constraints on possible solutions, valid candidates cannot be found by enumeration for more than a handful of assemblages. The search space must be "pruned" in some fashion to remove combinations that cannot possibly be part of a valid solution.

Overview of the IDSS Algorithm The technique we propose to accomplish these goals is called the Iterative Deterministic Seriation Solution (IDSS). IDSS builds deterministic frequency seriation DFS orders in an iterative process, starting with valid seriation solutions composed of the smallest possible number of assemblages and then employing these as building blocks for larger solutions. Solutions are grown from valid smaller solutions , instead of evaluating all instead of enumerating possible combinations. We start with combinations of three assemblages (triples), the fewest number that can be evaluated in terms of the degree to which they meet the demands of the model. With three assemblages(triples), we retain only those sets in which the frequencies for each of the classes show a steady increase, steady decrease, a middle "peak",," or no change at all (Figure 3Fig 4). Assemblage orders that have frequencies that decrease then increase are eliminated as building blocks.

Figure 4. For any three sets In DFS, assemblages must meet the frequency and continuity expectations of the model. Here, three assemblages (Assemblage A, valid seriation solutions consist Assemblage B, Assemblage C) are represented by rows of four possible patterns horizontal bars where the length of the bar is equivalent to the relative proportion of the type in the assemblage. The small black bars reflect statistical uncertainty of the proportions. At least three assemblages are required to evaluate orders based on the seriation model. Valid orders include type frequencies that include no change, types increasing in frequency, types decreasing in frequency, and types that have a single maximum frequency peak. These triplets Invalid orders are those with discontinuity in frequencies, those with more than one maximum frequency peak or in which the smallest subset frequencies of assemblages that types are valid according to increasing towards the expectations top and bottom of the seriation methodorders.

The next step in the procedure is to take use just the successful triples and see if any of the remaining assemblages can be added to either end to create a larger set of four assemblages while also avoiding violations of the seriation model. This process is then repeated iteratively until either there no assemblages remaining to be linked to the ends of the existing orders or until no larger valid seriation solutions can be found. Only the successful combinations of four The successful sets of four assemblages are then used to assess the potential combinations of five , assemblages, successful sets of five assemblages become the basis for looking at valid sets of six assemblages, and so on. This process is iteratively repeated until no additional larger seriation solutions can be validly created. The end product of this stage of the algorithm is one or more valid the set of all valid seriation orders with the possibility that some assemblages may appear in more than one ordering.

The logical basis of this procedure is that all larger solutions consist of, by definition, smaller subsets of valid solutions. Thus, the For example, a valid solution set of six assemblages labeled A-B-C-D-E-F also includes valid subsets such as B-C-D and B-C-D-E. So Thus, if we start with all valid triple solutions and sequentially check

which solutions include valid sets of four assemblages , and so onvalid solutions of N assemblages and iteratively evaluate N+1 assemblages in terms of the requirements of the seriation model, we are guaranteed to end up with the largest possible solution. This process vastly trims down the number of possible solutions since we no longer have Since the algorithm avoids having to search all of the future combinations that stem from an invalid solution. The invalid solutions, IDSS vastly trims down the number of possible solutions: the search space is pruned as the algorithm proceeds.

While this iterative approach reduces the numbers of combinations, the numbers of possibilities to examine still get large. This growth in numbers is due to the fact any large solution of M assemblages (a subset of N, where $M < N$) also includes the number of further subsets. So while we are able to avoid checking combinations that do not meet the criteria of the seriation method, the sheer number of valid solutions still can be extremely that must be examined is still very large. While many of these solutions of these combinations are ultimately trivial since they often become parts of larger orders, when one is iterative ordering assemblages constructing solutions by aggregation, the smaller subsets must always be searched before the overarching larger seriation order is discovered.

By itselfNonetheless, building solutions by iterative "agglomeration" "agglomeration" of smaller building blocks reduces the search space considerably, and by itself is enough to allow the analysis of reasonably sized and archaeologically-relevant data sets.

Scaling the algorithm to large larger numbers of assemblages , however, requires additional heuristics to further restrict the possibilities that must be evaluated.

Solving this secondary problem requires further application of the theory underlying the seriation method. Ford's [6] criterion states that for assemblages to be seriated, they must come from the same cultural tradition (see also [?] [1]). This criterion means that the differences in frequencies between any two assemblages can be assumed to mainly be a function of differences in the degree of interaction. In an ideal set of assemblages that reflect a single cultural tradition one would expect smoothly continuous frequency changes. When multiple cultural traditions are combined, the differences in frequencies will be discontinuous since more than one set of processes is in operationwhen considered as a group. What this means in practice is that discontinuity in frequencies reflect the potential for relative discontinuities in frequencies potentially indicate the presence of more than one cultural tradition or that the changes in frequencies cannot be distinguished from sampling error. Resolution of these options requires additional samples. Since arbitrary parts of a single large solution put together will also produce discontinuities, we potentially requires finding additional intermediate samples.

