PATTERNS IN SPACE AND TIME

SIMULATING CULTURAL TRANSMISSION IN ARCHAEOLOGY

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Marko Porčić

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PREFACE

With the rise of the latest scientific revolution in archaeology, it may seem that we do not need to worry any more about the old theoretical, methodological and empirical debates about style, archaeological cultures, diffusion, seriation, types, classification etc., as the hard sciences will provide the answers that we seek, just as analysis of ancient DNA resolved one of the long-standing questions about the nature of Neolithic expansion in Europe. Although I fully embrace the application of the hard sciences in archaeology, a part of me has always felt that the use of biology, physics and chemistry, with the aim to answer the traditional archaeological questions, was almost like jumping to the answers pages with the solutions to the exercise questions at the end of a textbook. On a more serious note: there is nothing wrong with this – the latest developments in archaeological science have pushed forward the boundaries of our knowledge in ways which were unimaginable a few decades ago; and we should take any scientific path that will generate positive knowledge about the past. But the patterns of material culture, which were the subject of traditional archaeological research, are still there, and they contain relevant information about the past. If archaeologists do not continue to persist in developing theories and methods to deal with this aspect of the archaeological record, no one else will.

This book is an exploration of archaeological theory, and represents an attempt to illustrate how cultural transmission theory, as a relatively novel tool in the archaeologist's intellectual toolbox, can be used to explore, understand and explain some of these traditional and fundamental issues in archaeology. The book grew out of research that I have performed intermittently over the last nine years, most of which has remained unpublished. My fascination with cultural transmission theory and evolutionary archaeology dates back to the days when I was a PhD student, but for various reasons, I have never been able to devote my full attention to it. During the past 15 years, I have been building and upgrading the skills necessary to do research in this complex field. The most important skill was the ability to make computer simulations. This allowed me to play and experiment with potential scenarios of the past. I quickly discovered that these experiments helped me to understand better the complex interplay between the properties of the cultural process and the archaeological record. I also discovered that the machinery I built can be used to test hypotheses and generate new theoretical knowledge. So, this is how this book came to be. It was written around the results I had accumulated over the years. My ambition with this book has not been to make a comprehensive study of the fundamental archaeological problems related to the formal variability of material culture in space and time, but to write about this subject from the perspective of the results of my own simulation experiments and the insights they provided. My hope is that the readers will benefit from this book in the same way as I did while I was creating the material for it – that it will deepen their understanding of the intricate connections between the spatio-temporal distributions of types and assemblages, and the processes which generated them.

I wish to express my deepest gratitude to the reviewers: Enrico Crema, Stephen Shennan and Aleksandar Palavestra. Their detailed comments and suggestions have helped me to improve the original text significantly – they have indeed offered true guidance, for which I am immensely grateful. I would also like to express my gratitude to Jonathan Boulting for the language editing. Of course, the responsibility for any remaining errors and omissions is exclusively mine.

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THE OLD PROBLEMS AND THE NEW TOOLS

Chapter 1

THE OLD PROBLEMS AND THE NEW TOOLS

1.1. THE OLD PROBLEMS

Lyman and colleagues started their major review of culture-historical archaeology in America by mentioning Gordon Willey's (1953) and Albert Spaulding's (1960) minimalistic definitions of archaeology as a study of the formal variability of material culture in space and time (Lyman et al. 1997: v). Indeed, it is difficult to find a more profound description of archaeology's essence than that. Why are two objects (e.g. two clay pots) or assemblages of objects from different places and times similar or different? In what ways are social structures and processes reflected in the spatio-temporal patterns of stylistic and technological variability within and between communities? These are the fundamental questions of archaeology. The intricate interplay of form, space, and time is the subject of this book. I will begin by outlining in broad strokes the old problems of archaeological inquiry, as they are both the subject and the main motivation for undertaking the research presented in the chapters to come.

Traditional culture-historical archaeology excelled in the description of the formal variability of material culture in time and space. The fact that the formal properties of the material culture change through time was utilized by the culture-historical archaeologists to create chronologies (Lyman et al. 1997; Lyman et al. 1998; O'Brien & Lyman 1999). The patterns in time became crucial for the reconstruction of relative chronological relations between artifacts and assemblages via the seriation method. Even though the reasons for the observed patterns were not well understood, the seriation method worked. And there are at least two reasons why these patterns in time still matter today. The first reason is that the patterns themselves hold clues about the processes that generated them, and these processes can be studied if the suitable theoretical framework is available. In other words, the temporal variability of material culture is not something that is only useful for relative dating, but can also reveal important information about past social and cultural dynamics. The second reason is that the development of methods of absolute dating did not eliminate the need for constructing relative chronologies. The precision of radiocarbon dating, which is the most commonly used method, is usually not sufficient to inform us about the temporal order of events all of which occurred within the same 100-200 years. Moreover, in such cases, knowing the relative temporal sequence of the dates can be used to narrow down the ranges of the dates within the Bayesian modeling framework. Therefore, we still need the methods of relative dating. A deep theoretical understanding of the processes which generate temporal patterns can be used to improve the seriation method and to obtain a better grasp of its potential and limitations.

The patterns of formal variability of material culture in space and the spatial distribution of culture became the central issues of anthropology and archaeology in the 20th century, and continue to be important today (Hodder 1978; Roberts & Vander Linden 2011). It became obvious very quickly to both archaeologists and anthropologists of the late 19th and early 20th centuries that culture was spatially clustered – that similar cultural elements are usually found in the same region, and that different regions usually display different cultural elements. The explanation of such patterns has represented a major theoretical challenge in both archaeology and anthropology (Shennan 1994). The processes of cultural diffusion and migration were invoked to explain this variability within the culture-historical paradigm. The mapping of cultural elements in space and understanding of the resulting patterns became a major concern of culture-historical anthropology in its various schools and versions, from Bastian and Ratzel in the 19th century, to the Vienna school of diffusionists, and particularly Franz Boas and his students in America (Палавестра 2011: 107-118).

In archaeology, the spatial clustering of material culture and its interpretation also became a major issue in the first half of the 20th century, especially in the works of Kossinna and Childe (Trigger 2006), giving rise to the important theoretical concept of *archaeological culture* (Shennan 1994; Clarke 1978; Roberts & Vander Linden 2011; Shennan 1978). The concept of archaeological culture is traditionally defined as *"... certain types of remains – pots, implements, ornaments and house forms – constantly recurring together" (Childe 1929: v-vi).* David Clarke (1978: 188) later reformulated Childe's classic definition of archaeological culture, as *"...a polythetic set of specific and comprehensive artefact-type categories which consistently recur together in assemblages within a limited geographical* *area”*. The implication of Clarke’s definition is that archaeological cultures are equivalent to statistical groups (e.g. clusters resulting from cluster analysis) of assemblages, because the groups are defined by stylistic similarity between units, and the units do not have to be identical in order to be in the same group (Porčić & Nešić 2014). The central question which emerged from the works of Kossinna and Childe was how to relate the archaeological cultures to the anthropological, ethnographic and historical units such as linguistic group, society, polity, and ethnic group.

The concept of archaeological culture has been employed in the traditional culture-historical approach to identify and organize the formal variability of material culture across time and space into convenient and manageable units. The assessment of similarities or differences was largely based on subjective estimates rather than statistical analyses (except in American culture-historical archaeology, which was more oriented towards quantitative analysis – see Lyman et al. 1997). Despite the polythetic nature of the concept, in practice, the definition of archaeological cultures was usually based on a single class of material culture, knapped stone artifacts for the pre-Neolithic, and pottery for the Neolithic and post-Neolithic periods (Furholt 2008; 2020). The resolution and meaning of these units in terms of an underlying anthropological and historical reality remains unclear (Porčić 2013b). In the traditional paradigm, archaeological cultures served both as empirical patterns and explanatory devices, and were often equated with ethnic, linguistic or socio-political groups (Shennan 1994). Thus, a map with a distribution of archaeological cultures from one specific period in time was usually understood as a historical or ethnographic map with the different polities represented in space. Although few archaeologists today would explicitly claim that archaeological cultures equate with ethnic or linguistic groups, many still use the term with the implicit idea that these entities represent vague equivalents of ethnographically recorded groups or reflections of some kinds of socio-political entities.

Spatially bounded groups of sites or assemblages with typologically similar material cultures can be characterized as the results of an informal cluster analysis. In this light, it is not unreasonable to assume that, in many cases, the traditional concept of archaeological culture did capture significant patterns of formal variability of material culture in time and space. After all, the formal cluster analysis also involves subjective elements in choosing the similarity/distance measure and the clustering algorithm[1] (Shennan 2004; Baxter

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[1] The cluster analysis may sometimes produce different groupings, depending on the clustering algorithm and the distance metric. Therefore, even the objectivity of the patterns themselves is not absolute.

1994). Therefore, the fact that archaeological cultures are subjectively defined is in most cases a minor technical issue, as the informal and formal clustering methods may produce similar results (but see Ivanovaitė et al. 2020; Sauer & Riede 2019), and they are all arbitrary to a degree. Of course, it is always better to have a quantified description of the archaeological record, but the identification and description of patterns are not the main problems here.

The true problem is in the nature of the patterns and their interpretation. A cluster analysis will produce groups regardless of whether such groups represent discrete sociocultural/ethnic/political/linguistic entities or not. For example, if a cluster analysis is applied to a sample of units with equidistant values in one dimension, the units will be organized in the output into discrete groups, even though such groups do not exist. There are statistical ways to evaluate the validity of groups created in such a way, but the point is that archaeologists always deal with some kind of pattern while they attempt to organize the variability of the past record into discrete units. But even if a true pattern of discrete grouping exists, it does not automatically reveal the mechanism which created it – or, in other words, these groupings or patterns need to be explained and interpreted after further probing. The problem goes beyond drawing boundaries based on the distribution of material culture in space. While the overwhelming evidence nowadays demonstrates the futility of the term ‘archaeological cultures’ as an interpretative framework (Shennan 1994), we may still legitimately wonder what stands behind the spatial patterns of material culture variability (Shennan et al. 2015; Porčić 2013b).

The problem of interpreting archaeological cultures also has a deeper epistemological dimension related to the distinction between essentialism (typological thinking) and population (materialist) thinking (Mayr 1994; O’Brien & Lyman 2000: 31-36). The concept of archaeological cultures corresponds closely to an essentialist ontology. The archaeological cultures are imagined as holistic entities with an essence which is materialized in each artifact or assemblage belonging to a particular culture[2]. In contrast, the population thinking approach regards the individual variation as real. According to this view, population properties are statistical summaries – they are abstractions, and represent the consequences of processes which operate on the level of individuals. The essentialist view is limiting, as it imposes one particular

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[2] This statement perhaps fits better with the view of archaeological culture in European archaeology than in American archaeology. Even though Binford and other New Archaeologists portrayed Americanist culture-historical archaeology as subscribing to the normative theory of culture in archaeology (Binford 1965), which is essentialist, just as is its European counterpart, Lyman and O’Brien (2004) debate this characterization and present a complex and more nuanced picture of the role of normative theory in Americanist archaeology.

interpretation upon the spatiotemporal clustering of material culture; whereas the population thinking approach is better suited to investigating the processes which have generated the formal variability of material culture.

In the previous paragraphs I was using the term ‘formal variability’ of material culture rather vaguely, to cover all kinds of variability between the objects and features of material culture. In this context, the form is understood in the most general sense suggested by Dunnell (1978) – as any artificial attribute without the specification of scale; so it can refer to the variation in attributes of objects, groups of attributes, types (variants) of objects, or the frequency structure of assemblages. This variability is associated with the stylistic and/or functional/technological aspects, depending on the choice of attributes. The functional and technological variations of material culture also represent the formal variation of material culture, and as such, are legitimate phenomena for research. But in this book I limit myself to the study of stylistic aspects of formal variation.

Sackett conceptualized style as *isochrestic variation* – whenever there are functionally equivalent ways of making or doing something, there is room for style (Sackett 1982; 1986). In Sackett’s view, style is in most cases passive, in the sense that stylistic variation (especially between groups) is not a product of the intention to differentiate but a consequence of the fact that in different communities there are different norms for doing things which are transmitted by socialization (see also Binford 1963). The key point is that style refers to those properties which do not have a function. It refers to items which perform the same function – they are functional equivalents (Binford 1963: 92).

The concept of style (vs. function) has been one of the most debated topics in archaeological theory (Hegmon 1992). Most of this debate was focused on whether style itself has a function and what the functions of style are. For example, Wobst (1977) suggested that style has a function in the realm of non-verbal communication – e.g. to signal group affiliation. Sackett (1986) also does not exclude the possibility that style may also have some kind of function, e.g. by taking on an iconological role. Wiessner defined two modes of style – *emblemic* and *assertive* (Wiessner 1983). *Emblemic* style refers to the variation in form used to signal group identity and boundaries. This kind of style cannot be used to measure interaction, as all or most members of the group use one variant. *Assertive* style is personal, in the sense that it does not refer to a group but is a consequence of personal choice and, as such, supports personal identity. According to Wiessner, assertive style can be used to measure interaction between people, as it is conducive to copying between peers (e.g. one may decide, for whatever personal reason, to prefer one variant over another from the repertoire that she or he is familiar with). Therefore, style can indeed fulfill some kind of function in the sociocultural system.

Hegmon (1992) finds the distinction between style as a component of human activity and style as a pattern of variation somewhat problematic; but I find it extremely useful to delineate what I mean by style in this book. Style as a component of human activity can and often does have a function from the social and cultural perspective (e.g. in reflecting individual or group identity); but, by definition, style as a formal property of an object cannot have a function from the perspective of the object – style resides in the properties of an object, which are free to vary without influencing the physical performance of the object i.e. the object's practical function. I will use the term *stylistic variability* primarily to denote the patterns of formal variation, whereas the mechanisms which have generated the patterns are kept separate conceptually. In this context, the most relevant feature of formal variation is that for each attribute or artifact type one can choose between different options which are functionally equivalent (Binford 1963), where function is understood strictly in terms of the object's use. For example, the choice between the zig-zag and cross-hatched decoration patterns placed on a cooking pot does not have any influence on the effectiveness of the pot in performing its function as a container for cooking food. In this sense, the term style, as used here, is closest to Sackett's conceptualization of style as *isochrestic variation*.

1.2. THE NEW TOOLS

All these problems were defined in the early days of traditional culture-historical archaeology, and theoretical constructs such as *diffusion*, *archaeological culture*, *style*, as well as methodological solutions such as *seriation*, are a legacy of the paradigm of culture history. In the heyday of processual archaeology, questions of stylistic variability usually took the back seat, as secondary to issues of subsistence, economy and socio-cultural evolution, but could still be found in the works of the New Archaeologists associated with ceramic sociology research (Longacre 1970; Hill 1966; Deetz 1968). In postprocessual archaeology, the formal variation of material culture was often interpreted in relation to individual agency, identity, gender, etc.

However, there was no coherent and comprehensive theory produced by any of the aforementioned schools of archaeological thought that would systematically answer the fundamental questions of how and why patterns are generated. In the late 20th century, a new anthropological and archaeological theory emerged as the perfect candidate for solving these old and fundamental archaeological problems. This is the evolutionary cultural transmission theory. This theory was developed as a part of the wider agenda to integrate biological and cultural evolution, and it is based on the thesis that cultural transmission has the properties of a Darwinian evolution (Boyd and Richerson 1985). Just as the evolutionary theory in biology provides an explanation for the change of frequency of genotypes and phenotypes in space and time, the cultural transmission theory should do the same for the spatio-temporal patterns of types and stylistic attributes of material culture in the archaeological record. As noted by Eerkens and Lipo (2007), cultural transmission was assumed in many anthropological and archaeological theories and models, but modern cultural transmission theory is specific for its evolutionary basis and its comprehensiveness in addressing the phenomena discussed above:

> *"While culture historians lacked an explicit theoretical basis and instead made their arguments based on a series of empirical generalizations (Lyman et al. 1997), CT [cultural transmission] today derives from a much more structured theoretical model, specifically Darwinian models of evolution. Thus, early and mid-20th century diffusion models were focused on the ''culture'' as a unit of study, and ideas were perceived as being diffused in and out of groups of people who comprise sets of bounded entities. Darwinian theory, of which modern CT is a part, is based more on the actions and decisions of individuals. Moreover, while diffusionists like Boas and Kroeber were interested in change, they were less interested in rates of change, rates of error during transmission, what conditions might foster greater or slower rates of error, different transmission mechanisms, and how diffusion could inform more generally on prehistoric cultures. For most culture historians, diffusion remained a sufficient explanation to account for similarity in the absence of the movement of people (i.e., migration) or goods (i.e., trade) (O'Brien et al. 2005). As a result, modern CT models are generally more rigorous in their definition and more quantitative in their application."*
>
> *(Eerkens and Lipo 2007: 241)*

In the last 25 years, the research performed within this relatively new theoretical framework has resulted in significant and unprecedented advances in our understanding of the traditional archaeological problems regarding the formal variation of material culture in space and time. In this book, I follow this line of research, and utilize cultural transmission theory for the purpose of archaeological theory building. The research presented in the central chapters of the book is theoretical research aimed at exploring three general questions:

1) How do different models of cultural transmission translate into patterns of stylistic variation in space?

2) What are the key factors determining the temporal patterning of material culture in the archaeological record?

3) How do the cultural transmission parameters and spatio-temporal observational scales and frames interact to produce the patterns in the archaeological record?

The research is based on computer simulation experiments designed to explore the implications of different scenarios and models of cultural transmission. This kind of research is well established in the field of cultural evolutionary studies in anthropology and archaeology (e.g. Madsen 2020; Gjesfjeld et al. 2020; Crema et al. 2014b; Kandler & Shennan 2013; Premo 2014; Porčić & Nešić 2014; Eerkens & Lipo 2005; Lipo et al. 1997), and is becoming a gold standard for theoretical explorations in evolutionary archaeology. As will soon become clear, one of the major advantages of the cultural transmission theory is that it allows the systematic construction of quantitative models which can further be implemented and explored by means of mathematical analysis and computer simulation. The relevance of such an endeavor is directly determined by the degree to which these models truly reflect the underlying reality, and whether anything similar can be found in the empirical record. I address this issue many times in the book. And I attempt to demonstrate that the models are capable of generating a wide range of patterns that we can actually observe in the empirical world.

1.3. THE PURPOSE AND OUTLINE OF THE BOOK

My ambition with this book is to illustrate how we can translate our traditional archaeological problems into the conceptual framework of cultural transmission theory, and how we can obtain theoretical and methodological benefits from it. The main aim is to show that the concepts and terms of cultural transmission theory are “good to think” with (to borrow the phrase of Levi-Strauss), as regards the fundamental problems of traditional archaeology.