We can use the same continuity principle to rule out valid subset solutions that we do not need to evaluate. For example, A-D-G is a valid but trivial subset of the solution A-B-C-D-E-F-G. The differences in type frequencies of these subset solutions will be larger than the larger set. By assigning a threshold of discontinuity measured by the maximum allowable difference between the summed frequencies of any pair of assemblages within an ordered set, one can rule out most of these the trivial solutions. Consequently, as we iteratively search for possible assemblages that can be added to either end of an existing one, we can rule out all of the possibilities that are too dissimilar for consideration. This step allows us to ignore removes comparisons between assemblages and reduce thus reduces our search space.

Of course, establishing a continuity threshold requires user inputand , which means that the search space is partially shaped by the researcher. We always implicitly choose a threshold when we choose the set of However, this is always the case as we must select assemblages to include in our seriation, by selecting some assemblages in an area and not others. Making analyses. In the traditional practice of culture historians, this was

accomplished by selecting those assemblages that come from a local area and that appear to come from the same cultural tradition [1]. In IDSS, we make this step explicit and thus amenable to automation and statistical evaluation , here we specify by specifying the maximum discontinuity allowable within a set of assemblages that can be considered as being directly related to one another. In practice, this means stipulating a maximum frequency difference in any one type or summed for the maximum allowable for the sum of frequency differences across all types. In an ideally generated set of assemblages , the maximal that provides a good sample of the interacting population, the greatest difference between the frequencies of types might would be relatively small (e.g., 5% or smaller) since good sampling should ensure continuous change in frequencies. The size of the threshold in many cases will be a reflection of the degree to which the assemblages have sampled are samples of the set of events that produced the assemblages in the first place. In most cases, the continuity threshold can be set higher to tolerate bigger gaps in the frequencies, but at the cost of a greater amount of processing required to search for solutions. The optimal value of the continuity threshold may also be determined algorithmically by repeating the analysis across several threshold values and examining how the structure of solutions change.

Initial Implementation We have coded the IDSS algorithm in Python (see Supporting Material S1 Text for the full algorithm). Tests of our IDSS implementation show that with artificially generated data in which an a priori *a priori* solution is known, solutions can be rapidly the correct solution set is always identified. In Panel A of Figure 4Fig 5, we show a set of 15 unordered assemblages each with 6 types. Using a threshold of 0.10 (i.e., the maximum search distance are assemblages that have type frequencies of acceptable difference between assemblage frequencies is no more than 0.1 difference10%), the IDSS algorithm was able to locate the optimal seriation order of these assemblages out of all possible valid solutions in just over 1470 seconds, using all available computing cores on a 2013-era quad-core computer. Compared to an estimated 22 years for This length of time might appear slow relative to quick hand-sorting but the results of intuitive shuffling of graphical representations cannot ensure that the largest possible order is identified nor can it find all the equally valid solutions that might be present. Traditional brute force sorting methods (Figure **??**), this achievement clearly brings frequency seriation to a position in which it can move from intuitive approaches that evaluate the entire search space can easily take many years (Table 1). Using IDSS instead of hand-sorting to automated and systematic analysis at least when the solutions include allows identification of all valid solutions from groups of 20 or fewer assemblages on a single desktop computer. Twenty or so assemblages is a common scale of analysis, at least for many archaeological cases conducted within local regions, and it is important for a deterministic frequency seriation DFS algorithm to be able to produce optimal solutions for this scale of data, on commonly available hardware. In particular, many large sets of assemblages break down into much smaller subsets when ordered deterministically and thus can be analyzed quickly. Solutions with larger numbers of assemblages or few solution subsets , however, require carefully setting the maximum differences between assemblages and possibly using a computing cluster to further parallelize the evaluation of solutions.

Graphical Representation Figure 4Fig 5, Panel A represents the traditional graphic form for seriations in which the width of the horizontal bars represents the magnitude of the frequencies of types for individual assemblages. This "stacked and centered bar" format is instantly recognizable by archaeologists, and is excellent for displaying the results of a seriation if there is only one causal factor driving the ordering

Figure 5. Example of the results of IDSS algorithm seriation in traditional (output for 15 assemblages with 6 types. This seriation order was generated using a threshold of 0.10. Panel A) takes the form of traditional centered-bar format where the empty bars indicate relative proportion of the type and small black bars represent confidence intervals of $\alpha = 0.05$ for the type proportions. Panel B is the same order in graph form(B). Note that while hand-sorting of this example data could be relatively easily done, the IDSS algorithm ensures that the longest possible solution or set of solutions is found. In real-world cases, patterns of type frequencies often includes the effects of sample size, space and other transmission processes. In these cases, a systematic deterministic method is necessary to ensure comprehensive and statistically sound solutions.

(typically, time) and if no assemblages participate in more than one seriation. When the situation becomes any more complex than a single chronological order, we need a better visual representation.

Graphs, a collection of vertices and edges, provide an alternative means of visualization that accommodate linear orderings as well as more complex relations [91–95]. We can create a graph representation of our seriation results by connecting assemblages via edges in the sequence produced by the IDSS algorithm (Panel B, Figure Fig 4). This simple graphic informs us about the relations between assemblages without the addition of the information regarding the composition of the types. The graph representation allows has an advantage over traditional centered-bar diagrams since it allows us to examine relations where assemblages may be shared in multiple valid solutions [94, 96].

The ability of graphs to reflect complex set sets of relationships, however, can result in difficult interpretation of the results. The strength of seriation is that solutions are linear relations where the order reflects some combination of differences in time and space. However, if assemblages are found in more than one solution, additional analytic steps must be taken to reduce the results to something that can serve as a hypothesis about the structure of transmission and the relations between assemblages. As shown in Figure 5Fig 6, we can proceed by "adding" accumulating valid solutions, and then pruning unnecessary edges. We begin , at the top , with three valid solutions , output from the basic IDSS algorithm. Each meets the criteria for unimodality and the frequency differences are within the tolerance limits for maximum frequency differences0.1 tolerance limit set for continuity. In the middle of the figure, we show the results of "adding" agglomerating the graphs together, where an edge exists between two vertices if those vertices possess an edge in any of the three source graphs. The weights assigned to edges are proportional to the summed differences in type frequencies between pairs of assemblages. This "summed" aggregate graph allows us to construct the final solution. We follow the approach described by Lipo [94], starting with just the vertices, and iteratively adding edges from the summed graph starting with those which possess the lowest weight as measured by Euclidian Euclidean distance between pairs of assemblages. This process produces a graph that includes all the vertices the maximal set of vertices from the starting solutions but using the minimum number of edges that represent smallest distances between vertices and includes all equivalent values as options. The result is what we call the "minmax" graph.

As an example, Figure 6 represents a Fig 7 represents a simulated case in which a set of assemblages that initially represent a single lineage with a single temporal order branches into two sub-populations, each having valid seriation orders. Such a scenario might happen, for example, if a group of individuals who begin by exchanging information later become becomes two distinct but smaller populations that only interact locally, or when a single location serves as a center node for two or more

Figure 6. **Seriation results when more than one solution is possible within a set of assemblages"Minmax" graph creation steps.** In this example, we begin with the graph representations of three valid seriation solutions (1-3) for the same a set of 9 assemblages (A-I). HereIn the figure, the thickness of the edges reflects the summed differences in frequencies between each pair of assemblages. The Each solution represents a valid and unique seriationsolutions are then added together . To combine the three seriations, we first sum the graphs to create a summed single aggregate solution consisting sum that is composed of all nodes and edges from the individual graphs. From Using the sum of the solutionsaggregate solution, we then reduce the graph to include by including the fewest edges that can be made between all vertices . This reduction step involves constructing a graph and starting with the edges that have the smallest weight, as calculated by the sum of the differences in frequencies. Edges that include new vertices are added sequentially until all of the connected vertices are included. Edges with equivalent weight values are includedretained as well.

relatively separate sub-populations. In this scenario(Figure 7), we discover that there , there are 8 possible valid seriations. In a traditional representation of this seriation we would be forced to show each solution separately and note textually or in captions that some assemblages are included in multiple seriationsseriation solutions. Using a graph representation and the process described above, however, we can easily reveal identify a pattern of relations in which the seriation branches into two different paths(Figures 8 and 9). Note that the graph in Figure 8 is complex, but it was constructed using the same steps as in Figure 5, and . The seriation solution we generate represents the minimum set of weighted edges which capture the smallest "weighted distance" between vertices. It represents, in this way, the minimal hypothesis about intensity of transmission and trait sharing needed to account for the observed pattern of frequencies.

Figure 7. **Frequency seriation A set of assemblages that comprise a illustrate branching lineage.** The "-A" and "-B" series (A) Raw data for 15 assemblages with 6 types. (B) Centered bar graphical representation of the relative proportions of types for the 15 assemblages with confidence interval of $\alpha = 0.05$. In this example, we can create valid DFS solutions that include all be seriated along with of the first 5 Assemblages 1-5 plus either the "-A" assemblages or the "-B" assemblages, but not both. (C) Seriation representation of the two lineages that make up the set of assemblages. Although they overlap for Assemblages 1 through 5, the two seriations cannot be seriated as merged into a single set without violations of the modelvalid solution, and thus are shown in bar form as two separate solutions.

Set of all valid seriation solutions in (A) traditional and (B) graph format.Each of these orders is a valid deterministic frequency seriation solution.

Sum of deterministic frequency seriation solutions in graph form.This figure consists of the sum of the edges and vertices in all of the valid seriation solutions in the graphs. The widths of the edges are proportional to the number of times the pair appears in the set of solutions.

The final graph representation of the 'branching' example in Figure 8 that includes seriation relationships for all assemblages added in the order of the smallest distances between pairs.The width of the edges is proportional to the summed frequency differences between the types in each pair of assemblages.

Statistical Evaluation   In generating valid seriations that reflect variability in the   587
archaeological record related to inheritance, we assume that the assemblages are   588
described with sufficient three or more stylistic classes [24,33] to avoid problems of   589
closed arrays [97] [2,97–100]. We also assume that the assemblages have been evaluated   590
in term terms of minimum sample size requirements. Sample sizes must be great enough   591
to ensure a minimum of statistical confidence in the frequencies of classes– otherwise .   592
In cases where samples are insufficient, the frequencies may reflect a lack of proper   593
sampling and not the character of the archaeological record. Early culture historians   594
used a fixed number such a as 50 to be the minimum size required [10]. Better are   595
bootstrap tests that are sensitive to aspects of assemblage richness and diversity   596
Bootstrap tests are a more robust means of assessing when samples are large enough to   597
meet a specified statistical confidence level [32,101].   598