It is conceptualized as a hybrid between a review text and original research. For many of the computer simulation experiments presented in the core chapters of the book, the results can be anticipated on the basis of the existing literature, as they represent another confirmation and illustration of the already established hypotheses. These experiments fulfill the didactic purpose of the book – they are used as tools to illustrate how cultural transmission theory works when applied to archaeological problems. On the other hand, I use computer simulation to test specific hypotheses and generate new knowledge, in order to demonstrate the research potential of the approach. Therefore, the book is primarily intended for experts in the field, but also for postgraduate students and archaeologists interested in archaeological theory and method.

The book consists of seven chapters. In the introductory chapter, I lay out the motivation for my research – the interpretation of the formal variability of material culture in space and time. In the next two chapters, I introduce the theoretical and methodological foundations of the research presented in the book. Chapter 2 represents a short review of the basic concepts of cultural transmission theory and its application in archaeology. It is not a comprehensive review of the field, as some important topics such as cultural phylogenetics and models of cultural transmission related to technology and function, are only briefly mentioned. The first two chapters are suitable for the non-expert audience, as they lay out the fundamental theoretical problems and provide a review of cultural transmission theory and its application in archaeology. Familiarity with the most relevant topics in the history of archaeological thought is assumed for the understanding of this chapter (e.g. Trigger 2006).

Chapter 3 presents the main methods and techniques used to address the key issues. To be able to understand the methods and techniques of analysis, the reader should have a good grasp of the basic principles of the quantitative methods and their application in archaeology. Consulting standard texts on this issue, like Shennan (2004) or Van Pool & Leonard (2011), would be a good idea for readers who do not have a solid foundation in quantitative methods, as these text completely cover the topics needed to understand the statistical instruments used in the book.

Chapters 4, 5, and 6 constitute the core of the book. Chapter 4 explores the spatial patterns generated by the implementation of cultural transmission models, whereas Chapter 5 explores temporal patterns. In Chapter 6, I bring the spatial and temporal perspective together into a single analytical framework. In each of the core research chapters, I perform *in silico* experiments to explore the spatial, temporal and spatio-temporal patterns generated by various cultural transmission scenarios; but I also draw upon archaeological and ethnographic case studies to show that comparable patterns are indeed found in the empirical world. The opening and closing (discussion) sections of the core chapters can be read by the general archeological audience, whereas the description of the simulation experiment results and statistical analysis are technical and will primarily be of interest to experts in the field of cultural transmission studies in archaeology and anthropology.

In the last chapter, I summarize the main results, and present the limitations of my approach as well as the prospects for future research. This chapter is of general interest, as I come back to fundamental archaeological problems and concepts and try to put them into perspective in the light of the findings presented in the core chapters.

The technical details, such as the computer simulation code and mathematical elaboration of the seriation coefficient, are presented in the appendices in order to make the main text easier to read for the non-expert. A Glossary is also provided, for quick reference and clarification of the jargon associated with culture transmission theory.

2

CULTURAL TRANSMISSION AND ARCHAEOLOGY: THEORETICAL AND EPISTEMOLOGICAL PERSPECTIVES

Chapter 2

CULTURAL TRANSMISSION AND ARCHAEOLOGY: THEORETICAL AND EPISTEMOLOGICAL PERSPECTIVES

> *Cultural transmission is analogous to genetic transmission in that, although basically conservative, it can give rise to a form of evolution.*
>
> *(Dawkins 1976: 203)*

2.1. INTRODUCTION

This chapter has two aims. The first is to introduce basic information about the cultural transmission theory as a general anthropological theory, and how it became the basis of the evolutionary archeology approach. I will focus on those aspects of the theory, i.e. the first principles, the key concepts, and the particular cultural transmission models which will be used and explored in this book from the archaeological perspective.

The second aim is to clarify the relationship between cultural transmission theory and archaeology, so that the research presented in this book can be contextualized and evaluated from an epistemological point of view. In the second part of the chapter, I will try to be more precise, by first defining the levels and kinds of theory relevant for archaeological work, and then by contextualizing cultural transmission theory within this framework, so that the archaeological problems I investigate in this book will become clear.

2.2. CULTURAL TRANSMISSION THEORY AS PART OF THE DUAL INHERITANCE EVOLUTIONARY THEORY OF CULTURE

2.2.1. First principles

Cultural transmission theory, which is the subject of this book[3], is part of the general anthropological *dual inheritance theory* also known as *the gene-culture coevolution theory* (Boyd & Richerson 1985; Richerson & Boyd 2005; Cavalli-Sforza & Feldman 1981). The main idea of the dual inheritance theory is that humans have two channels of inheritance. The first channel is the biological genetic inheritance, and the second channel is cultural transmission or social learning. The two channels are separate in the sense that information about behavior, social institutions, ideas, attitudes or material culture is not encoded in the genes, and vice-versa, that genetic information cannot be transmitted via cultural transmission (Kronfeldner 2021). Even though the channels are separate, they can interact and influence each other in often complex ways. For example, the cultural environment may generate selection pressures that act on genes, and biological factors may induce cultural response (Levinson & Dediu 2013). Of course, the capacity for culture was necessarily the product of biological evolution. Only in this sense does biological evolution have primacy over cultural evolution in this theoretical framework. Once the capacity for cumulative culture[4] (Eerkens & Lipo 2007) evolved, cultural evolution became a separate process with its own channel of transmission. In other words, there are no genes for the Serbian (or any other) language, or for matrilocal residence, Zoroastrian (or any other) religion, or painted pottery designs.

Cultural transmission theory is part of dual inheritance theory, and its subject is the channel of cultural inheritance. The concept of cultural transmission predates dual inheritance theory, as there are older theories (especially within culture-historical anthropology and archaeology) where this concept (usually under the banner of cultural diffusion) was of central importance (Eerkens & Lipo 2007). However, the specificity of cultural transmission theory, which is the main subject of this book, is that it has been developed within

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[3] There are other brands of cultural evolutionary theory which are not in the focus of this book, such as *cultural attraction theory*, which will be discussed shortly below.

[4] Cumulative culture refers to the potential to preserve cultural inventions by means of social learning, and to build upon them, making the culture more complex in time , thus generating behavior and cultural elements that no individual could invent or learn individually (Boyd & Richerson 1996; see also Mesoudi & Thornton 2018). The capacity for cumulative culture is not uniquely human, as persistant cultural traditions have been recorded among birds and some primates, but the scale of human cumulative culture is more advanced by several orders of magnitude, giving rise to the phenomenon of cultural evolution (Boyd & Richerson 1996).

the Darwinian evolutionary framework[5] (Eerkens & Lipo 2007). It is based on the premise that some aspects of culture can be conceptualized and modeled as general Darwinian evolutionary process (Mesoudi 2015; 2011; Mesoudi et al. 2006; Boyd & Richerson 1985; Dawkins 1976; Cavalli-Sforza & Feldman 1981). The theory of evolution was originally developed to explain the diversity and origin of biological species. Biological evolution represents a change in the frequency of genotypes, and by implication, phenotypes, over time. If some variants (alleles) of certain genes have a higher adaptive value, i.e. if they increase the probability of their own replication in the next generation by generating phenotypic traits that increase the probability of reproduction of the carrier organism, then we call this process *natural selection*. If the alleles have the same adaptive value, their frequency in a population over time can still change as a consequence of purely stochastic processes and random events. This process is called *drift*, and it drives *neutral evolution*. In biological evolution, the genes that consist of the DNA molecules represent the physical medium of inheritance. Genes can mutate, which constantly introduces new variations into the system, and variability exists both at the levels of the genotype and of the phenotype. Both natural selection and drift, along with mutations, represent descent with modification.

The crucial point is that the principles of Darwinian evolution apply to any system where there is a variability of information at the population level and the possibility of its transmission (equivalent to heredity) and modification, regardless of the nature of the medium for the storage and transmission of the hereditary information (Mesoudi 2011; Richerson & Boyd 2005; Mesoudi et al. 2006; Mesoudi 2015; Dawkins 1976; Lycett 2015a; Mesoudi et al. 2004). Therefore, the theory of evolution as well as the process of evolution can be generalized (i.e. separated conceptually from the biochemical basis of the genes and the DNA) as being any process which has the aforementioned abstract features. This generalization of Darwinian principles to encompass phenomena outside of biology is known as *universal Darwinism* (Dennett 1995: 58; Blackmore 1999: 10–23). Universal Darwinism elevates the principles of the Darwinian theory of evolution to a higher epistemological level – as a basic set of principles behind the theories which explain different phenomena in the world where Darwinian mechanisms operate, from diversity of life on Earth, to computer viruses, and human culture.

The core of evolutionary cultural transmission theory is the assumption that certain aspects of human culture, which may include its ideational, behavioral,

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[5] For this reason I will use the terms 'cultural transmission theory' and 'cultural evolutionary theory' as synonyms.

and material aspects, have the properties of the universal or general Darwinian evolutionary system (Mesoudi et al. 2006; Mesoudi 2015; Lycett 2015a; Mesoudi et al. 2004) – that “similarity in behavior and artifacts may be caused by the exchange of information using a nongenetic mechanism” (Eerkens & Lipo 2007: 240). This means that some cultural phenomena can be modeled as population-level phenomena, and that the system is characterized by the current frequency distribution of variants, if the variants are conceptualized as discrete units, or by the probability (density) distribution of possible cultural states, if they are continuous. The basic process is the transmission of cultural information via social learning between the members of the population, with the possibility of modification by copying error or intentional invention. The evolutionary change is the change in the frequency or probability density associated with cultural variants. The differential transmission of information that results in frequency change may come from the stochasticity of the transmission process itself (the neutral evolution and drift), or can be caused by other factors that increase or decrease the probability of the particular cultural information being transmitted to another person or object (selection).

It should be noted that this is a completely different paradigm of cultural evolution compared to what is usually considered as evolutionism in anthropology (Palavestra & Porčić 2008; Dunnell 1980). In social and cultural anthropology, the terms “evolutionism” and “sociocultural evolution” are usually associated with the classic sociocultural evolutionism of the 19th century, established by Edward Tylor, Henry Morgan and Herbert Spencer, and its updated version, the neoevolutionism of the mid-20th century championed by Leslie White, Julian Steward, Elman Service, and Marshall Sahlins. In these theories the term “sociocultural evolution” can be replaced with the term “sociocultural change” without a loss in meaning, as the structure of these theories does not have anything to do with the structure of Darwinian evolutionary theory (Dunnell 1980). Both 19th century evolutionists and neoevolutionists were concerned with changes in the scale and organization of human societies. The neoevolutionists were particularly concerned with defining the forms of human organization which would reflect specific evolution, as an adaptation to a particular ecological niche, and general evolution, which would reflect the scale and social complexity (hence the categories such as band, tribe, chiefdom and state) (Sahlins & Service 1960). The most important questions revolved around how one organizational type transformed into the other, and particularly how social complexity increased. These transformations can indeed be thought of as macroevolutionary changes in the Darwinian framework, but the units and processes employed by the sociocultural evolutionists had nothing to do epistemically with a theory of Darwinian evolution, as the mechanisms of change did not involve population thinking and descent with modification (Dunnell 1980). Evolutionary change was understood as the holistic transformation of an entire cultural system caused or mediated by external or internal factors such as climate, population pressure, intensity of warfare, etc.

In biology, the basic unit of transmission is well known. Hereditary information is carried by a gene which consists of the sequence of three nucleotides (in the case of protein-encoding genes), the building blocks of the DNA molecule. But what about cultural transmission? Richard Dawkins famously coined the term *meme* as the cultural equivalent of a gene:

> *"Examples of memes are tunes, ideas, catch-phrases, clothes fashions, ways of making pots or of building arches. Just as genes propagate themselves in the gene pool by leaping from body to body via sperms or eggs, so memes propagate themselves in the meme pool by leaping from brain to brain via a process which, in the broad sense, can be called imitation. If a scientist hears, or reads about, a good idea, he passes it on to his colleagues and students. He mentions it in his articles and his lectures. If the idea catches on, it can be said to propagate itself, spreading from brain to brain."*
>
> *(Dawkins 1976: 206)*

A similar concept, the *culturgen*, was introduced by Lumsden and Wilson (1981).

Unlike for genes, there is no consensus on whether memes should be used as a metaphor for the cultural information transmitted by any means and at any level of complexity, or whether we should try to define them physically e.g. as "self-replicating brain structures, actual patterns of neuronal wiring-up that reconstitute themselves in one brain after another" (Dawkins 2006: 323). In this book, I will use the word 'meme' as a synonym for a cultural trait or cultural variant, without subscribing to any particular interpretation of its nature and scale.

Another important issue is copying-fidelity and the question of whether memes are particulate units of inheritance:

> *"This brings me to the third general quality of successful replicators: copying-fidelity. Here I must admit that I am on shaky ground. At first sight it looks as if memes are not high fidelity replicators at all. Every time a scientist hears an idea and passes it on to somebody else, he is likely to change it somewhat. I have made no secret of my debt in this book to the ideas of R. L. Trivers. Yet I have not repeated*

> *them in his own words. I have twisted them round for my own purposes, changing the emphasis, blending them with ideas of my own and of other people. The memes are being passed on to you in altered form. This looks quite unlike the particulate, all-or-none quality of gene transmission. It looks as though meme transmission is subject to continuous mutation, and also to blending."*
>
> *(Dawkins 1976: 209)*

However, the issue of discreteness and absolute fidelity are not fundamental for the theory to work. It has been shown that discrete models are useful even if the mental representations being transmitted are not discrete gene-like replicators; and cultural transmission does not involve the accurate replication of discrete memes (Henrich et al. 2008; Mesoudi et al. 2004). This is because some meme states are more probable than others, since they are easier to think – these are the cognitive attractors which reduce the variation of the meme representations by concentrating them around a smaller number of values:

> *"Instead of a continuum of cultural variants, most people will hold a representation near an attractor. If there is only one attractor, it will dominate. However, if, as seems likely in most cases, attractors are many, other selective forces will then act to increase the frequency of people holding a representation near one attractor over others. Under such conditions, even weak selective forces ("weak" relative to the strength of the attractors) can determine the final distribution of representations in the population."*
>
> *(Henrich et al. 2008: 121)*

The concept of cultural attraction is the corner stone of another major evolutionary theory of cultural transmission – the *cultural attraction theory*, also known as *cultural epidemiology* (Morin 2016; Sperber 1996; Claidière & Sperber 2007). Cultural attraction theory envisions the transmission process as a reconstruction and biased transformation of cultural representations (i.e. cultural variants, or meme variants), rather than the simple differential replication of memes. The crucial thesis of cultural attraction theory is that the way in which mental representations are transformed will usually not be random but biased towards cultural attractors. Cultural attractors are cultural variants which are, for some reason, cognitive or ecological, more probable transformation outcomes than other. The factors of attraction are not exclusively cognitive and psychological, but can be ecological i.e. external to the mind (Scott-Phillips et al. 2018; Acerbi & Mesoudi 2015; Claidiere et al, 2014). As

Mesoudi (2021) has noted, there is no fundamental contradiction between the cultural selection and biased transformations positions on cultural evolution – both kinds of dynamics may be present with different weights in different domains of culture.

In this book I do not explore the implications of cultural attraction theory, but focus on the 'standard' cultural transmission theory of Boyd and Richerson. The main reason for such a decision is pragmatic, and contingent upon the history of the evolutionary approach in archaeology. The models of standard cultural transmission theory are more developed and they have been more widely used in archaeology in comparison to cultural attraction theory. This does not mean that cultural attraction theory has no relevance for archaeology. On the contrary, the potential of this theory is underutilized in archaeology, and may turn out to be crucial for understanding copying errors and innovation related to material culture (see Crema et al. 2023). This issue is briefly discussed in the final chapter of the book.

2.2.2. The properties of cultural transmission

The conceptualization of the cultural transmission process as the evolutionary process had profound implications for the structure and potential of the theory, because it enabled the use and modification of the long established quantitative models from the population genetics (Boyd & Richerson 1985; McElreath & Boyd 2007; Cavalli-Sforza & Feldman 1981). Unlike previous cultural transmission theories, the evolutionary cultural transmission theory has an epistemic advantage of being a quantitative theory. The theory of cultural transmission thus consists of quantitative models specifically constructed to capture the variety of cultural processes which may generate a change in the frequencies of cultural elements at the population level.

The study of cultural evolutionary systems requires the construction of a new theory and models based on the modifications of the original biological evolutionary theory. This is because cultural evolution has properties for which no analogues exist in biological evolution. When it comes to the pathway of transmission, cultural transmission is not limited only to parent-offspring transmission of cultural information (*vertical transmission*), but may occur between members of any generation regardless of biological relatedness (Cavalli-Sforza & Feldman 1981). If it occurs between members of the same generation it is *horizontal transmission*, whereas if it occurs between unrelated members of older and younger generations, it is called *oblique transmission* (Cavalli-Sforza & Feldman 1981). Usually, the direction of the transmission is from the older to the younger generation, but in principle there is nothing to prevent cultural transmission from going the other way round, although this may be quite rare. In addition to the one-to-one (asexual reproduction) or two-to-one (sexual reproduction) relations present in the biological inheritance, in the cultural case, the transmission can be one-to-many or many-to-one.

In cultural evolution theory, the transmission of memes occurs by means of social learning. There are several mechanisms of social learning. Hoppit and Laland (2013: Chapters 2 and 4) provide a classification of social learning mechanisms, which includes a list of twelve social learning mechanisms; but it should be noted that there is no universal classification upon which all of the researchers in the field of social learning will agree (cf. Rendell et al. 2011). So, the details of each classification attempt are open to debate. The distinction between social learning mechanisms is conceptually useful, although in practice the situation is usually complex and the boundaries between the mechanisms may be blurred, or the mechanisms may be difficult to identify (Hoppitt and Laland 2013, see also Singh et al. 2021). In a review of cultural evolutionary approaches in archaeology, Lycett offered a taxonomy which includes four general mechanisms: stimulus enhancement, emulation, imitation, and teaching (Lycett 2015a). Stimulus enhancement is perhaps the least relevant for most modern human situations, as it is a kind of indirect learning where no actual copying takes place – the learning is social simply because one individual influences the behavior of another individual by exposing the other individual to the context (directing the attention) which amplifies the probability of a certain behavior being acquired. Emulation is when one individual tries to copy the end result of the behavior of another individual (e.g. to make the same artifact), without observing the sequence of steps that lead to that end result. Imitation is the kind of social learning when the student tries to reproduce each action of the role model in the sequence; whereas teaching assumes the active role of the model i.e. explicit instructions for how to do something. The distinction between the mechanisms of social learning can have important implications, especially in archaeology, where the degree of copying error and the generation of mutations may depend on the kind of social learning mechanism – copying error is greater in the case of emulation than imitation (Schillinger et al. 2015).

2.2.3. Models of cultural transmission

The second important difference between biological and cultural evolution concerns the evolutionary forces, the specific biases that may increase or decrease the probability of transmission for the different variants. The evolutionary forces that cause the differential transmission of variants are more diverse and complex in cultural evolution compared to the biological evolution. For this reason, the existing models from population genetics had to be modified and new models had to be formulated (Boyd & Richerson 1985). These models of transmission form the core of cultural evolution theory.

Just as in biological evolution, neutral evolution and natural selection are also present in cultural evolution. Neutral evolution is captured by the *unbiased* or *neutral model* of cultural transmission. In the unbiased model, it is assumed that the probability of replication of each variant of a meme (e.g. painted pottery ornament) is proportional to its current frequency in the population. In finite populations, the sampling effects would slightly increase the proportion of some variants over others in one generation, and the cumulative effect of these small stochastic deviations would lead to the differential replication of meme variants, even if all meme variants have the same adaptive value. The smaller the population, the stronger the effect of differential replication – this is the drift. It is important to stress that even though meme frequencies are changing in such a way that some variants become numerous while others decrease in frequency and disappear, there is no selection, as all meme variants have the same adaptive value. The frequencies are changing only due to chance. Imagine that we start with a finite population of size *N*, where the frequencies of four meme variants are uniformly distributed. In time step zero, the relative frequencies of all variants are the same. In the next time step, the frequency of one of the variants increases by one unit, and the frequency of one of the remaining three decreases by one unit simply by chance (as the sampled frequencies are never exactly equal to the theoretical frequencies, especially in small samples). This changes the probabilities of replication for the meme variants in the next episode of transmission. Now the variant whose probability of replication has increased slightly by chance has a slightly greater probability of being transmitted in the next iteration of the transmission process. The cumulative effect will be the increase of frequency of some variants at the expense of others, which in the absence of the introduction of new variants into the system (mutations or inventions) would lead to the fixation of a single variant in the population.

What would be the anthropological rationale for such a model? How could human behavior possibly be modeled as a random process of copying? Why would anyone decide which hairstyle to choose based on the random number generator, with hairstyles weighed by their current frequency distribution in the population? For example, Leroi et al. (2020) criticize the conclusions of Hahn et al. (2003) and Bentley et al. (2004) that the neutral model is a good explanation for the frequencies of first names in the USA in the following manner. They argue that if American parents choose first names for their children randomly (i.e. in proportion to their relative abundances), then many Christians would end up naming their children with typical Muslim names, which is obviously absurd and, in their view, disqualifies the neutral model as a reasonable explanation for the frequency distribution of first names. But this criticism misses the point of the neutral model. It is important to realize that models are not reality, but simplified representations of reality. The anthropological interpretation of the neutral or unbiased model of cultural evolution is that each individual has idiosyncratic reasons for choosing a particular meme variant over another, but the net result of these multiple decisions made by different members of the population is such that it is *as if* they were chosen randomly, with the sampling probability of each variant being equal to its current relative frequency in the population (Shennan 2011). Therefore, in this model, each individual decision is a black box, but their cumulative net effect is such that the transmission is driven by the current relative frequencies of the variants. This captures the assumption that each meme variant has the same adaptive value and that there is no systematic or inherent preference for one variant over another. In the example with first names, as Bentley et al. (2021) note, the issue of scale is important – at the scale of the entire USA the neutral model is a good model. It does not mean that people are randomly choosing names for their children, only that, at a given scale, the resulting patterns are *as if* they were doing so. Therefore, the neutral model is a representation of reality at a certain scale – it does not model motivation for individual decisions but the aggregate outcome of a large number of individual decisions. It is best seen as a theoretical tool, as it is robust in the sense that it can approximate the complex reality of many competing non-neutral processes in the world (Bentley et al. 2021). As will be discussed soon and showcased throughout the book, the neutral model is a very important, if not the most important model of cultural transmission in archaeology.

Classic natural selection may also be an evolutionary force in cultural evolution. If a certain meme is vertically transmitted and increases the probability of biological reproduction, the frequency of such a meme will increase through time, as the ones who carry it will have more children than the ones who do not, and the children of the meme-bearers will also carry that meme due to vertical cultural transmission. The adoption and spread of farming is an excellent example of natural selection acting on memes (Shennan 2002: 53). The acceptance or non-acceptance of farming can be thought of as two cultural traits or memes (or meme complexes). The farming economy enables people to have higher fertility i.e. more children who will themselves also become farmers owing to social learning from their parents. The net result will be the increase of the farming population compared to the non-farmers, "outcompeting them in classic natural selection terms" (Shennan 2002: 53). In this way, the meme for farming is naturally selected.

In addition to drift and natural selection, which are the main forces of biological evolution, the specifics of cultural evolution give rise to new forces, for which new models have been formulated (Lycett 2015a; Richerson & Boyd 2005; Henrich & McElreath 2003). I will use a simplified version of the Rendell et al. (2011) taxonomy for the classification and presentation of the most important cultural transmission models (Figure 2.1).

In cultural transmission there are numerous biases which increase or decrease the probability for a particular meme to be replicated, and models have been formulated to capture the essence of these processes. The most general line of division is between *content biases* and *context biases* (Lycett 2015a). A content bias will be present if a particular meme variant has a real or perceived (dis) advantage over other cultural variants, or if it is cognitively preferred/repellent for some reason. For example, metal axes may be preferred over stone axes due to their greater efficiency (Henrich & McElreath 2003), and a story about a celebrity's love life (or any other gossip) is more likely to be retold than a story about what someone bought in a regular visit to a supermarket. Content biases result in *cultural selection* in the strict sense, as the content of the cultural information influences its probability of being replicated.

In the case of context biases, the probability of replication for a particular meme is not influenced by its contents but by the various contextual aspects. Context biases can be divided into frequency-dependent biases and model-based biases. The frequency-dependent biases arise when the probability of replication of a meme depends on its relative frequency in the population. The frequency-dependent biases can be further subdivided into conformity and rarity (anti-conformity) biases. The *conformist model* of transmission assumes that people will tend to conform – that they will choose more often than by chance to copy the most frequent meme in the population. The *anticonformist model* based on rarity bias assumes exactly the opposite – that people will tend to copy the least numerous (which is often the novel) meme variants in the population. I have singled out the conformist and anti-conformist models as the most popular models in archaeology, but it should be emphasized that other frequency dependent models are possible (see Rendell et al. 2011 for a more detailed list of frequency-dependent biases).

The model-based biases give rise to a class of cultural transmission models where the probability of copying of a cultural variant depends on which person or group possesses the variant. This category can also be subdivided. *Prestige bias* means that people will tend to copy preferentially the memes associated with individuals and groups (or artifacts, see Lycett 2015a) who are for some reason considered to be prestigious, whereas *success bias* assumes that people will try to imitate the most successful person in some field. These biases are sometimes labeled as indirect biases, because people are usually copying traits or behaviors which have nothing to do with the actual reasons for the success (e.g. one may have the same hair-style or the same tattoo as a famous musician or sports player, but this has no real impact on the person's sport or musical skill). The *similarity bias* is another category of model-based biases – when this kind of bias is present, people tend to preferentially copy cultural information from the individuals who are more similar to themselves. The *Axelrod model* is an example of cultural transmission model with similarity bias (Axelrod 1997). Other criteria for the choice of models are also possible, such as age (e.g. copying traits in older people) or religious or professional affiliations.

A model which also needs to be mentioned is Boyd and Richerson's (1985) *guided variation* model. In this model, there is no bias in the transmission process but in the process of mutation. In this model, the mutation is not random, as in biological evolution, but it is directed towards certain culturally preferred values. Individuals modify the cultural variants they have copied towards some culturally preferred standard, and then the resulting distribution of memes is used as a basis for the next episode of unbiased transmission. The guided variation model of Boyd and Richerson partially resembles the ideas of the cultural attraction theory, although the transformation towards the attractor in this model occurs only within the mutation event, it is not an integral part of the transmission process.

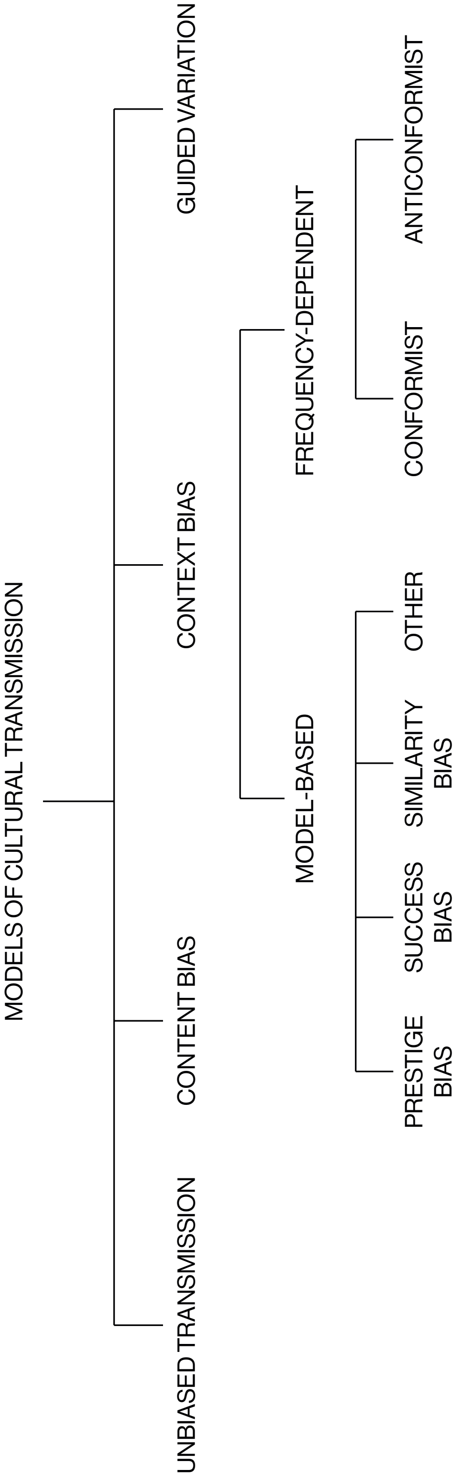

Figure 2.1. A taxonomy of the models of cultural transmission (adapted and modified after Rendell et al. 2011: Fig.1 and Lycett 2015a: Fig.1)

2.3. CULTURAL TRANSMISSION THEORY IN ARCHAEOLOGY

2.3.1. Darwinian evolution in archaeology

Even though the application of evolutionary cultural transmission theory in archaeology is a relatively recent phenomenon, some of the key concepts and ideas can be traced at least to the late 1960s and 1970s. Many of the ideas presented in David Clarke's *Analytical Archaeology* (Clarke 1978) closely resemble modern cultural transmission theory, as Clarke envisioned the patterns in the archeological record as reflecting the flow of cultural information at the population level through time at different scales (Lycett & Shennan 2018; O'Brien & Lyman 2000: 261-265). He formulated a taxonomy of observational scales and relevant processes associated with each scale, as well as methods for their quantification and analysis. The only component that was missing was an explicit reliance on Darwinian evolutionary theory, although it was heavily implied in Clarke's ideas (Lycett & Shennan 2018; O'Brien & Lyman 2000: 261-262).

Robert Dunnell explicitly advocated the application of Darwinian evolutionary theory in the interpretation of the archaeological record (Dunnell 1978; 1980; Dunnell 1989). Dunnell proposed a completely different concept of style – one which was explicitly defined in terms of the evolutionary process. In Dunnell's scheme, the variation is defined as stylistic if it is not selected in any way, which means that no variant has an adaptive (functional) advantage over another[6]. Therefore, Dunnell (1978) suggests that stylistic traits can best be accommodated by stochastic processes, as they exhibit random behavior. In terms of cultural transmission theory, the model of unbiased transmission comes to mind first as a candidate for modeling style, but other models, such as conformist or anti-conformist transmission, are also potential candidates, as long as the features being transmitted are not functional in the sense that they affect the physical or symbolic performance of the object.

The evolutionary approach to archaeology was advocated by various researchers during the 80s and the 90s (e.g. O'Brien & Holland 1990; Leonard & Jones 1987; Teltser 1995b; Rindos et al. 1985). However, there were few empirical applications, as most publications were programmatic statements. It was not entirely clear how to perform empirical research in this theoretical framework.

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[6] As O'Brien and Lyman noted, this idea was not new, as Kroeber and Binford also viewed style as selectively neutral and therefore a result of a stochastic process of transmission; but neither of them pursued the theoretical and methodological implications of this insight (O'Brien and Lyman 2000: 265-266).

Moreover, the proposed approaches were only loosely or not at all connected to the cultural transmission models developed within the dual-inheritance theory of Boyd and Richerson.

2.3.2. Neiman's breakthrough and beyond

The major breakthrough in the development and application of cultural transmission theory came with the work of Fraser Neiman and his seminal paper "Stylistic Variation in Evolutionary Perspective: Inferences from Decorative Diversity and Interassemblage Distance in Illinois Woodland Ceramic Assemblages" (Neiman 1995). In the theoretical section of the paper, Neiman adapted the population genetics mathematical theory to model the cultural transmission of material culture. He used computer simulation to show that the neutral (unbiased) model of cultural transmission produces specific patterns of change in the relative frequency of cultural variants in time. These patterns resembled the patterns of temporal dynamics of the relative frequency of types that are often encountered by archaeologists for various classes of artifacts. When the assemblages are ordered in the true chronological sequence (e.g. by means of stratigraphy or absolute dating), the relative frequencies of each type usually behave in accord with the unimodal trend – the relative frequencies of an initially rare type may increase, reach some maximum relative frequency and then start to slowly decrease towards disappearance. This empirically established pattern was the basis for the seriation method of reconstructing the relative chronological sequence of assemblages – assemblages with unknown stratigraphic relations and unknown absolute chronology should be ordered in such a way that the relative frequencies of types conform as much as possible to the aforementioned trend (O'Brien & Lyman 1999). What Neiman did was to show that evolutionary cultural transmission theory was able to explain the temporal variability of material culture. Such a result was anticipated by Dunnell (Dunnell 1978; Dunnell 1989) and Teltser (Teltser 1995a), who suggested that stylistic variability was a result of neutral evolution. Neiman demonstrated this explicitly – by showing that the implication of the theory concerning the temporal dynamics of type frequency is consistent with the empirical evidence. Before Neiman's work, the fact that seriation works, i.e. that the relative frequencies of types have approximately unimodal distributions in time, was explained by invoking the principle of popularity – some variants were more popular than other at different times (O'Brien & Lyman 1999). The problem with this explanation is that it does not actually explain why the frequencies change the way they do – it just rephrases the problem into more intuitive terms ('popularity') and leaves it where it is. Neiman, on the other hand, managed to show that such a pattern of frequency change is predicted by the neutral model of cultural transmission.

In the continuation of his paper, Neiman adapted the mathematical theory of neutral biological evolution to make connections between the parameters of cultural transmission, such as population size and mutation rate, with the archaeologically observable and measurable traits, such as assemblage diversity and inter-assemblage distances[7]. The diversity of an assemblage *sensu lato* (i.e. its variability) can be measured in two ways. One way is to simply count the number of variants which are present (e.g. the number of vessel types represented by at least one specimen) in the assemblage. This count is called the *richness* of an assemblage. The other way is to combine the information on richness with information about the distribution of relative frequencies of variants. This is diversity *sensu stricto*.

Using a very simple and elegant mathematical model, Neiman showed that under neutral transmission, the cultural diversity[8] of a population at equilibrium is approximately equal to:

$$2N_e\mu + 1 \quad \text{(Eq. 2.1)}$$

Where N_e is the effective population size[9] and μ is the mutation rate. The mutation rate is the probability that an agent will introduce a novel cultural variant (e.g. type) to the system, instead of copying from the existing pool of variants. The product $2N\mu$ is usually referred to as the *theta* (θ) parameter. This equation is telling us that the diversity of types in an assemblage, if the underlying process of transmission is neutral, will be proportional to the population

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[7] Euclidean distance between a pair of assemblages is based on the relative frequencies of types in each assemblage. Each assemblage is represented by a vector, with the number of elements equal to the total number of types present in all assemblages under study. The vector element entry for each type is equal to the relative frequency of that type in a particular assemblage. Therefore, the relative frequencies of types in an assemblage represent the coordinates of an assemblage in multidimensional space, with the number of dimensions equal to the total number of types present in assemblages under study. The distance between two assemblages is then calculated as a simple Euclidean distance based on the assemblage coordinates.

[8] In this context, the diversity refers to the reciprocal value of homogeneity of a population – it is a theoretical construct. Homogeneity is defined as the "probability that two randomly chosen individuals in the population carry variants that are copies of a common antecedent variant" (Neiman 1995: 12).

[9] Effective population size is not the same as census population size (the number of individuals in a population). It is a theoretical concept from population genetics, which reflects the population size of an idealized population (constant population size, evolution driven by random drift, random mating, non-overlapping generations), that corresponds to a real population with the same genetic diversity. In order to apply the theoretical results where effective population size is a relevant parameter, it is assumed that the census and effective population sizes are correlated; but this may not always be the case, as the relationship between census population size and effective population size is complex (Premo 2016).

size and the mutation rate. The important thing is that the *theta* parameter can be empirically estimated from the relative frequencies of types (diversity *sensu stricto*) or by using the information on assemblage richness (see below). Neiman used this important theoretical result to argue that changes in assemblage diversity are monitoring changes in the components of the *theta* parameter.

How does Neiman interpret the changes in the *theta* parameter? The assemblage diversity will increase or decrease depending on how the components of the *theta* parameter, the population size and the mutation rate, change through time.

> *"Recall that θ is twice the product of the effective population size (N_e) and the innovation rate (μ), where the latter includes the combined effects of both in situ innovation (v) and the introduction of novel variants from other groups (m). If $m = v + \mu$, then $N_e \mu = N_e v + N_e m$. Now, it seems reasonable to suppose v, the probability that a group member will introduce a novel variant into their own group in each time period, is roughly constant across demes (e.g., Dunnell 1978: 197; Leone 1968:1150). On the other hand, m, the probability that an individual in a given group learns from a member of another deme, is likely to be more variable in time and space. Under these circumstances, most of the variation in θ with the parameter μ will be caused by variation in intergroup transmission rates. In addition, we can expect θ to be independently affected by variation in N_e. Variation in θ, derived from either or both of these sources, implies variation in the absolute number of intergroup transmission episodes per unit time ($N_e m$), that is, the number of times local group members learn from members of other groups. Variation in θ is a conservative measure of intergroup transmission levels, because a proportion of donor group members carry variants that already exist in the recipient group as a result of transmission into it in previous time periods."*
>
> *(Neiman 1995: 17-18)*

Therefore, Neiman uses *theta* estimates, based on assemblage richness (diversity *sensu lato*), as a proxy for measuring the degree of intergroup interaction, as the mutation rate is modeled as consisting of two components. The first component is the probability of introducing a completely novel variant (by copying error or deliberate innovation), and the second component is the probability of introducing a novel variant by copying from another community. Having established this result by deriving it from cultural transmission theory, Neiman goes on to use it to investigate empirically the changes in intercommunity interaction through time in the Illinois Woodland period.