Even when minimum sample size requirements are met, the comparisons between   599
any pair of assemblages must be evaluated in terms of statistical reliability. The larger   600
the sample size, the greater the confidence one has that the patterns between the   601
frequencies of classes reflects the archaeological record and not the happenstance   602
configuration of the sample's description or other circumstances. This uncertainty   603
propagates through the entire seriation order: all solutions obtained have statistical   604
confidence based on the overall strength of the pattern between the pairs of assemblages.   605

To specify the statistical confidence of our seriation solution, we can construct   606
confidence limits for the frequencies of individual classes. These confidence intervals   607
then serve as the basis for assessing the strength of the pattern of frequencies. In terms   608
of statistical models, a set of proportions from M classes is a sample from a multinomial   609
distribution with M categories. Calculating confidence intervals for multinomial   610
proportions is remarkably complex and there is not an exact method that is generally   611
recognized. When the number of classes is "large" (i.e., $M > 10$), the Glaz and   612
Sison [102] method is generally thought to be the best, while $M < 10$, Goodman's   613
method [103] is preferred. Since assemblages can vary in how many classes are   614
represented, a better method is to use a bootstrap means for calculating the values for   615
the bootstrap confidence intervals at a requested significance level for each pair of   616
assemblages. This step consists of creating a large number of new bootstrap   617
assemblages with the same sample size by resampling the original assemblage with   618
replacement. In our implementation of IDSS, we calculate class frequencies for each of   619
the bootstrapped assemblages. Using the pool of assemblages as the basis for the   620
distribution of frequencies, we then determine the limits of the confidence intervals for   621
the designated level of significance (α).   622

We can then use bootstrap confidence limits when we make comparisons of   623
frequencies between assemblages during the iterative assemblage testing steps. The   624
differences between frequency classes must exceed the limits of the confidence interval in   625
order for the pairs of assemblages to be evaluated having frequencies as "greater than"   626
or "less than" one another. All comparisons in which frequencies frequency values fall   627
within the confidence intervals are scored as "matching." Since matching frequencies do   628
not violate the assumptions of the frequency seriation model, this process has the effect   629
of creating a greater number of valid solutions all of which are statistically valid orders   630
at a given level of significance. Figures 10 and 11 provide Fig 8 provides an example of   631
how bootstrapped confidence intervals can produce different solutions than using direct   632
frequency comparisons especially when sample sizes of the assemblages or differences in   633
frequencies being compared are small.   634

The graph solutions include for the assemblages in Figure 10 using the process   635
described in Figure 5. In A, the seriations are created through direct comparison of the   636
frequency values. In B, the seriations are created through statistical comparisons using   637

Figure 8. Example set of In A and B, 7 assemblages that cannot be seriated together due to composed of material with 5 types are shown with a violation in the continuous distribution of frequencies. Assemblage 6 lacks material Comparing frequencies between assemblages relative to the DFS seriation model with a specified confidence interval of Type 1 $\alpha = 0.001$ and thus is not continuous with Assemblage 5 the bootstrap process described above, two valid solutions must be formed (C and 7. D). These two solutions share Assemblages 1-5 but differ as to whether they include Assemblage-6 or Assemblage-7. (E) shows the two overlapping solutions in graph form.

bootstrapped confidence intervals for the type frequencies ($\alpha = 0.001$). When confidence intervals are considered, there are a greater number of possible valid solutions. As a result, we can find the longest solution that meets our specified level of significance.

Results

Example From Phillips, Ford And Griffin (1951) And Lipo (2001)

Archaeological research conducted in the Lower Mississippi Valley (LMV) provides a useful example of how the concepts behind cultural transmission form the basis for generating explanations of the archaeological record, and no better case study exists than the long-term efforts of Phillips and his colleagues [10]. Through a series of surface collections of decorated prehistoric ceramics and the use of seriation to order assemblages through time, this work provided a remarkably their work produced a solid chronological framework for the Mississippi River valley and established the region as one of the primary foci a primary focus of American archaeology [2, 70, 104].

Using a subset of data from the LMV assemblages and new ceramic collections from seven deposits in northeastern Arkansas [32, 88] and shown in Table 2, Lipo used seriation-based techniques and simulations of cultural transmission to account for patterns of stylistic similarity in varying spatial and temporal configurations among 20 late prehistoric locations. Through his analysis, Lipo [86, 88] demonstrated that data generated from the original collections are well suited for examining transmission.

In his analysis, Lipo [86, 88] constructed deterministic seriations for the assemblages using a manual graphical technique and found that the no single solution could be obtained using the 20 assemblages. Instead, the set of assemblages had to divided into 8 different spatial groups (Figure 12-13Figs 9–10). These groups reflected the effects of local transmission among communities that overwhelms the effects of longer-range interaction within the region. Interestingly, two valid seriation solutions in the "Parkin" area (Groups 2 and 3 in Figure 12Fig 10) overlap with one another in that they both share the assemblage 11-N-1, the Parkin site. Lipo [88] explained this result as the effect of Parkin acting as a central "node" in a network and possibly indicative of emerging social complexity among otherwise functionally redundant settlements.

While Lipo's result demonstrates the potential for seriation as a means of explaining patterns of cultural transmission, the results and the approach as a whole are limited in practical utility for a number of key several reasons. First, the seriation results were created by hand sorting following graphic methods outlined by Ford [6, 10] though assisted using spreadsheet macros in Microsoft Excel [88]. Consequently, we have no way of knowing whether the final sets of orders are the largest set or whether all possible solutions are represented. Second, while Lipo ensured that the assemblage sizes were adequate for comparisons of richness and diversity, we cannot specify the

Figure 9. The set of deterministic frequency seriations DFS solutions created by hand sorting by Lipo [88] late prehistoric ceramic assemblages in the Memphis and St. Francis areas of the Lower Mississippi River Valley Survey [10] [10, 88]. Here, the assemblages have been standardized in terms of type descriptions and are all of sufficient sample sizes. The error bars indicate the 99% confidence interval for the type frequencies. The largest seriation solutions formed eight spatial sets. The assemblage from Parkin (11-N-1) falls into two different sets, suggesting that it served as a central node of interaction between communities. The Holden Lake assemblage appears as a valid addition to all of solutions, supporting the seriation suggesting idea that it is earlier than the other samples in the analysis.

Figure 10. Spatial distribution of seriation groups with St. Francis and Memphis Assemblages consisting of Lipo [88] [89] and Phillips et al. [10] samples. Labels for groups refer to seriation solutions numbered in Figure 12Fig 9. While each seriation group also includes Holden Lake, this assemblage is removed here for visual clarity. The groups are strongly spatial in their configuration. Interestingly, the Parkin (11-N-1) assemblage falls into groups 2 and 3 suggesting that it served as a central node, possibly indicating emerging social complexity.

confidence interval around the final set of solutions chosen created confidence intervals for each class frequency and tested the pairwise ordering of assemblages, the inability to assess the chosen solution with respect to the entire search space limits confidence in the results. Finally, the use of frequency graphs as the graphical representation for the set of solutions reveals the limitation of the visualization. While, Lipo demonstrated how Lipo showed that seriation orders overlapped or intersected with one another and that this overlap potentially allows one to infer information about prehistoric social structure, the frequency bar graph is incapable of representing anything other than linear ordersbut the use of stacked and centered bar charts prevents effectively visualizing such relations. This limitation impacts the degree to which the approach can be systematically applied, especially as cases become increasingly complex.

IDSS Analysis of PFG Assemblages

Using the IDSS analysis we can systematically produce examine the full set of possible frequency seriation solutions (Figures ?? Figs 11–??13). Despite the large number of possible solutions ($N = 2.56 \times 10^{18}$), iteratively finding the maximum set of set of 97 possible solutions required less than two seconds of processing due to the fact that the largest possible seriations were composed of only 4 assemblages. No larger sets can be built without introducing violations of unimodality, so the algorithm did not need to continue its search and terminated. Using a confidence interval of 0.995% $\alpha = 0.05$ allowed us to generate a solution that included all assemblages. The results of the seriation analysis reflect many of the features of the original analysis but add additional details regarding the structure of interaction between communities. Fig 11 clearly shows how the traditional linear ordering breaks down as a visualization mechanism, especially in the presence of many valid solutions. A number of assemblages participate in multiple solutions, and it is impossible to get a sense of the overall nature of the solutions when confronted with many separate orderings. Thus, as described above, we focus here on the graph representation of results (Fig 12).

Fig 12 displays the combination of valid seriation solutions as a "minmax" graph, constructed by combining individual valid solutions and retaining those connecting edges which minimize the total frequency differences between assemblages. Each branch in the graph represents an ordering, which may be temporal, spatial, or a combination

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Figure 11. An "atlas" of the 97 valid DFS solutions for the Memphis and St. Francis area assemblages that can be created using the IDSS algorithm, a continuity threshold of 0.30 and $\alpha = 0.05$ confidence intervals for frequency comparisons. The confidence intervals for each assemblage are determined using 1000 bootstrap samples for each pair of assemblages. Note that many assemblages (e.g., 12-O-5) appear in multiple seriations. Also, note that many assemblages are present in more than one solution, which demonstrates the difficulty of understanding the overall pattern of change using the traditional linear representation.

of spatiotemporal causes. Most notably, the pattern of the seriation solutions is strongly spatial: assemblages are more likely to be linked to neighbors than others farther away (Figure ??Fig 13). To assess the statistical significance of the spatial patternis greater than chance, we resampled the original set of assemblages, and calculated the sum of the frequency distances between the pairs. Doing this 1000 times provided a probability distribution against which we compared the original resultsover the clustering of assemblages into groups. In the case of the IDSS results results shown in Fig 13, we estimated p=0.04 $p = 0.04$ which suggests that the spatial pattern is statistically significant.

Figure 12. The largest set of valid frequency seriation solutions created using the IDSS algorithm 'minmax' graph produced for the Memphis and St. Francis and Memphis area assemblages from the 97 valid DFS solutions generated the IDSS algorithm (as shown in Fig 11) using a continuity threshold of 0.30 and $\alpha = 0.05$ confidence intervals for the comparison of frequencies. The "minmax" graph was generated using the procedure described by Lipo [88]in Fig 6. Significantly, the results show remarkable structure with a series of spatially clustered branches that are formed from overlapping but distinct sets of seriation solutions. Parkin (11-N-1) forms the center of a branch that extends in 3 different directions (to 11-N-9, 13-P-1 and 11-O-10). Assemblages 13-O-7 and 13-O-10 also have this same configuration. 13-O-7 has an extra branch leading to Holden Lake, a presumably earlier deposit. The branches are numbered and colored to correspond with the spatial groups in Fig 13.