After Neiman's work, there was a steep increase of archaeological studies based on cultural transmission theory, with several major theoretical and methodological publications appearing almost at the same time (Shennan 2002; Lipo 2001; O'Brien & Lyman 2000; O'Brien & Lyman 2003). Shennan and Wilkinson (Shennan & Wilkinson 2001) and Lipo (2001) advanced the state of the art considerably by building upon Neiman's key theoretical result that relates the neutral model and the typological diversity of assemblages. Neiman (1995) presented two possible ways of estimating the *theta* parameter for the assemblage:

1) theta can be estimated from the relative frequencies of variants (i.e. from diversity *sensu stricto*) using the following formula (Neiman 1995:14, Eq. 7):

$$t_f = \frac{1}{\sum_{i=1}^{k} p_i^2} - 1 \quad \text{(Eq. 2.2)}$$

where p_i is the proportion of the *i*-th type or variant in the assemblage.

2) given the observed sample size (N) and richness (k), defined as the number of different variants in the assemblage, the theory implies (Ewens 1972) that if the sampled assemblage is the result of a neutral process, the underlying theta for a given sample size (N) and richness (k) is estimated by solving the following equation for *theta* (Neiman 1995:16, Eq. 9):

$$E[k] = \sum_{i=0}^{N-1} \frac{\theta}{\theta + i} \quad \text{(Eq. 2.3)}$$

where $E[k]$ is the expected richness[10], and N is the observed sample size. Neiman labeled this estimate of *theta* as t_e (Neiman 1995).

Shennan and Wilkinson (2001) argued that the magnitude of difference between the two *theta* estimates can be used as a test criterion for the null hypothesis that the frequency of variants in archaeological assemblages changed

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[10] In practice, the observed richness k is used as the $E[k]$ in the formula to numerically estimate *theta*.

in accordance with the expectations of the neutral model[11]. The t_f is a purely empirical estimate of *theta* as it is calculated from the frequencies of types in an assemblage, and does not depend on assumptions about the generating process. Shennan and Wilkinson suggested that, on the other hand, the t_e estimate can be interpreted as the *theta* value expected for an assemblage of a given size and a given richness, if the underlying generating process was neutral transmission. The implication is that the difference between t_f and t_e is the measure of the divergence from the neutral model (Shennan and Wilkinson 2001). The neutral model was set as a baseline model, a null hypothesis to be tested against the data. If the t_f is equal to the t_e, then the neutral model is a good explanation for the data. If the t_f estimate is higher than the t_e estimate, this indicates that the anticonformist transmission model better fits the data than the neutral model. If the t_f estimate is lower than the t_e estimate, this indicates the conformist model of transmission as the assemblage generating process.

The neutrality tests provided means to empirically evaluate different hypotheses about the nature of the social and cultural processes standing behind the formal variation of material culture in time and space (Lipo & Madsen 2001), and it is no wonder that many other researchers were quick to follow this path (Kohler et al. 2004; Steele et al. 2010). As the research accumulated, it became clear that there were many problems that needed to be solved, such as time averaging, equifinality, equilibrium assumptions etc., but the field remained vibrant, with the researchers constantly trying to improve the method by exploring the potential problems and offering novel solutions (Madsen 2012; Premo 2014; Premo & Scholnick 2011; Porčić 2015; Kandler & Shennan 2013; Kandler & Crema 2019; Crema et al. 2016; Crema et al. 2014a; Bentley et al. 2004; Gjesfjeld et al. 2020; Madsen 2020; O'Dwyer & Kandler 2017). The general problem that these studies aimed to solve is best summarized by Stephen Shennan:

> *"The question then becomes, to what extent is it possible to identify the action of the various cultural evolutionary processes outlined above on the basis of distributions of through-time variation in the past, given the often poor temporal resolution of the archaeological record and the enormous range of complex processes that have affected it? This is a classic 'inverse problem' of a type very familiar to archaeologists: inferring the microscale processes producing a pattern from the pattern itself, as opposed to carrying out designed experiments or making naturalistic*

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[11] I will only describe the method by Shennan and Wilkinson (2001) as it is more widely known and it is conceptually simpler to present, whereas it should be noted that, at the same time, Lipo (2001) developed his own version of the neutrality test which builds upon the method published in Ewens (1972).

> *observations of processes in the field and examining their consequences. The problems are analogous to those faced by population geneticists in identifying the operation of selection and other processes given the evidence of gene distributions, but in that case the problems are less complex, the amounts of data available are now enormous and very powerful methods have been developed with a strong and well-justified theoretical background. However, as with the development of the theoretical models that created the basis for the field of cultural evolution, the existence of these methods is something from which empirical cultural evolutionary studies can benefit."*
>
> *(Shennan 2011: 1078)*

Another important line of research that has arisen from the conceptualization of culture as an evolutionary process is *cultural phylogenetics* – the application of the theory and methods from the biological fields of cladistics (Kitching et al. 1998) and comparative phylogenetic analysis (Harvey & Pagel 1991; Felsenstein 1985) to (material) culture (O'Brien & Lyman 2003; Lipo et al. 2005; Straffon 2016; 2019; Borgerhoff Mulder 2001; Mace et al. 1994). Cultural phylogenetic methods are used to study cultural macroevolutionary patterns such as the distribution of cultural elements in space. The essence of this research is to test evolutionary hypotheses about culture, usually to see if different aspects of culture conform to the tree-like model of evolution, and if they do, to reconstruct the cultural phylogenies – the relations between cultural entities in terms of their evolutionary (transmission) history, as represented by the tree showing the branching of clades from common ancestors. The key for reconstructing cultural phylogenies is the identification of homologies. Homology is a cultural element shared between two or more cultural entities due to their shared cultural ancestry. When it comes to the application of the phylogenetic method in archaeology, it should be emphasized that the assumption of the tree-like structure is not simply assumed, but empirically tested in each case. Moreover, it has been shown that the strength of the phylogenetic signal in cultural data confirms it to be as strong as the strength of the signal in the biological data (Collard et al. 2006). The study by Collard et al. (2006) is indeed an impressive demonstration of the relevance of evolutionary transmission theory to the cultural realm.

In addition to using cladistics to look for phylogenetic signals and to reconstruct phylogenetic relationships between cultural entities, comparative phylogenetic methods are also applied in anthropological and archaeological research (Mace & Pagel 1994; Borgerhoff Mulder 2001). For example, the phylogenetic independent contrasts (Mace & Pagel 1994) represent a potential solution to one of the fundamental problems in comparative anthropological research – *Galton's problem*. Galton's problem refers to the problem of applying standard statistical tests to cross-cultural data, as the observations may not be independent due to shared cultural ancestry or cultural diffusion (Mace & Pagel 1994). Comparative phylogenetic methods can and have been used to include the information on historical and genetic information, in order to test cross-cultural hypotheses.

To conclude this short review (for comprehensive and detailed reviews see Marwick 2005; Lycett 2015a; Walsh et al. 2019; Shennan 2008; 2011; García Rivero 2016; Straffon 2019), cultural transmission theory in archaeology became the basis for an entire line of diverse and productive research, thus promoting evolutionary archaeology to the ranks of major schools of archaeological thought. It does not mean that this kind of approach is a theoretical panacea; but when it comes to the fundamental problems of traditional archaeological research, cultural transmission theory offers more than previous approaches.

2.4. THE EPISTEMOLOGICAL PERSPECTIVE

2.4.1. The levels and kinds of theory in anthropology and archaeology

What is the relationship between cultural transmission theory, anthropology and archaeology from the epistemological perspective? Before I try to answer this question, I first need to make a short digression and discuss the levels and kinds of theory in archaeology and anthropology. There are many opinions on this subject, and therefore the selection of concepts and views presented here reflects my own preferences and understanding of the matter, rather than a consensus in the discipline (there is none). My position in this regard is openly Binfordian, in the sense that I accept the distinction between the two basic levels of theory: the *middle-range* archaeological theory and the general anthropological theory (Binford 1977; 1981). Having said that, it is important to stress that, in this context, this position is primarily epistemological – it does not assume the primacy of any particular brand of archaeological or anthropological theory. But let us start with the relationship between anthropology and archaeology.

Anthropology is the science[12] of culture. The general aim of anthropology to provide a systematic description and rational explanations (theory) for the emergence and diversity of human cultures is what makes it a universally valuable enterprise, the intellectual equal to other sciences, social or natural. In the North American tradition of scholarship, archaeology is a constituent part of anthropology, as one of its four fields. In Europe, archaeology is usually taught and practiced as an independent discipline. But I assume that no one would deny the fundamental theoretical and epistemological connections between archaeology and anthropology. The science of culture can never be complete without its attempting to explain the origins of culture and its development through time. The theories and hypotheses about major anthropological phenomena such as social inequality, social complexity, technological development, the origins of agriculture, human-environment interactions, social institutions, ideologies, the evolution of *Homo sapiens* and the life-history traits of our species, usually contain the dynamic aspects i.e. the temporal change in key variables. The only way to estimate the values on the relevant variables for the largest part of the human past, and to enable the testing of anthropological theories and hypotheses about human culture, is by using the methods of archaeology.

But archaeology is much more than just a substitute for history and the ethnography of the past. As a matter of fact, in most cases, archaeology cannot produce ethnographic-like descriptions of the past at all, as it operates with evidence that enables insight into processes that operate on different temporal and spatial scales than the events and processes recordable by ethnographers or historians (Perreault 2019; Shennan 2002: 9). This is both the weakness and the strength of archaeology. It is strength when the anthropological theories and hypotheses deal with processes and temporal depths that only archaeology can tackle. It is a weakness when the anthropological hypothesis or theory is expressed at ethnographic time-scale, because archaeology is in most cases unable to generate compatible data and information – and in such cases archaeology will be unable to fulfill its role in anthropological theory-building. Traditional culture-historical archaeology fell into this trap in its attempt to match anthropological to archaeological phenomena existing at different time scales, a point beautifully illustrated by Clarke (1973: 10): "... to interpret the French Mousterian sequence, of more than 30,000 years duration, in terms

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[12] In time, for better or for worse, anthropology has become more than a science, as the postmodernist impact has opened the anthropological agenda to ethical and political considerations, as well as activism and action related to gender issues, minority groups, rights of native peoples, etc. It is not my intention to reiterate the arguments of the never-resolved debate as to what anthropology is or should be – my perspective is simply focused on the original scientific aspirations of anthropology to provide a rational account of the cultural diversity of humans, while acknowledging its complexity as a culturally, historically and politically contextualized discipline.

of the acrobatic maneuverings of five typological tribes is tantamount to an attempt to explain the Vietnam war in terms of electron displacements." But culture-historical archaeology was not concerned with general anthropological theory in the first place. The problem of potential non-compatibility became most visible in postprocessual archaeology, where the agenda was set to explore exactly those anthropological topics that are not suitable for archaeological research (most such hypotheses are not testable, because they cannot be falsified), such as individual agency, agency of material culture, gender issues, psychology and individual perception, biographies, perceptions of landscape, etc. (Shennan 2002: 9). These topics demand ethnographic descriptions of the past which are rarely possible.

On the other hand, archaeology depends on anthropology in several ways. In the most general sense, anthropology gives meaning to archaeology[13]. One might protest and say that archaeology can be performed not to contribute to the needs of anthropology but simply to reconstruct what happened in the past, just like traditional history. But this is both a folly and a delusion. It is a folly because its contribution to general anthropological theory is what makes archaeology a part of the meaningful pursuit of knowledge, a part of the bigger picture, rather than just a parochial and exotic pastime which generates sets of unrelated trivia about the past. To reject the anthropological perspective in archaeological research is to deprive archaeology of its most valuable intellectual aspect. Likewise, the idea that one can do pure archaeology (or history), completely independently of anthropology, is a delusion, because the concepts used to structure the observations and inferences are ultimately anthropological concepts. The phenomena that we explore are also anthropological phenomena, and it is impossible to explain the past without recourse to anthropology. One may be unaware of this, but it would be just another case of not seeing the woods for the trees. Therefore, archaeology has a double role in its relation to anthropology – it contributes to general anthropological knowledge by providing means of testing anthropological theories and hypotheses that no other discipline can; but it also depends on anthropology for an observational and explanatory framework of the past.

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[13] This does not imply that other social sciences such as economics and sociology are not important. On the contrary, they are very important, in a way similar to that of anthropology – they need archaeology to test the temporal aspects of their general theories; whilst archaeology borrows models and theories from economics and sociology to explain the past. The reason for emphasizing the importance of anthropology is because it is holistic, and as such, it incorporates to some degree both economics and sociology. Therefore, even though anthropology is practiced as a separate academic discipline, i.e. it is separate from economics and sociology (which focus mostly on Western civilization and the contemporary world), in the wider picture it encompasses both of these disciplines. In this context, I am taking the broadest possible view of anthropology.

Archaeological theory in the strict sense of the term is a theory that links the empirical observations of the archaeological record to the dynamics of the past. This is the middle-range theory[14], a term famously coined by Binford in order to distinguish conceptually archaeological theory *sensu stricto* from general anthropological theory (Binford 1977; 1981; see also Raab & Goodyear 1984). As noted by Raab and Goodyear (1984), other prominent theorists, such as Clarke (1973) and Schiffer (Schiffer 1975; 1976), also recognized the need for such a theory. The second kind of theory that we need is one that will tell us why things happened in the past the way they did – to explain the past in the terms of some general principles. This is general anthropological theory.

The relationship between general theory and archaeology is two-fold. We can invoke general theory to explain a past phenomenon or we can use archaeological research to provide means for the testing of general theory. For example, the theory of the Agricultural Demographic Transition suggests that populations which make a transition from the foraging to the farming way of life will have increased fertility and will consequently increase in size (Bocquet-Appel 2011). This is a general theory, as it is relevant for any time or place. The major test of this theory included a large corpus of archaeological data on inferred fertility and the chronology of various prehistoric communities (Bocquet-Appel 2002; Guerrero et al. 2008; Kohler et al. 2008). Likewise, an already established theory, such as the scalar stress theory, can be used to explain why the maximum settlement population had to be relatively small in non-hierarchical societies (Johnson 1982; Feinman 2011; Alberti 2014); or the optimal foraging theory can be used to explain the frequencies of different animals in the faunal assemblages or settlement patterns (Winterhalder & Smith 2000), and so on.

Middle-range theory and general anthropological theory are the two basic levels and kinds of theory in archaeology. They represent two levels because archaeological inferences about past events and behavior must logically precede the explanation of these events and behavior. These two theories are also different in kind, as they refer to two distinct domains of reality. Archaeological middle-range theory deals with translating archaeological observations into anthropologically meaningful statements about the past, whereas general anthropological theory explains the diversity and processes of anthropological phenomena themselves, regardless of whether they come from the past or present. It may seem that this discussion and elaboration of different kinds

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[14] It should not be confused with the concept of the middle-range theory in sociology, which was proposed by Robert Merton (1968) as an epistemic strategy to formulate a set of independent theories and models as explanations for particular social domains which have clear empirical implications (Raab and Goodyear 1984).

of theories is simply a scholastic exercise; but if we want to understand the complex relations of cultural transmission theory and archaeology from the epistemological perspective, this categorization is useful and necessary. I will argue that cultural transmission theory can have both epistemic roles[15]. In particular cases, it is not always easy or possible to decide in which mode the theory is used (as it can be used in both), but we can at least maintain this difference at the conceptual level.

2.4.2. Cultural transmission theory as a tool for constructing the middle-range theory

Even though the cultural transmission theory is a general anthropological theory, it can be used to formulate the middle-range theory in archaeology – to make predictions about what kind of patterns we should expect to find if past social processes unfolded in accordance with a specific model of cultural transmission:

> *"The vast majority of CT research in archaeology has revolved around the use of CT theory as a means to understand and explain variation and covariation within and between assemblages of artifacts or traits of artifacts. Thus, archaeologists measure patterns in the attributes of artifacts to deduce ancient transmission patterns, which are then extrapolated to make claims about the nature of past societies and what may have prompted individuals to use one type of transmission system over another. For example, societies might be characterized either as employing primarily social learning to transmit information, resulting in higher within-community conformity, or as encouraging individual learning and experimentation. Alternatively, societies might be characterized as using primarily oblique versus vertical transmission. While such differences may represent an alternative social structure and/or ethos and may be interesting to know in individual prehistoric cases, such descriptions are rarely extrapolated to larger interpretive or theoretical frameworks. They are used only to explain the archaeological record of a particular window of time in space. "*
>
> *(Eerkens & Lipo 2007: 260)*

In this mode, the principles of cultural transmission theory are assumed to be true and are used to derive predictions about the archaeological record by specifying the connections between cultural processes or structures with

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[15] It should be emphasized, however, that the role of cultural transmission theory as archaeological theory ***sensu stricto*** is incomplete, as it does not include the formation processes of the archaeological record.

the variability of the material culture in space and time. In such cases, we are describing past processes in terms of the models and concepts of cultural transmission theory. For example, Neiman assumed that the neutral model is the appropriate model for the transmission of the Woodland ceramics. If this model was true, the theory suggests that the assemblages' homogeneity/diversity reflect the degree of intergroup transmission i.e. interactions, in terms of the number of people moving between the communities. Neiman then empirically investigated whether and how the diversity of assemblages changed through time and interpreted these changes in terms of community interactions. Cultural transmission theory is used as a justification for the proxy which Neiman used, but the ability to monitor the degree of intergroup transmission is not the same thing as being able to explain the reasons for the changes in interaction frequency. For this particular phenomenon some other theory may be relevant.

2.4.3. Cultural transmission theory as a general anthropological theory

Cultural transmission theory is a general anthropological theory in the sense that it explains or provides a model for certain classes of cultural phenomena. Perhaps the most illustrative example of the use of cultural transmission theory as a general theory for explaining rather than reconstructing the past can be found in the seminal works *of Shennan* (2001) and Henrich (2004), regarding the relationship between the demographic dimensions of preindustrial populations and technological complexity. Shennan and Henrich used cultural transmission theory to deduce that the development and persistence of complex technologies is possible only if the population size is sufficiently large to compensate for the lack of perfect replication fidelity. Shennan argued that this might explain both the development of modern human behavior (as reflected in complex technology and symbolic behavior) after and, sporadically, before the beginning of the Upper *Paleolithic around* 45k years ago (Shennan 2001). Henrich suggested that the loss of technological complexity in Tasmania, when the effective population size was reduced as Tasmania was separated from the Australian mainland by the rising ocean level in the early Holocene, can be explained by the cultural transmission model of social learning (Henrich 2001).