Figure 13. Graph representation The spatial distribution of all seriation solutions for the St. Francis edges of graph shown in Fig 12 and Memphis the spatial groups of assemblagessummed together. The width groups outlines represent the branches of the "minmax" graph depicted in Fig 12. Note that the edges reflects have a measure of differences between strong spatial pattern in that assemblages calculated as the sum next to each other are more likely to be paired within seriation solutions than those assemblages that are farther away. A bootstrap assessment of the differences significance of frequencies between typesthis spatial pattern shows that $p = 0.04$. Not all The color of the assemblages can be added each spatial group corresponds to the set of solutions as shown by major branches in the vertices without edges"minmax" graph in Fig 12.

The graph created from the sum of the deterministic frequency seriation solutions for the St. Francis and Memphis area assemblages.

All of the valid deterministic frequency seriation solutions for the Memphis and St. Francis area assemblages using a 0.995% confidence intervals ($\alpha = 0.005$) for frequency

comparisons.The confidence intervals for each assemblage are determined using 1000 bootstrap samples for each pair of assemblages.

Graph representation of the sum of all valid deterministic frequency seriations solutions generated the IDSS algorithm (Figure ??) and using 0.995% confidence intervals ($\alpha = 0.005$) for the comparison of frequencies.

Graph for the valid deterministic frequency seriations solutions generated the IDSS algorithm using 0.995% confidence intervals ($\alpha = 0.005$) for the comparison of frequencies and using the procedure describe in Figure 5.Parkin (11-N-1) forms the center of a branch that extends in 3 different directions (to 11-N-9, 13-P-1 and 11-O-10). 13-O-7 and 13-O-10 also have this same configuration. 13-O-7 has an extra branch leading to Holden Lake, a presumably earlier deposit.

The spatial distribution of the edges of graph shown in Figure ??.Note that the edges have a strong spatial pattern in that vertices next to each other are more likely to be paired in seriation solutions than those that are farther away. A bootstrap assessment of the significance of this spatial pattern shows that $p = 0.04$. Spatial groups of assemblages for the PFG. The groups outlines represent the set of assemblages that are linked to their nearest neighbors.

There are significant differences from the original seriation analysesThe analysis with IDSS shares many of the large scale features of Lipo's original analysis [88], but there are also significant differences. First, we can now see the continuous nature of the interaction: while there are locally connected sets of assemblages, the seriation solutions grow increasingly inclusive over space as one includes more assemblages with few indications of discontinuity. In Figure ??, we have created arbitrary all possess interconnections which point to a "nested" interaction structure between communities. In Fig 13, we found 4 groups composed of those sets of assemblages connected to their nearest spatially-local neighbor. Divisions between the groups are identified by edges connect assemblages beyond the nearest neighbor distance. The seriation orders reflect the identified groups are shown by edges that connect assemblages which minimize intra-group frequency distance. Overall, the IDSS solution reflects the pattern in which assemblages form spatial sets in which are in turn related to each other at higher scales of analysesanalysis.

This pattern is exemplified by Group 1 in Figure ?? Fig 13. Group 1 is composed of a single set of assemblages that fall northeast of 11-N-1 (Parkin). Parkin remains a member of more than one seriation solution with branches going to 11-N-9 (Group 1a) and and another going to a group formed by assemblages 11-O-10 /and 11-N-4(Group 1b). Interestingly, on the basis of these new analyses the IDSS results, Rose Mound (12-N-3) now appears to be more closely related to the southeastern Group 2 to the south rather than being part of related to the group with Parkin. This configuration might explain the proximity of the two large deposits so close together. We propose that this set of archaeological deposits were created by separate lineages whose use of the landscape is focused in different directions: Parkin towards the north and Rose Mound to the south. Alternativelyit , the configuration of assemblage relations may reflect use of the landscape by groups over slightly varying points in time. Further study regarding the relations between these deposits is needed.

Group 2 in Fig 13 includes assemblage 13-P-1, 13-P-10 and 13-N-21 on the east side of the valley. The inclusion of 13-N-21 here can be potentially explained by independent knowledge that the deposit is significantly a series of testable hypotheses: (a) the deposit was created substantially earlier than the other assemblages , the outcome of a lack of

intermediate assemblages from the study or by the in the study, (b) the assemblages 768
used in the study are incomplete and lack intermediate assemblages or (c) the 769
composition of the deposit reflects the movement of populations from one community to 770
the otheroutside this local community and thus forms a discontinuity. The same set of 771
hypotheses can be built for the relation of 10-P-1though , although in this case the lack 772
of additional local assemblages around the deposit is the most likely caseexplanation. 773
Assemblage 13-P-1 shares solutions in the same way in which 11-N-1 does in Group 1. 774

The assemblages located in the south and southwestern portions of the study area 775
(Group 3 in Figure 20Fig 13) form a large group in which the likelihood of falling into a 776
solution decreases with distance. The assemblages form two subsets (3a and 3bgroups 777
(Groups 2 and 3) that overlap with at 13-O-7. Like 11-N-1 and 13-P-1, 13-O-7 forms a 778
central node with overlapping seriations, one to the south and one to the north. 779

The fact that each of the groups of locally interacting assemblages also includes an 780
assemblage that is found in multiple overlapping seriation solutions lends weight to the 781
notion that patterns of interaction reflected in the frequencies of decorated pottery 782
types is informing on the social relations within these communities. Overall, the 783
distance between neighboring communities structures interaction between populations. 784
Interaction, in other words, has a strong "nearest-neighbornearest neighbor" quality. A 785
few communities, however, do not follow this pattern and exhibit evidence of greater 786
interaction throughout the region regardless of their frequency distance to other 787
localitiesassemblages. This pattern is likely the consequence of hierarchical organization 788
to the cultural transmission patterns structure in the interaction among such 789
communities, and potentially represents the beginnings of more complex social 790
organization [86, 88]. 791

Significantly, the spatial pattern of the nearest neighbor groups (Figure ??) generally 792
matches the pattern observed in Figure 2 showing the results hierarchical cluster 793
analysis of the correspondence analysis for the same data set but with greater detail . 794
Unlike correspondence analysis where the output is a statistically generalization of the 795
assemblages, the IDSS results are theory-driven and allows us to relate a seriation to 796
actual transmission events. 797
Additionally, the IDSS algorithm provides a means of distinguishing the 798
within-group temporal relations from the between-group spatial ones. 799

Returning briefly to the correspondence analysis from Figs 2 and 3, the clustering of 800
assemblages is roughly similar, but the IDSS results resolve more detail about 801
connections between assemblages. We argue that this detail is available in a 802
deterministic algorithm such as IDSS but not in the correspondence analysis because 803
the transformation of frequency data to similarity coefficients obscures detail, which the 804
traditional frequency seriation model (as embodied here in IDSS) is able to utilize. 805

Discussion 806

Deterministic frequency seriation DFS has a long history in archaeological research. 807
Indeed, it seriation is one of the few unique analytical tools developed wholly within 808
archaeology . Much of entirely within archaeology and its use led to the success of the 809
discipline in the first half of the 20th centuryis derived from the use of seriation and the 810
culture historical concepts associated with sorting observations through time. Beginning 811
in the 1960s, a growing fascination with numerical techniques and spatial 812
reconstructions resulted in the perception that the utility of deterministic frequency 813
seriation was regarded as a non-systematic and outdated "dating" technique that was 814

been generally the perception grew that DFS was an unsystematic and outdated method of producing chronologies that had been superseded by radiocarbon chronometrics.

The demise of seriationas a central tool of archaeological inquiry comes from our lack of Radiocarbon dating, however, is not the principal cause for seriation's demise in recent decades. Despite having broader applicability than just relative dating, the lack of a theoretical rationale and an automated means of systematically generating solutions , along with a rising interest in cultural reconstruction rather than matters of chronology. Similarity-based approaches have largely served to solve chronological issues at the cost of seriation's connection to archaeological theory. While numerical techniques offer fast ways of producing orders, the degree to which they rely on simple similarity matrix ordering and discarded the more detailed requirements of the original deterministic frequency seriation method made their products largely useless and this lack of effectiveness stymied the development of seriation as a method. And the growing dissatisfaction was quite reasonable: if the method cannot be guaranteed to produce any specific knowledge or if it depends on unknown or even incorrect assumptions, there is little value to be gained from its use.

generating solutions led investigators to look elsewhere. We suggest that the deficiencies of seriation can be addressed by framing the method in terms of cultural transmission theory and ultimately, evolutionary theory itself. Once integrated into theory and implemented through practical and well-performing algorithms for generating solutions, we argue that seriation has an important place in the archaeological tool kit beyond its former use as a dating method.

Theoretical developments of the last 20 years have started to provide a theoretical basis for the method [24, 27, 32, 33, 40, 88, 105]. Seen as a general means for studying transmission that provides temporal orders under particular empirical and measurement conditions, deterministic frequency seriation has great potential. This potential, however, has been ultimately hindered by the legacy techniques used to implement the method.

Hand sorting descriptions of assemblages, while faithful to a minimum set of underlying theoretical requirements, is simply impractical, difficult to evaluate and limited in statistical rigor.

The approach presented here by the IDSS algorithm certainly does not solve all the problems inherent in deterministic frequency seriation. We the creation of an automated DFS algorithm, but is a step in the right direction. Ultimately, we need a greater understanding of the relations between the structure of classification used to measuring artifacts and the patterns generated by these descriptionsthe classifications used to categorize and the effect of this structure on seriations. We also need the development of techniques that can handle arbitrarily large sets of assemblages through some combination of careful parsing of valid analytic sets, massive parallelizationcluster computing, or clever sorting algorithms. Ideally, we should be able to run deterministic frequency seriation DFS analyses on sets of assemblages and then evaluate the results as a function of varying classification strategies, sample sizes and other sources of input. For each source of arbitrary input in the method, we should be able to we can evaluate the degree to which those choices influence the structure and character of the results. And we should be able to more tightly link our results to the theoretical rationale that forms the need a tighter link between theory and method. For example, what happens if we eliminate the need for unimodality as a sorting criterion? How do assemblages representing different durations affect the structure of outcomes and can we use

patterns observed in seriation results to detect duration? Do particular regional models of transmission yield particular patterns in the resulting seriation solutions? Such questions point to new areas of research that are opened up by having an algorithmic means of generating deterministic frequency seriation DFS solutions.