2.4.4. Archaeology and the testing of cultural transmission theory

When it comes to the use of cultural transmission theory as a source for proxies and for the prediction of patterns in the archaeological record, the key question is whether this theory is valid. Is it really true that certain aspects of culture do behave in such a way that they can be modeled as evolutionary systems? This is the question regarding the validity of cultural transmission theory as a general theory. How do we actually know that the cultural transmission theory is true? It is one thing to assume that cultural evolutionary models are good models for certain aspects of culture and then go on to explore the implications of these models under this assumption; but it is a completely different thing at the conceptual level to test this assumption:

> *"Ultimately, such descriptive studies represent a wholesale and fairly uncritical borrowing of ideas from CT rather than attempts to falsify the theory, as science should strive to do (e.g., Popper 1959)."*
>
> *(Eerkens and Lipo 2007: 260)*

Not only can archaeology benefit from cultural transmission theory, but it can provide the means for its testing as a general anthropological theory (Garvey 2018). Let us revisit Neiman's classic work (Neiman 1995). What would constitute a test of cultural transmission theory in this particular example? In Neiman's paper, we can actually find a good example of testing cultural transmission theory in the first part of the paper, and we can use the research presented in the second part as an inspiration to formulate another hypothetical test of the theory. Neiman's comparison of the patterns produced by simulations of the neutral model to the battleship shape of type-frequency dynamics usually encountered in the archaeological record constitutes a partial empirical test of the relevance of cultural evolutionary models. If the theory is true, suggesting that some aspects of the culture, including the transmission of material culture, can be modeled as an evolutionary system (transmission of information with modification), then we have a clear prediction of what the dynamics of variant frequencies will look like. This prediction can be compared to the actual changes in variant frequency through time in contexts where the temporal position of assemblages is determined by stratigraphy or some independent method of absolute dating, such as radiocarbon or dendrochronology. This is what Neiman did, and he found a good match. It should be noted, however, that this is only a partial test, because there are other models of transmission which also produce similar patterns (Acerbi et al. 2012; Klimek et al. 2019; Newberry & Plotkin 2022; see also section 5.7 in this book). Therefore, the neutral model is a sufficient, but not a necessary condition for this pattern to arise. Nevertheless, what is important here is that Neiman was able to show that an evolutionary cultural transmission model can reproduce the observed empirical patterns.

In the second part of the paper, Neiman used assemblage diversity as a proxy for interactions between communities. I have presented that as an example of the use of cultural transmission theory in the middle-range mode. But if Neiman had independent evidence for the degree of interactions between different local communities in different time periods, e.g. by means of strontium isotope analysis or ancient DNA, he would have been in the position to directly test the cultural transmission theory. If the theory was true, the assemblage diversity would indeed correlate with the degree of intergroup interaction as established by independent lines of evidence.

In the research presented in this book, cultural transmission theory is mostly used in the mode of middle-range theory. The models to be presented in the next chapters provide predictions of the spatial and temporal patternings of material culture under different regimes of cultural transmission, taking into account the formation of the archaeological record and the transformations which are specific to this process, like time-averaging and sampling. This corresponds to middle-range theorizing in archaeology. But the theoretical exercise which constitutes the core of the book can also be understood as middle-range theory-building in the Mertonian sense of the term, i.e. as a theory-building which is midway between the empirical world and the abstract general theory (Merton 1968: 39). I develop and investigate the behavior of specifically parametrized models corresponding to a set of past cultural processes (on specific spatial and temporal scales) which are less abstract than general cultural transmission theory (e.g. the models of cultural evolution as presented in Boyd and Richerson 1985).

3

EXPERIMENTING WITH CULTURAL TRANSMISSION: SIMULATION AND DATA ANALYSES

Chapter 3

EXPERIMENTING WITH CULTURAL TRANSMISSION: SIMULATION AND DATA ANALYSES

“As prehistorians we may be unable to decide why a particular unit has the spatial pattern it does, but we may be able to build stochastic models of contact and diffusion which interrelate aspects of culture into different arrangements and configurations.”

(Hodder 1978: 269)

3.1. COMPUTER SIMULATION AS AN EXPERIMENTAL TOOL

In this chapter, I will present the main methods that were used to perform the theoretical research which constitutes the core of the book. In the first part of the chapter, I describe the basic computer simulation design, whilst in the second part, I present the statistical techniques and instruments used to analyze the simulation output. The purpose of the simulation is to serve as the engine for the implementation of the cultural transmission models. As the main aims of the research are to explore and illustrate how various processes of cultural transmission generate patterns of material culture variability in space and time, computer simulation is a tool that I use to generate the expected patterns given a particular model and scenario of cultural transmission.

The method of computer simulation is of great epistemic importance for the social sciences (Gilbert & Troitzsch 1999), and especially for the historical sciences. Its importance stems from the fact that computer simulation brings us as close as possible to the experimental method, which is the gold standard in science. The experiments have limited applicability in the social sciences, for both ethical and practical reasons, whilst experimentation is completely impossible in the historical sciences (Romanowska et al. 2021; Premo 2007).

The computer simulation method does not allow us to experiment with the past reality itself, but with the models of the past.

The computer simulation method is one of the most important methods in the field of cultural transmission and cultural evolution research (for an excellent practical guide to constructing and exploring computer simulations of the most important cultural transmission models, see Acerbi et al. 2022). It should be noted that computer simulation is certainly not the only way to explore the models of cultural transmission. Building mathematical analytical models using difference or differential equations is also a standard method in cultural transmission research (McElreath & Boyd 2007). However, I choose to use the agent-based simulation approach as it enables me to mimic more closely the processes specific to the archaeological application of the cultural transmission models, as my primary aim is to contribute to archaeological middle-range theory. An additional benefit of the computer simulation approach is that it makes it easier to handle the stochastic processes.

There are two kinds of computer simulations in archaeology – the simulations which support theory-building (and hypothesis-testing), and the simulations with the purpose of testing archaeological methods (Lake 2014; Crema 2018). Throughout the book, I use the method of computer simulation primarily in the former mode, as a tool for theory-building. It is used to implement models of cultural transmission in order to generate artificial archaeological data. The general idea is to implement models of cultural transmission with specific parametrization, in order to explore their implications and the patterns they produce in terms of the formal variability of (simulated) material culture in space and time. The term specific parametrization refers to the fact that the spatial, temporal and demographic parameters of the simulations are chosen in such a way as to broadly reflect generic autonomous prehistoric or preindustrial sedentary agricultural communities. The patterns in the simulated data are then explored in relation to the processes that generated them, for the purpose of archaeological (middle-range) theory-building. The simulations presented here are static, as they do not allow any temporal or spatial heterogeneity in the transmission model and its parameters (e.g. no changes in population size through time, or switch from one model to another). Such realistic details can be included in the simulation, and such simulations already exist (Kandler & Shennan 2013; Crema et al. 2016; Kandler & Crema 2019), and are preferable and superior in practice when the aim is to identify and reconstruct transmission models from empirical data. For the purposes of this book, where the primary aim is to conduct theoretical explorations, these simple models will suffice and will provide the baseline for adding layers of complexity.

The simulations presented in this book can be classified as agent-based models (ABM) (Lake 2015; Romanowska et al. 2021), with some properties of cellular automata when it comes to simulations that include spatial processes. The core of the simulation engine is the same for all of the simulations presented in the next chapters. The modifications of the models and parameter values will be described at the appropriate places in the chapters to come. I will present the basic structure of the simulations on the example of the Neiman's (1995) formulation of the neutral transmission model, which is the model most often implemented and used in the book.

3.2. DESCRIPTION OF THE SIMULATION

3.2.1. The multiple community case: processes in space and time

I will describe the simulation used to generate the patterns of simulated material culture variation in space and time. Note that, as a special case, such a mechanism can simulate only temporal effects if the spatial extent is reduced to a single location.

The simulated world is a spatial grid which consists of a x b square cells. The grid is bounded, not toroidal, in order to make the spatial setup more realistic, as a spatial snapshot of some wider region. It is assumed that the dimensions of each square cell are 10 x 10 km, which implies that the square would roughly correspond to the catchment area of a generic preindustrial small settlement, which should be imagined at the center of the cell. Each cell in the grid contains N items which act like agents in a simulation (Figure 3.1). Each item can be thought of as representing a single artifact (e.g. a pot or figurine), used by a single person, of a certain type or meme variant (the terms type and variant will be used here interchangeably), labeled by an integer. This is the systemic (living) assemblage (*sensu* Schiffer 1972; 1976). The systemic assemblage refers to the set of artifacts in a certain settlement which were in contemporaneous use (e.g. all axes or all chairs that were in use at certain point in time). In the context of simulation, the contemporaneity refers to one simulation time step. I am assuming an approximately 1:1 ratio between the number of artifacts and the number of people for this hypothetical class of material culture, so the N loosely corresponds to the settlement population size as well.

This relationship between the census population size, the number of artifacts (objects) and the number of artifact makers needs some additional clarification. The basic items of the simulations are artifacts (i.e. meme variants carried by the artifacts), not human agents, as the algorithm operates directly on the memes and their frequencies. This is the agent-based model, so the agents, in the technical sense, are the memes. But it would be preferable to have an interpretation of the simulation in terms of the actual human agents as well. This is possible under certain assumptions, which I will explain by means of an example. Let us imagine that the items/artifacts are ceramic bowls, and that most people in the settlement use one such bowl (e.g. they eat lunch every day from that bowl). It is unrealistic to imagine that each person is a potter; therefore the number of potters must be much smaller than the total number of people. For example, if we assume that the each household produces its own pottery, and assuming 5 people per household, the number or potters would be 20 in a population of 100 people. If each potter makes the same number of bowls, then the number of bowls made by each potter is 5. The assumption that I am making is that for each new bowl that is made, the potter is independently choosing a meme variant. This means that one potter is not going to use the same decoration and/or shape for all his bowls, but will decide for each new bowl which decorative motif to apply or how to shape it. Of course, the validity of this assumption is not absolute, it may be questioned and different assumption can be made. I make the assumption explicit here, as this is the way to interpret the number of items as approximating the settlement population.

In each iteration of the simulation, which is interpreted as a one year time step, for each item from each cell in the grid, the computer first decides whether it will move the item from the systemic assemblage to the archaeological assemblage associated with this particular time step. The decision is probabilistic and depends on the *average use-life parameter* (L). The probability that an item will enter the archaeological record at any time step is equal to $1/L$. For example, if the average use-life is 2 years, this means that a half of the living assemblage (randomly sampled) will go to the archaeological assemblage in one time step of the simulation[16]. This simulates the fact that each artifact is discarded at some point (as it is broken or ceases to be useful for some other reason) and enters the archaeological record. Therefore, for each time step

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[16] The establishment of the correspondence between real-world time and simulation time in iterations depends on establishing the correspondence of the average use-life of items in the simulation and iterations. This is completely arbitrary. For example, one way of interpreting the setup presented in the previous paragraph is as described (one iteration = one year). But if we decide that one iteration corresponds to two years, then the use-life of two iterations, corresponds to an average use-life of four years. This offers the opportunity, if necessary, to re-scale the simulation results for items with different use-lives than the one I took as a standard.

the computer records the contents (the variant frequencies) of the archaeological assemblage produced, which consists of discarded items. Whenever *L* is different from 1, we have a situation of overlapping cultural generations in the archaeological record. This is a more realistic scenario than simulations presented in Porčić and Nešić (2014) and Porčić (2015), where an entire systemic assemblage went into the archaeological record at each time step – the non-overlapping cultural generations case.

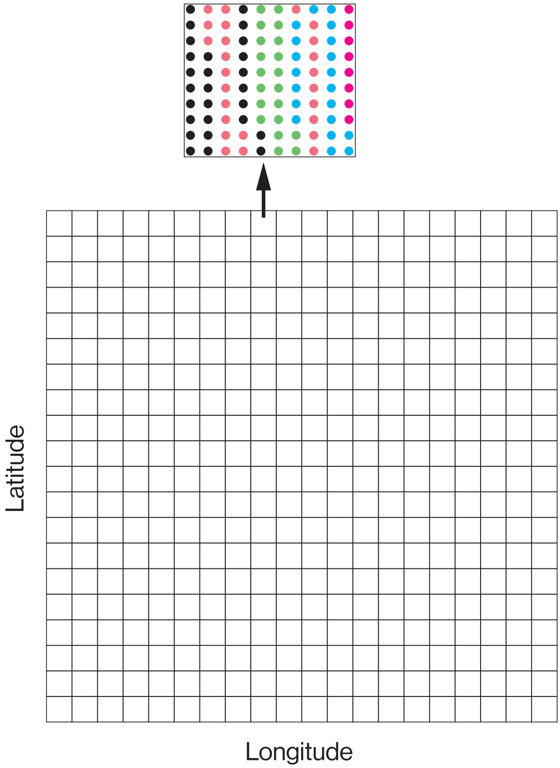

Figure 3.1. A schematic representation of the default simulation space and cell structure. The spatial grid consists of *a* x *b* cells (20 x 20 in this case). In each cell there is a population of *N* items (100 in this case) with particular frequency distribution of meme variants or types, marked by different colors.

Each discarded artifact during a time step needs to be replaced. This is where the cultural transmission comes in, because a type or variant needs to be assigned to the item which is newly introduced into the systemic assemblage in order to replace the discarded object. As I stated earlier, I will describe only the simulation of the neutral model here. There are three options for how to assign the cultural variant to the new item according to the neutral model that is used for the baseline:

1) Copy a variant from a randomly chosen item in the living assemblage population of the particular cell from the beginning of the time step (before the discard). The probability of copying each variant will be proportional to the relative frequency of the variant in the living assemblage of the particular cell before the discard.

2) Generate a mutation – introduce a globally (not just in relation to the particular cell) novel variant into the system. In this case the next free integer (not present within a particular cell or other cells in the grid) will be assigned to the item. This is equivalent to the *infinite allele models* of mutations in population genetics (Ewens 2004: 111–119). The probability of mutation is given by the ν parameter (from Neiman's model, I use the same notation). For example, if the probability of mutation is 0.005 ($\nu = 0.005$), this implies that in 5 out of 1000 cases, a type will not be copied from the existing pool of types, within or outside a given cell, but a completely novel type will be introduced. The mutation can occur in two ways. It can arise as a deliberate and intentional act to create something completely new and not to copy any of the existing variants, or it can be a consequence of the copying error. According to Eerkens and Lipo (2005; but see also Crema et al. 2023), copying errors are generated through a) errors in perception generated by cognitive limits in evaluating metric differences between two objects, and b) errors due to imprecision in manual dexterity:

   copying error = error in perception + error in execution (motor skills).

   How to choose the realistic values for the mutation rate parameter? This is a very difficult question. Shennan suggests obtaining the estimates from the data (Shennan 2011). This seems to be the best approach, as it takes into account the fact that the mutation rate may be idiosyncratic to the class of material culture under investigation and to the specific historical situation. But the estimation of mutation rates is difficult to make in practice, as there is more than one way of making the estimate (Shennan & Wilkinson 2001), and the estimates may be biased in small samples (Porčić 2015). In the absence of clear guidelines, I experiment with different values and different orders of magnitude, as one of the research tasks is to explore the influence of this parameter on the spatial and temporal patterns. The theory suggests (see Chapter 2) that what determines the nature of the neutral transmission process (the diversity of variants and the dynamics of frequency change) is actually the parameter *theta*, which is a product of population size and mutation rate. Therefore, different combinations of population size and mutation rate can result in the same theta value which determines the outcome of the evolutionary process. From this point of view, it is sufficient only to vary the theta parameter, but I want to keep its components separately in order to have a better anthropological comprehension of what is actually going on and because population size and mutation rate are estimated in different ways from the archaeological data

3) Copy a variant from a randomly chosen item from a *different* cell (a cell other than the cell to which the item which is being replaced belongs). This represents the intercommunity interaction and the probability of this option is given by the *m* parameter. If this parameter value is, for example, 0.1, this means that in 1 out of 10 cases, a type from another settlement will be copied. The choice of the cell from which a variant will be copied is probabilistic, and the probabilities are proportional to the distribution of the inverse square of Euclidean spatial distances of all other cells from the given cell. The distance is between the centroids of the cells. Therefore, the probability of interaction with another simulated community is determined by the geographical distance and it is based on the model of interaction supported by empirical research:

> *"Much research has shown that intermigration between two populations is approximately proportional to a simple function of the distance between them. One such function currently employed is* d^{-c}*, where d is the distance, and c is close to 2."*
>
> *(Cavalli-Sforza and Feldman 1981: 163).*

First the matrix of Euclidean distances *D* between the centroids of cells for all pairs of cells is calculated. Then this distance matrix is transformed into a similarity matrix *S* by applying the equation

$$s_{ij} = \frac{1}{d_{ij}^{2}} \quad \text{(Eq. 3.1)}$$

where d_{ij} is the Euclidean distance between the centroids of the cells. Then for each cell, the probability of interaction with any other cell is calculated by normalizing the row vector of similarities corresponding to each cell, so that it adds up to 1. This is done by dividing each s_{ij} value by the sum of s_i values in the corresponding row (excluding the value of the similarity of the cell to itself).

Such a model of spatial behavior translates into interactions that are usually localized. Interactions with cells that are further away are highly unlikely, as the probability of copying from different communities decreases rapidly with distance in such model. Increasing the probability of interaction increases the frequency of agents that "choose" to copy a variant from an item from a different cell. It should be noted that in this case, the introduced variant does not have to be globally novel – it may be already present in the local community, if it was present in all cells from the beginning or if it was introduced in an earlier episode of the interaction. Therefore, unlike with Neiman's model, the $m + v$ should be thought of as the maximum possible local overall mutation rate. This maximum is never reached and is much closer to v, as the neighboring cells, which are the most likely to be sampled from, usually have the same or similar repertoire of cultural variants as the considered cell.

What would be an anthropological interpretation of interactions, and how can it help us to specify the realistic parameter (of interaction) values? As this is a very general model, different interpretations are possible. For example, we can interpret interactions as marital migrations – persons coming from another settlement, or as trade visit episodes. Other possibilities would include trade and exchange of material culture between microregions (e.g. Graves 1991). Even warfare could lead to an increased social interaction between communities that would manifest itself as the introduction of traits from other communities (Lycett 2019). A better alternative to thinking about ways to adapt the interaction parameter to reflect a certain anthropological scenario would be to construct a more complex agent-based model, where processes such as marital residence migrations, visits, and trade are explicitly modeled. However, in the models used in this book, this parameter remains a black box.

3.2.2. The single community case: a process in time

The single community simulation is used to explore the patterns in time. There is no space in this simulation, as we are only looking at the single community (e.g. from a single cell). The algorithm of the simulation for the neutral model is the same as for the multiple community case, with the difference that there is no interaction parameter. Therefore, in each time step, when an item is discarded (becomes a member of the archaeological assemblage associated with a particular iteration of the simulation) and is replaced, there are only two possibilities compared to the multiple community model:

1) Randomly copy a variant in accord with the neutral model presented above.

2) Generate a mutation, again assuming that the mutation is the consequence of the deliberate innovation or the copying error. In this case, the mutation rate μ is a single parameter (its components are not modeled separately), which may be conceptualized as a combination of true *in situ* mutation or mutation due to the introduction of a variant from some other community (which is not simulated in this case) which was not previously present in the given community (i.e. this is Neiman's model – the only difference is that the cultural generations may be overlapping).

3.2.3. The reproducibility of the simulation results

I did not systematically present the results of the sensitivity analyses and repeated simulation runs for some of the simulations, but the multiple experiments I performed suggest that the patterns are very robust. The reader does not have to take my word for it, as I provide a full code for all of the simulations in the Appendices of the book, so this can be tested and checked. In Appendix 1, the codes for the neutral, the conformist, and the anti-conformist (not explored in the book for the multiple community case) models of cultural transmission in the multiple community case is presented. In Appendix 2, the code for the Axelrod model (Axelrod 1997) for the multiple community case, or more precisely, an interpretation of the Axelrod model, is given. In Appendix 3, the reader will find the code for the single community case for the neutral, conformist, and the anticonformist models. In addition to the simulation code, I also provided the code for data-collection and time-averaging. The computer simulation code and output data aggregation code are written in the *R* programming language (R Core Team 2019). Additionally, R code from the Appendices along with the specific code used in the data analysis is available in the Zenodo repository (doi: 10.5281/zenodo.7778260).

3.3. THE STATISTICAL INSTRUMENTS FOR SUMMARIZING AND ANALYZING THE SIMULATION OUTPUT

3.3.1. The time-averaging of simulated assemblages

As archaeological assemblages coming from the settlements are almost always time-averaged – as a result of multiple discard episodes (Bailey 2007) - we cannot look at the simulated archaeological assemblages from single iterations as realistic units of analysis. For this reason, the assemblages which represent the main units of analysis are generated by aggregating archaeological assemblages from several individual iterations (Madsen 2012; Premo 2014; Porčić 2015). The frequencies of variants are then counted for each aggregated assemblage. This is how I simulate the time-averaging of the archaeological record. The levels of time-averaging varied in different experiments and the details are presented in the corresponding chapters.

3.3.2. Analyzing the configuration of assemblages in the typological space

In order to extract a single measure of assemblage structure (i.e. the major dimension of the typological variation) and to reduce the dimensionality of the typological space, I apply *correspondence analysis* (CA) (Shennan 2004: 308-345; Greenacre 2007) to the variant frequencies from accumulated assemblages. The CA is a multivariate technique for dimensional reduction, and the scores on the CA axes can be interpreted as scores on the general typological dimensions, as they are mathematically constructed in such a way as to encompass the largest portion of (co)variability in variant frequencies between assemblages. The distances between the assemblages in the CA plot, which is usually the defined by the first and second CA axes, can be interpreted as typological distances. The closer the two assemblages are on such a plot, the more similar they are in terms of relative variant frequencies, and vice-versa. When it comes to patterns in time, CA is used as a seriation technique (Chapter 4). When it comes to patterns in space, CA is used to extract the summary measures of typological variability in order to explore the patterns in the typological space produced by different transmission models, and to explore the relations between the typological and spatial dimensions.

The typological distance matrix between pairs of cells (settlements) is calculated by using the *Brainerd-Robinson* (BR) coefficient (Brainerd 1951; Robinson 1951), which is a similarity metric specifically designed to measure the (dis) similarity between archaeological assemblages. The value of the BR similarity between assemblages i and j is equal to the sum of the differences of the variant percentages between assemblages i and j for all n individual variants, subtracted from 200:

$$200 - \sum_{k=1}^{n} \left| P_{ik} - P_{jk} \right| \qquad \text{(Eq. 3.2)}$$

- where P_{ik} is the percent of the k_{th} variant in the i-th assemblage, and P_{jk} is the percent of the k-th variant in the j-th assemblage.

The greater the value of the BR index for a pair of assemblages, the more similar they are in terms of the relative frequencies of attributes/types and vice-versa. In order to turn the BR similarity index into a distance measure, it is simply subtracted from 200; therefore the formula for the BR distance is:

$$BR_{ij} = \sum_{k=1}^{n} \left| P_{ik} - P_{jk} \right| \qquad \text{(Eq. 3.3)}$$

- where P_{ik} and P_{jk} are percentages of variant *k* in assemblages *i* and *j* respectively. The BR distances are calculated in *R* using the *BRsim* function (Alberti 2021b).

In addition to calculating a distance matrix based on the variant frequencies, I also calculated a distance matrix based on the presences and absences of variants. The measure of inter-assemblage distance is the *Jaccard coefficient* (Shennan 2004: 228-230; Jaccard 1912), which measures distances[17] between a pair of assemblages based on the presence and absence data. This lowers the resolution of the analysis, as it neglects the information on variant frequencies, but given that the presence/absence resolution is usually the best that can be achieved in empirical research, it is useful to explore the data using the statistical instrument that is comparable to the larger number of empirical studies.

I also use hierarchical cluster analysis to create groups of squares with similar assemblage structures – similar in terms of variant frequencies. The cluster analysis uses all of the variant frequency information from the data, as the typological similarity matrix is created from a full dataset, but the number of clusters needs to be specified by the analyst (it is usually set to 4 in this case). Cluster analysis is used in Chapter 4 to mimic the construction of archaeological cultures as statistical groups.

As for the clustering algorithm, the analyses are performed using the *Ward method* for the BR metric and the *average linkage method* (see Shennan 2004 or some other general textbook on cluster analysis for details about these standard clustering algorithms) for the Jaccard distances.

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[17] The Jaccard distance is obtained from the Jaccard similarity coefficient simply by subtracting its value from 1.

3.3.3. The correlations between typology, space and time

In the research presented in the following chapters, I explore the relations between the typological dimension on one side, and the spatial and temporal on the other, in two general ways:

1) By correlating the major typological dimensions extracted by CA with the major spatial directions and/or time.

2) By calculating and analyzing the correlations between the typological, spatial (Euclidean distances between cell coordinates), and temporal distance (Euclidean distances between midpoints of assemblage temporal spans) matrices between assemblages. I use the *Mantel matrix correlation* for this purpose (Mantel 1967). Technically, the correlation between two matrices is calculated as a simple correlation coefficient, where the units of observation are pairs of cells and the variables are the corresponding distance values from the two matrices. Mantel (1967) constructed a specific technique of significance testing for such a correlation, based on the permutations of the matrices, because the standard way of calculating the statistical significance (*p* value) is not valid in this case, as the assumption of the independence of observations is violated (as one cell is in several pairs). Although I rarely make use of the actual permutation test (the *Mantel test*), as the simulations allow me to work with entire populations rather than samples (so the effect size is more important than the *p* value), I will still refer to this kind of correlation as Mantel's correlation, to indicate the fact that we are looking at the correlations between distance matrix entry values rather than individual variable values. It should be noted that Mantel correlation analysis has its problems, and that it represents a very rough tool which should be interpreted with caution (Guillot & Rousset 2013; Nunn et al. 2006).

The correspondence analysis, the cluster analysis, and the Mantel matrix correlation are analytical instruments which are often used in archaeology for studying the formal variation of material culture in space and time. I use the same statistical instruments to analyze the simulation output data. This is crucial for archaeological theory-building, as it allows us to directly compare the simulated and empirical observations. In this chapter, I have only presented the statistical instruments at the most general level. The specifics of the individual analyses will be described in detail at the appropriate places in the forthcoming chapters.

4

PATTERNS IN SPACE

Chapter 4

PATTERNS IN SPACE

> *"It might be suggested that prehistorians have insufficient knowledge and theoretical ideas to interpret distribution maps of material culture items satisfactorily."*
>
> *(Hodder 1977: 239)*

4.1. THE LAYOUT OF EXPERIMENTS

In this chapter, I use computer simulation in order to demonstrate and explore how spatial patterns of formal variability can arise from simple cultural transmission models. The aim is to simulate particular transmission scenarios to see the implications of particular models for the distribution of type frequencies in space. Of course, time plays its part here as well, as cultural transmission must unfold in time, but the focus of this chapter will be on the spatial patterns, while holding time constant. This is achieved technically by looking at the spatial patterns from the same temporal slices. Again, this does not exclude the role of time in making two assemblages similar or different (e.g. through drift), but this kind of influence is not systematic. Drift assumes the passage of time, but time itself cannot systematically influence the patterns in space that we are interested in. Given the quasi-realistic setup of the simulations, this will enable us to see how long it takes for some kind of equilibrium pattern to emerge, or simply to see what will happen in the first 1000 years even if this is not the equilibrium state, from the initial conditions which also have some broad anthropological interpretation (e.g. when all assemblages are identical at the start - this corresponds to a situation which immediately follows some fast migration). I will use the statistical instruments presented in the previous chapter to explore the relationship between typology and space.

I will start with the simplest model of cultural transmission, which is often used as the baseline model or null hypothesis for the evolution of style – the neutral (unbiased) model of cultural transmission (Shennan & Wilkinson 2001; Neiman 1995; Bentley et al. 2021; Bentley et al. 2004; Hahn & Bentley 2003). The main idea is to demonstrate how this model can produce patterns in space which may resemble population structure even if there is none. In the first two experiments with the neutral model, the aim is to see what kinds of patterns in space are generated, and to see how the intensity of inter-community interactions affects the patterns. In the third experiment, I explore how the shape of the study area influences our perception of the patterns.

After exploring the neutral model, I move on to two models – the *conformist model* and the *Axelrod model* – which are more complex, in the sense that they assume something about how social and cultural factors influence individual decision-making. There are two main questions that I try to answer by experimenting with the conformist and the Axelrod models: 1) Can these models generate relatively discrete spatial clusters of typologically similar cell assemblages which correspond to the traditional idea of archaeological culture, starting from the initial cultural situation where all cell assemblages are identical at the beginning? 2) If discrete cultural groups are there to begin with (i.e. there are two distinct spatially clustered groups of cell assemblages), can these two models generate continuity, i.e. make the initial situation of cultural boundaries in space persist through time?

For the conformist model, in the first two experiments I explore the influence of the community interaction at relatively high levels of conformism in the case where there is no spatial structure to begin with (i.e. all assemblages are identical in the first iteration). Then I conduct two additional simulation experiments, to investigate what happens if there is a spatial population structure at the onset of the simulation and how the level of conformism determines whether the initial population structure will persist through time.

For the Axelrod model, I explore whether it can generate discrete spatio-cultural groups from the initial uniform cultural situation, and if it can preserve the already existing structure. I conducted 5 experiments to see how the degree of interaction and the degree of homophily influence the results in two contrasting situations – when the initial cultural situation is uniform and when the spatial structure of material culture is there to begin with.

4.2. THE NEUTRAL MODEL EXPERIMENTS

The neutral model was already described in Chapters 2 and 3, as it is the flagship model of the book, so I will only present a quick reminder here. This model assumes random copying of cultural variants within settlements with a possibility of mutation (the v parameter) and copying from an agent from another settlement (the m parameter). In the cases when agents choose to copy from a different settlement, they copy from a randomly selected agent from another settlement. The frequency of this behavior is determined by the simulation parameter m, which is the probability of interaction. The probabilities of choosing a particular settlement to copy from are proportional to the inverse square of the spatial distances between pairs of settlements.

In Chapter 3 I described how this model is implemented in a computer simulation; and it is now time to run the simulation experiments with concrete parameter values. The spatial grid consists of 20 x 20 cells. We should imagine that a settlement with 100 agents is present at the center of each cell. The probability of mutation is 0.005 (v), meaning that in 5 out of 1000 transmission events, an agent will not copy a variant from another agent but will introduce a new one. The choice of this concrete mutation rate value is admittedly arbitrary, but in the absence of a better solution I chose this value to be in the same order of magnitude as mutation rate estimates in Shennan and Wilkinson (2001) and Shennan and Bentley (2008). The average use-life of each agent is 2 iterations, implying that 50 items will enter the archaeological record in each iteration of the simulation. The starting systemic (living) assemblage of each settlement is the same for all cells, unless stated otherwise. Each agent (item) is randomly assigned to one of the 10 initial variants. Each agent represents a single artifact (a bowl for example). The simulation is run for 4000 iterations, starting from these initial assemblages. The 4000 iteration is an arbitrarily chosen value – to give sufficient time for the patterns to show at a millennial time scale, if there are any.

Time-averaged assemblages are created by aggregating the variant counts from the simulated archaeological record from 50 successive iterations. These accumulated assemblages correspond to site-phases or horizons. The size of each accumulated cell assemblage (per interval) is equal to the size of the cell assemblage entering the archaeological record in each iteration, times the number of aggregated iterations – 50 x 50 = 2500 items. To establish a correspondence of the simulation setup with reality, we should imagine that each cell of the grid is 10 x 10km, and each iteration corresponds to 1 year. With these assumptions, our simulation refers to an area of 40000 km^2, over a period of 4000 years. From each square of the grid we have assemblages of 2500 items each from the accumulated 50 iterations, given the average use-life of 2 iterations.

It is important to emphasize and reiterate an important point here: the neutral model does not assume that individuals are deciding which variant to copy by running random number generators in their heads. The neutral model assumes that each individual has her/his own reasons for choosing one variant over another – when decorating a pot for example –, but that the aggregate result is such that it is as if each individual chose the decoration variant randomly according to the probabilities of the current frequency distribution of variants in the population (Shennan 2011). Therefore, the neutral model does assume agency and intention, but this agency is a black box at the individual level.

4.2.1. The low interaction neutral model scenario (Experiment 4.1)

I will start with the low interaction scenario where the probability of interaction (ν) is 10%.[18] To reiterate, this means that in 10% of cases when a new item needs to be made, a variant will be copied from a randomly chosen agent from some other cell, with the probability of cell choice being proportional to the inverse of the squared distance between the cells.

In Figure 4.1 we can see the spatial distribution of variant frequencies after 50 iterations as summarized by the first CA axis. There is no spatial clustering of typologically similar cells in this graph. Most of the squares are more or less similar to one another, reflecting the initial conditions. After 500 years, when we look at assemblages from different cells, generated by accumulating the archaeological assemblages produced by the simulation between 451 and 500 iterations, a clear pattern emerges which remains relatively stable further on (cf. situation after 1000 years in Figure 4.1). A clear gradient in the correspondence analysis (CA) axis 1 scores is visible along the diagonal running in the SW-NE direction (Figure 4.1). As the entire region is square, both diagonals represent major spatial directions; therefore it is by chance alone that that particular diagonal is the direction of the gradient. The gradient along the other diagonal is usually captured by the CA axis 2 (Figure 4.1).

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[18] The adjective low is used only in the relative sense, as I explore a scenario with a three times higher probability of interaction later in the chapter. As the nature of intercommunity interaction is a sort of a black box in terms of a precise anthropological interpretation in my simulations (see Chapter 3), the terms low and high should only be understood in relative, not in absolute terms.

It should also be noted that the value of explained inertia[19] by the first two axes is almost identical, which is the consequence of the existence of the two equal major spatial directions[20] along the diagonals of the square. We can clearly see that for the time slice between 451 and 500 iterations. The CA axis 1 and CA axis 2 explain around 0.9% of total inertia each[21]. When the scores of the CA 1 axis are plotted in space, we can see a gradient in the SW-NE direction, whereas when the CA axis 2 scores are plotted in space, the gradient is in the SE-NW direction.

After 1000 iterations, the gradient is also present, but it is more closely aligned with the W-E direction rather than the diagonal. As I will discuss below, in the case of the square study region, the direction of the major typological gradient seems to oscillate around the diagonals in the dynamic equilibrium, whereas in the case where there is a single major spatial direction (e.g. if the study area has the shape of a rectangle), the typological gradient aligns with the dominant spatial direction.

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[19] ‘Inertia’ is the equivalent of variance in CA analysis jargon (Greenacre 2007; Shennan 2004).

[20] The term ‘major spatial direction’ refers to the longest axis of the study region. In the case of the square study region there are two major spatial directions – the diagonals.

[21] As noted in Porčić and Nešić (2014), the low percentage of inertia (variance) explained by the first two axes is due to the fact that there are a great number of variants that appear only once. There is no covariation between the presence of these variants, therefore they need to be individually accounted for by different CA dimensions. The sheer number of such variants produced in each iteration – with this parameter setup, 50 new variants are produced in each iteration, and most of them are never copied – “eats” up most of the inertia in the data.

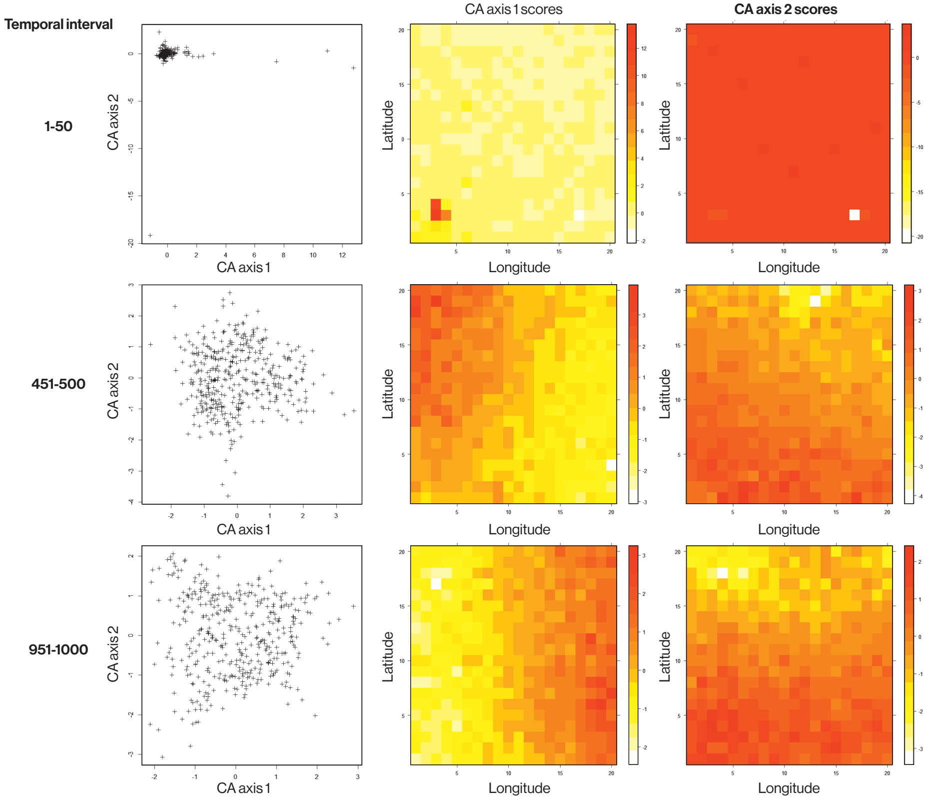


Figure 4.1. The configuration of cell assemblages in the typological space defined by the first two CA axes (the first column of panels), and the plot of CA 1 and CA 2 scores for each cell in space (the second and third column), at different time points, with time-averaging, for the low interaction neutral transmission scenario (Experiment 4.1).