The IDSS algorithm reflects an opportunity to achieve some of the promise of seriation as suggested by earlier efforts. Our preliminary results suggest indicates that we can avoid many of the limitations of deterministic frequency seriation DFS as traditionally done yet add needed features such as statistical evaluation, automation, and new visual representations to assist in disentangling the roles of time and the potential for complex patterns of interaction which blend factors of time and space. The spatial proximity in solutions. Our example from the Lower Mississippi River Valley survey illustrates these features and indicates the potential of the developments to comeillustrates the key features of the approach and demonstrates how IDSS can offer new details about the patterns of prehistoric cultural transmission and inheritance along with statistical assessment of solution quality.

Table 2. **Late Prehistoric Ceramic Assemblages prehistoric decorated ceramic assemblages from the Memphis and St. Francis areas of the Mississippi River Valley** as described by Lipo [88] [89] and Phillips et al. [10]. Analyses by Lipo [89] demonstrate that these assemblages have adequate sample size, classification consistency, no sherd size effects, and that the depositional environment equivalences environments are approximately equivalent. Given these analyses, we have confidence that the relative frequencies of ceramic types reflect patterns in the archaeological record and not the procedures involved in collection and description.

	Parkin Punctate	Bar-ton/Kent/MPI	Painted	Fortune Noded	Ranch Incised	Walls Engraved	Wallace Incised	Rhodes Incised	Vernon Paul Applique	Hull Engraved
10-P-1	39	62	46	0	0	0	0	0	0	6
11-N-9	528	198	13	0	19	0	0	0	0	0
11-N-1	865	323	59	17	35	0	0	0	4	0
11-O-10	404	208	6	16	4	0	0	0	0	0
11-N-4	764	470	18	5	9	0	0	0	0	0
13-N-5	35	11	33	0	0	0	0	0	0	0
13-N4	71	67	96	0	3	4	0	0	0	0
13-N-16	42	56	69	0	1	3	0	0	0	0
13-O-11	35	65	24	0	0	2	0	1	0	1
13-O-10	61	74	79	0	2	8	0	2	0	0
13-P-1	244	40	18	1	16	21	0	14	0	6
13-P-8	83	25	43	0	18	17	0	3	0	3
13-P-10	30	15	12	0	12	12	0	7	2	1
13-O-7	590	498	67	10	21	19	12	8	7	1
13-O-5	923	637	42	12	33	27	15	13	5	2
13-N-21	426	69	105	4	4	0	1	4	1	0
12-O-5	204	156	42	7	8	4	2	1	0	0
Holden Lake	27	294	7	24	2	0	2	1	3	0
13-N-15	728	364	160	9	5	8	14	3	7	2
12-N-3	549	328	77	19	4	0	3	1	2	0

Supporting Information 878

S1 FigText 879

Number of total solutions with multiple seriation groups and processing 880
time for sets of assemblages $4 < N < 100$, testing solutions across a computer 881
with 64 cores.Once the number of assemblages is greater than 14, brute 882
force methods requiring one to search all possible options clearly becomes 883
impossible even with the fastest available computers working in parallel. 884

S2 Text 885

Pseudo-code representation of the IDSS algorithm. 886

Acknowledgments 887

urlstyle

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Algorithm 1 Algorithm for IDSS seriation

Require: Input file I format:
 1: Tab-delimited text, column 0 contains assemblage name
 2: Remaining columns contain type counts as integers
 3: **procedure** IDSS(I)
 4:     Read input file I
 5:     Calculate relative frequency of each type
 6:     Calculate max frequency difference between assemblage pairs
 7:     Create list of assemblages A
 8:     **for all** triplets of assemblages T **do**
 9:         **if** using continuity threshold t_c **then**
10:             **if** max frequency difference $> t_c$ for pairs $\in T$ **then**
11:                 Skip triplet
12:             **end if**
13:         **end if**
14:         **if** triplet T is valid given unimodality for all types **then**
15:             Store triplet in candidate solutions **C**
16:         **end if**
17:         $R \leftarrow$ assemblages $\notin$ **C**   ▷ Remaining assemblages
18:         **repeat**
19:             **for all** assemblages $a \in R$ **do**
20:                 **if** using continuity threshold t_c **then**
21:                     **if** max freq difference $> t_c$ for a and all **C then**
22:                         Skip assemblage a for this loop
23:                     **end if**
24:                 **end if**
25:                 **if** assemblage a + candidate solution $c \in$ **C then**
26:                     Replace c in **C** with $c + a$
27:                     Remove a from R ▷ Grow existing solutions
28:                 **end if**
29:             **end for**
30:         **until** $R =$ or loop repeats with no changes
31:         **for all** candidate solutions $c \in$ **C do**
32:             **if** c is strict subset of another solution in **C then**
33:                 Remove c from **C**
34:             **end if**
35:         **end for**
36:     **end for**   ▷ **C** now contains the set of solutions
37:     Output **C** in various formats
38: **end procedure**

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