In order to illustrate how the illusion of discreteness can be formed from a continuum, I perform cluster analysis on the BR and Jaccard distances between the time-averaged cell assemblages from the time interval of 951-1000 iterations. I present the results for the 2, 4, and 8 cluster solutions. The results of the cluster analysis suggest that there are spatial blocks with squares which have a similar frequency structure of variants (Figure 4.2). When the cluster analysis is applied on the Brainerd-Robinson (BR) distance matrix, the resulting spatial pattern is fuzzy, but when it is applied on the Jaccard distance matrix, the resulting pattern is clear cut (Figure 4.2). Counter-intuitively, the lower resolution metric based only on presences and absences of type – the Jaccard distance –, gives more clear-cut results than the Brainerd-Robinson, which utilizes the full frequency information. But this can easily be explained by the fact that the Jaccard coefficient is better at detecting the spatial signal when it comes mainly from the low frequency types. Namely, if assemblages have similar frequencies of high-frequency types and they differ mostly on low-frequency (rare) types, which is the case here, then the BR distances will be dominated by high-frequency patterns and *will generally* be low, whereas the Jaccard distances will be able to capture the underlying pattern of rare variants as they are given equal weight in the calculation process, as variant frequencies are reduced to presences (1) and absences (0).

In any case, the application of cluster analysis to the neutral model output will produce typological clusters which are also spatially clustered. If we accept the assumption that the discovery of archaeological cultures in traditional culture-historical archaeology was a kind of informal cluster analysis (see Chapter 1), then this exercise clearly shows how the illusion of discrete groups can be created even if the underlying model assumes no groups or social mechanisms of group formation or cohesion, and the pattern itself is a continuum rather than a discrete grouping.

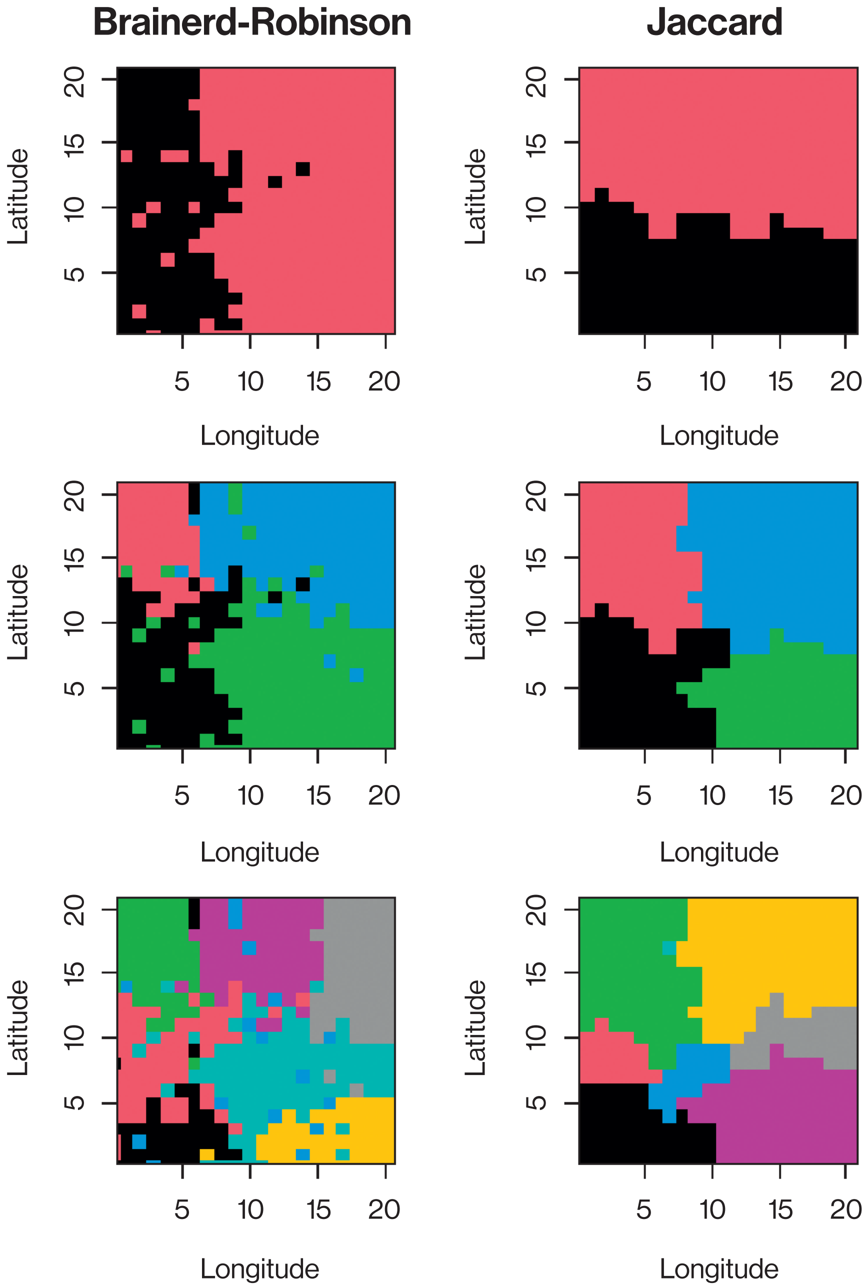


Figure 4.2. Cluster membership of each cell plotted in the study space. Cluster solutions with different number of clusters (2 in the upper, 4 in the middle, and 8 in the lower panel) are presented for the BR and Jaccard distances between time-averaged cell assemblages for the low interaction neutral transmission scenario for the 951-1000 iterations interval (Experiment 4.1). Different clusters are marked by different colors, but the association of color and cluster is arbitrary.

Therefore, this example demonstrates that as time goes by, the spatial structure is formed where initially there was none, and this happens very fast, within the first 500 years. All assemblages were identical in the beginning, but the result would be the same if they were all different to begin with (the reader can try this using the R code from Appendix 1). When all assemblages are the same at the beginning, the variation starts to build up, but then it gradually collapses as the interactions force the spatial pattern; whereas if all assemblages start differently, the collapse of the existing variation starts immediately. The correlation between the typological and spatial distances becomes stronger until dynamic equilibrium is reached, where the Mantel correlation coefficient oscillates around 0.4 when typological distances are measured with the BR distance, and around 0.7 when the Jaccard distance is used (Table 4.1, Figures 4.3 and 4.4). This is the classic *isolation by distance* pattern (see also Crema et al. 2014b and Porčić & Nešić 2014). The typologically similar assemblages cluster in space, but the noise created by the stochasticity of the transmission process within the cells decreases the correlation between the spatial and typological distances.

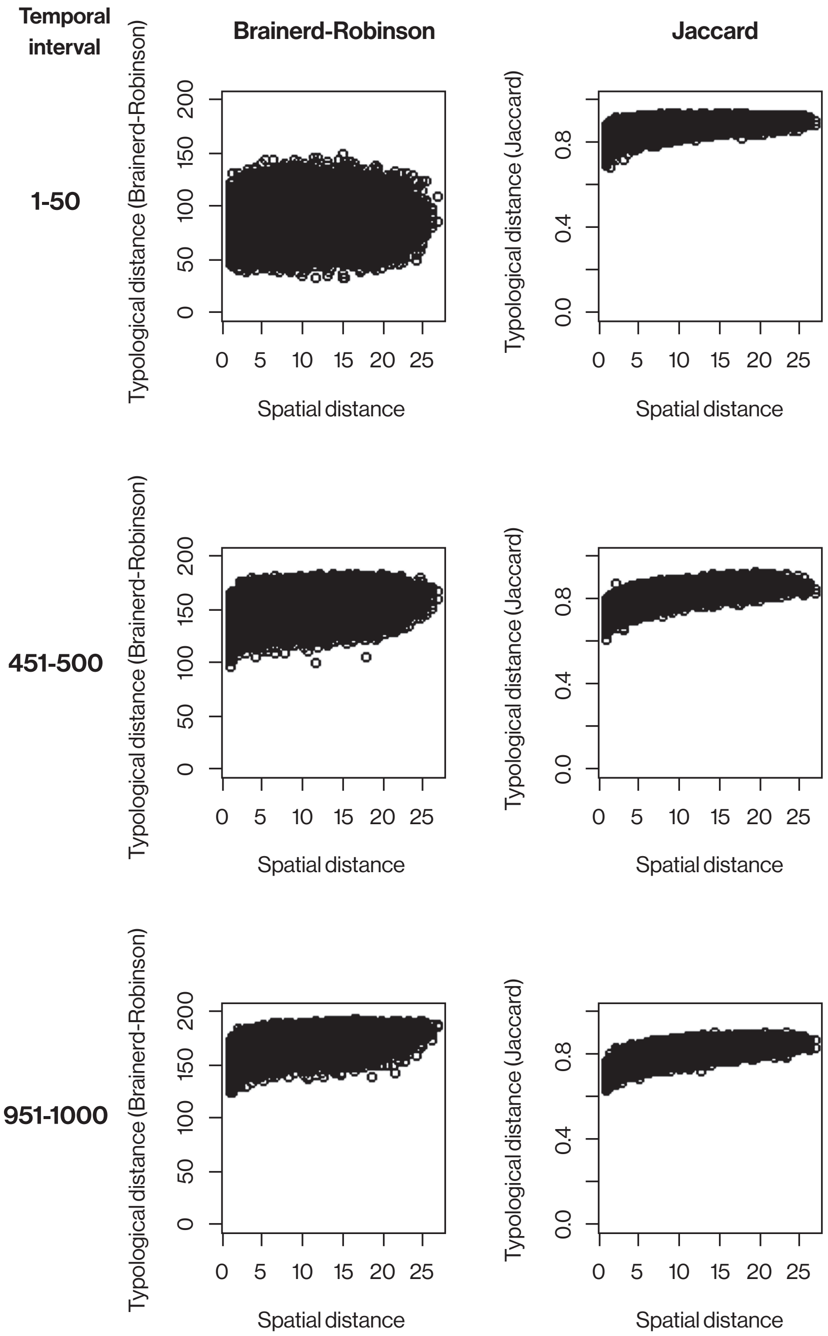
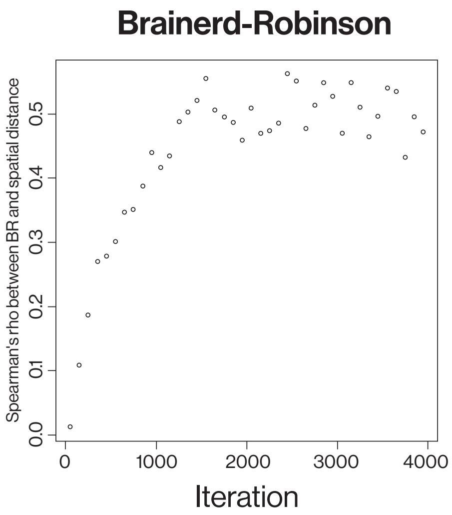


Figure 4.3. The typological (as measured by BR or Jaccard distances) vs. spatial distance between time-averaged cell assemblages at different times for the low interaction neutral transmission scenario (Experiment 4.1).



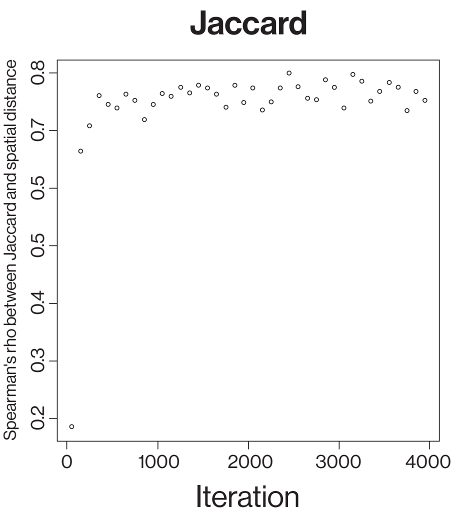


Figure 4.4. The temporal dynamics of the correlation coefficient (Spearman's rho) between typological and spatial distances for the low interaction neutral transmission scenario (Experiment 4.1).

4.2.2. The high interaction neutral model scenario (Experiment 4.2)

In the high interaction scenario, where the probability of interaction (m) is increased to 30%, the same pattern is found, only in this case the spatial patterning is stronger (i.e. there is a higher correlation between typology and space) and the spatial structure forms more rapidly than in the low interaction scenario – the Mantel coefficients quickly increase with time and reach the equilibrium value (Figures 4.5-4.6, Table 4.1). Again, the space-typology correlations are higher when the typological distances are measured with the Jaccard distance than with the BR distance. In the high interaction scenario the equilibrium Mantel correlation between spatial and BR distances is higher than in the low interaction scenario – it is around 0.6.

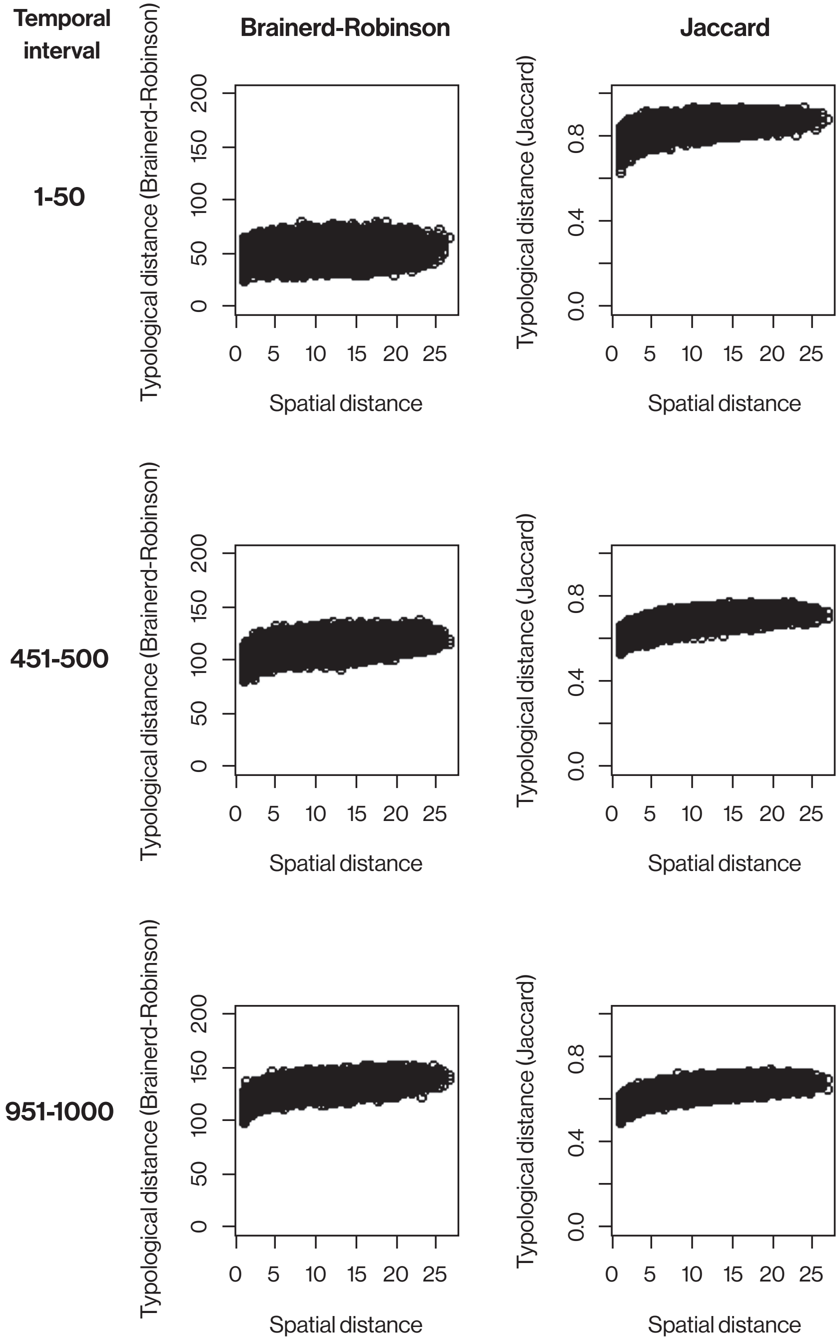
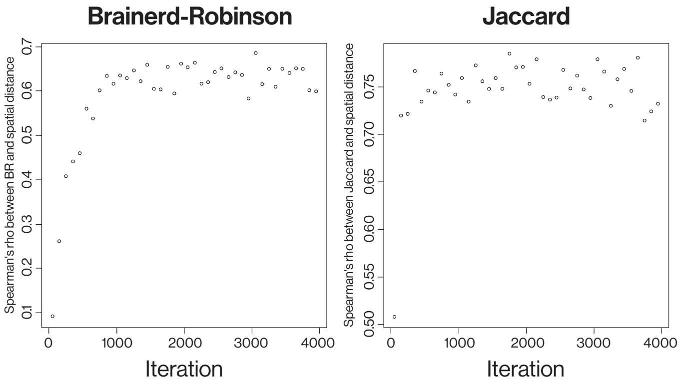


Figure 4.5. The typological (as measured by BR or Jaccard distances) vs. spatial distance between time-averaged cell assemblages at different times for the high interaction neutral transmission scenario (Experiment 4.2).


Brainerd-Robinson

Jaccard

Figure 4.6. The temporal dynamics of the correlation coefficient (Spearman's rho) between typological and spatial distances for the high interaction neutral transmission scenario (Experiment 4.2).

We can see in Figure 4.7 that the gradient is already visible after the first 50 iterations, and the correlations between typological and spatial distances are already moderate. Again, the Jaccard distances are more strongly correlated with the spatial distances than the BR distances. The configuration of assemblages in the typological space defined by the first two CA axes resembles the rotated rectangular shape of the study area.

Degree of interaction	Accumulation interval	Mantel correlation (BR distance vs. spatial distance)	Mantel correlation (Jaccard distance vs. spatial distance)	CA axis 1 inertia	CA axis 2 inertia
Low ($m = 0.1$)	1-50	0.025 (min = -0.02; max = 0.06)	0.23 (min = 0.15; max = 0.31)	0.9%	0.8%
	451-500	0.31 (min = 0.23; max = 0.37)	0.74 (min = 0.7; max = 0.78)	1%	0.9%
	951-1000	0.48 (min = 0.41; max = 0.52)	0.75 (min = 0.72; max = 0.78)	1%	0.9%
High ($m = 0.3$)	1-50	0.11 (min = 0.04; max = 0.22)	0.53 (min = 0.49; max = 0.56)	0.8%	0.8%
	451-500	0.54 (min = 0.47; max = 0.63)	0.75 (min = 0.72; max = 0.77)	1.3%	1.3%
	951-1000	0.64 (min = 0.57; max = 0.68)	0.74 (min = 0.7; max = 0.78)	1.4%	1.3%

Table 4.1. The mean, minimum, and maximum Mantel correlations between typological and spatial distances for the high and low interaction scenarios of the neutral model, based on the 30 simulation repetitions.

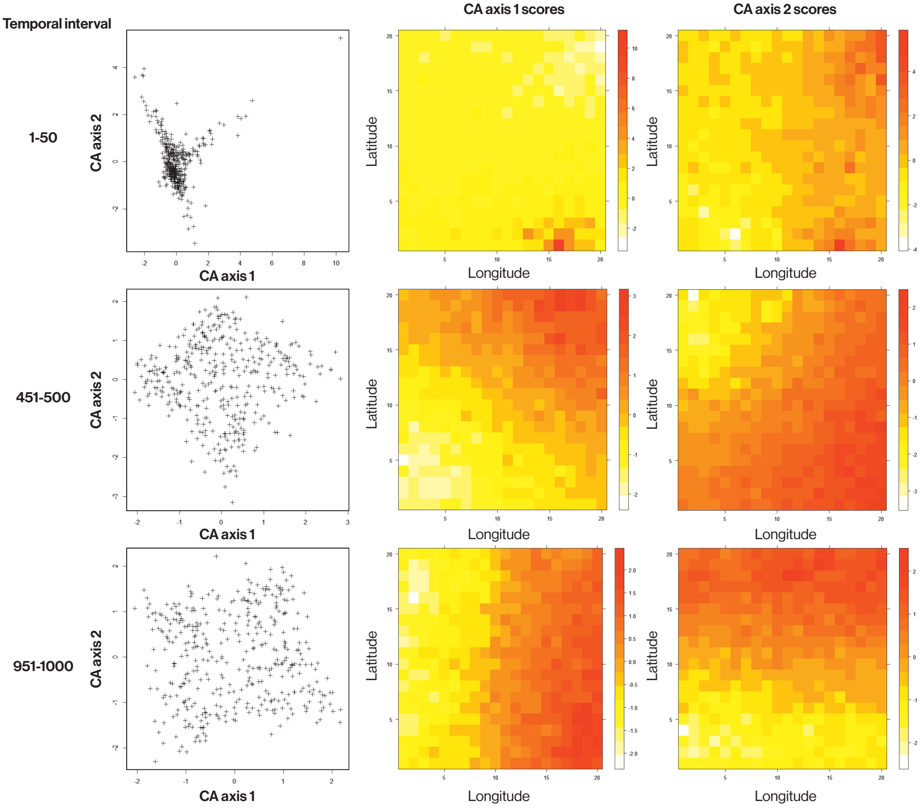


Figure 4.7. The configuration of cell assemblages in the typological space defined by the first two CA axes (the first column of panels), and the plot of CA 1 and CA 2 scores for each cell in space (the second and third column) at different time points, with time-averaging, for the high interaction neutral transmission scenario (Experiment 4.2).

4.2.3. The nature of typological gradients (Experiment 4.3)

The typological gradients can be seen more clearly if the simulated region is not square but rectangular in shape. In this experiment, I run the low interaction neutral transmission scenario when the shape of the study region is rectangular, with a grid of 40 x 10 cells. Figure 4.8 shows the configuration of cell assemblages in the typological space as defined by the first two CA axes and the plot of the CA axis 1 scores in space after 500 iterations of the low interaction neutral transmission with time-averaging (aggregation interval 451-500 iterations). The assemblages in the CA space form the recognizable horseshoe (arch) pattern. The horsehoe pattern is indicative of the chronological signal in the data when the seriation is performed by CA or multidimensional scaling (MDS), and the direction between the ends of the horseshoe reflects the passage of time (Porčić 2018; Baxter 1994; Alberti 2021a). Here, we can see that if the study area is dominated by a single spatial direction, the same pattern will arise, and in this case the typological gradient is purely spatial, as all the assemblages come from an identical temporal interval.

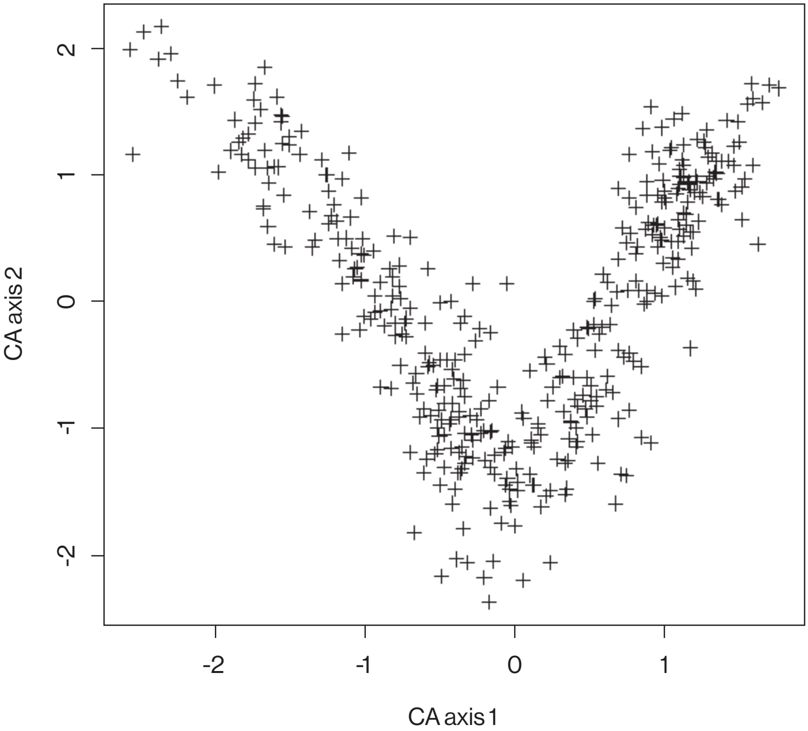


Figure 4.8. The configuration of cell assemblages in the typological space defined by the first two CA axes for the rectangular region (40x10 grid). CA axis 1 accounts for 1.3% of the inertia; CA axis 2 accounts for the 1% of the inertia (Experiment 4.3).

The dominant typological gradient is aligned with the longer side of the study area rectangle which is the dominant spatial direction (Figure 4.9). The scores on the second CA axis form an interesting pattern in space. The similarity in cell assemblages drops of away from the center of the study region (i.e. away from the vertical line which divides the study region in half along the longer side of the rectangle) (Figure 4.9). This does not mean that assemblages towards the edges of the study region are similar – they are only similar in the sense that they differ from the central cell assemblages.

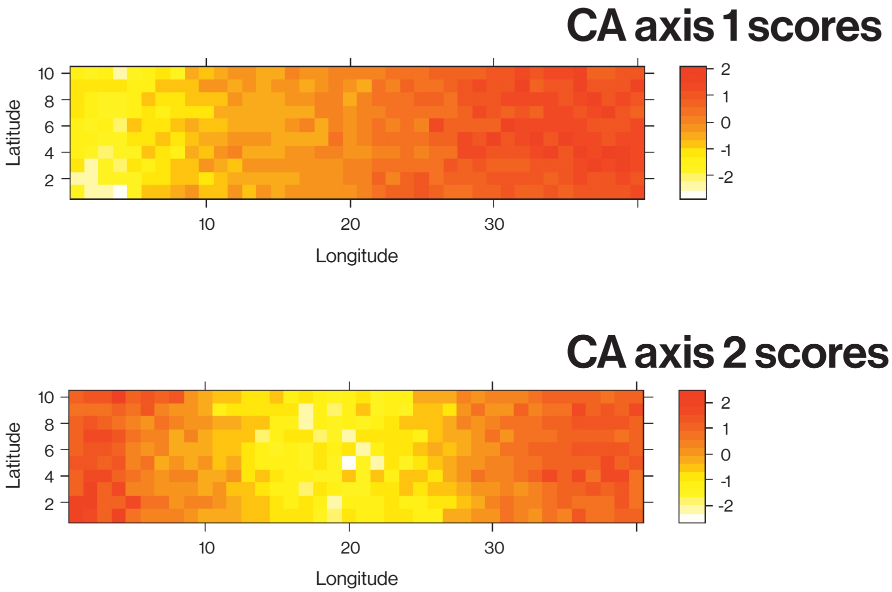


Figure 4.9. The plot of CA axis 1 and 2 scores in space for the rectangular study region.

We may be tempted to think of the major spatial directions as the major directions that channel cultural transmission, but this would not be correct. There is no directionality in the transmission process. From the perspective of the individual cell, all directions are approximately equally likely[22] for between-square interactions. The gradients are not real in any absolute sense. They always align with the major spatial direction of observation (see also Porčić & Nešić 2014: Figs. 5 and 7). We can see this clearly if we take two orthogonal transects from the results of the high interaction simulation scenario (Figure 4.10).

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[22] Technically, the cardinal directions are more likely from the perspective of a single cell, because the distance between that cell and the other cell which is immediately to the north/south or east/west is equal to one cell side, whereas the distance between the cells and its NW, NE, SW and SE neighbors is higher by the factor of the square root of 2.

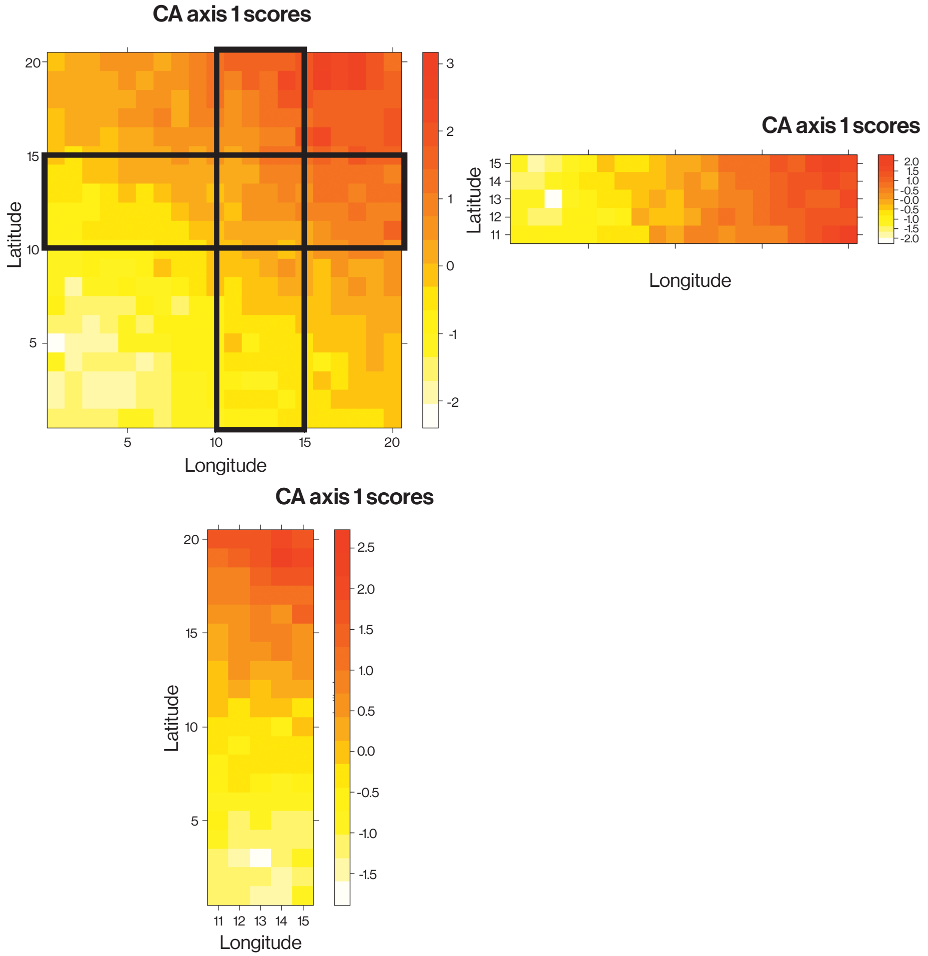

Figure 4.10. Horizontal and vertical subsections of the study region. The plot of the CA axis 1 scores for the high interaction neutral transmission scenario after 550 iterations (aggregated assemblages from 501-550 iterations), based on the CA of the entire set of cells. For the entire area, the typological gradient follows a NE-SW direction. The cell assemblages from the vertical and horizontal transects shown in the figure are selected for the separate CA analysis. The direction of the typological gradient for the horizontal transect is horizontal, whereas it is vertical for the vertical transect.

If we apply the CA only to the squares of the horizontal transects and plot the CA axis 1 scores in space, we will find that the gradient now follows the East-West spatial direction, which is the major spatial direction of the transect (Figure 4.10). Bear in mind that no new simulation was run. We only took a sample of squares from the already existing results after the entire simulation was run in the entire original rectangular region, as if we excavated or considered the sites exclusively from this transect. The equivalent result arises if we only take the vertical transect – the typological gradient as measured by the CA axis 1 now follows the North-South direction (Figure 4.10). If we look at the distribution of the assemblages in the typological space defined by the first two CA axes, we will again notice the horseshoe pattern suggesting the presence of a spatial gradient of type frequencies (Figure 4.11). Therefore, depending on the size and shape of the study area, different typological gradients and different spatial patterns of style can arise from the same data generated by the same simulation run. This demonstrates that the observed typological gradients are not real in the sense of their representing a feature of the transmission process.

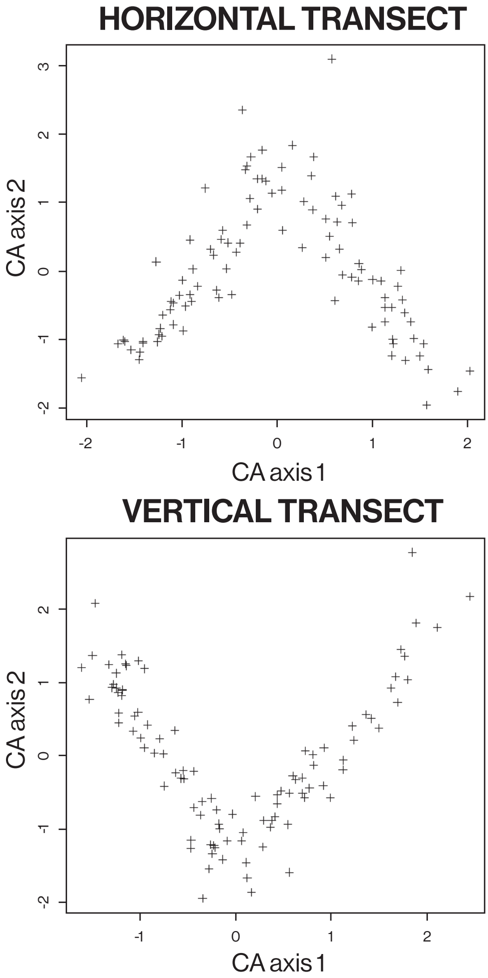

Figure 4.11. The plot of cell assemblages from the horizontal and vertical transects in the typological space defined by the first two CA axes.

Moreover, when the simulated space is square, the direction of the typological gradient is in a dynamic equilibrium. Due to constant cultural transmission, the typological gradient will actually oscillate in its alignment between the diagonals of the square. There will be transitional periods when the typological gradient will align with some of the sides of the square. This is clear from the graph, where the absolute value of the linear correlation coefficient between the first CA axis and the major spatial direction is shown at different times during the simulation history that lasts for 4000 iterations[23] (Figure 4.12). The value of the correlation oscillates between approximately 1, indicating the alignment of the typological with the major spatial gradient, and approximately 0.7, indicating the transition of the gradient direction, when the typological gradient is more in line with one of the sides of the study area rectangle than with the diagonal. This effect may also have to do with the fact that in the technical setup of the simulation not all directions are equally likely from the perspective of a single cell – the cells on the cardinal directions (in the rook neighborhood) are more likely candidates for the interaction, as the distance between cells is calculated as the simple Euclidean distance, and so the cells on the diagonals are more distant than the ones on the cardinal directions.

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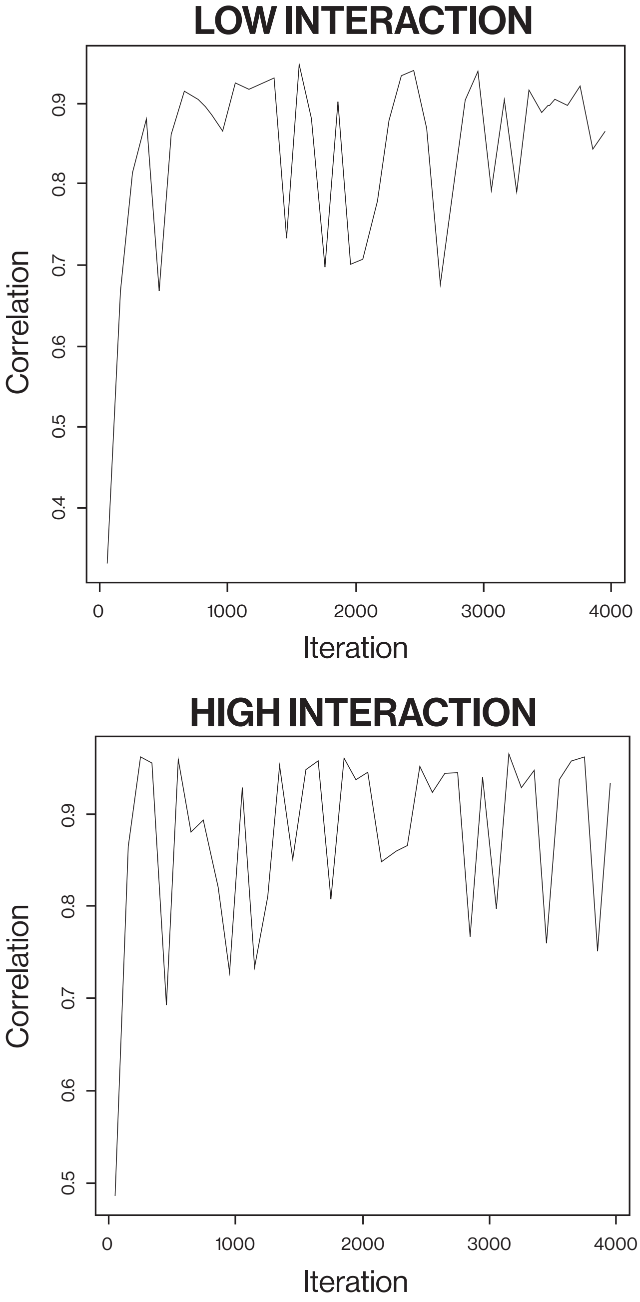
[23] When the principal component analysis (PCA) is applied to the spatial coordinates of the cells, which form the rectangle, the PCA 1 and PCA 2 dimensions will actually represent the diagonals of the rectangular study region, as these are the two major spatial directions of a square. CA 1 may align with the first or the second diagonal. The linear correlation coefficient is calculated for both diagonals at certain points in time (with time-averaging, using the interval of 50 iterations), and I take the absolute value of the higher coefficient value as indicative of the current relation between the major typological and spatial directions (the absolute value is taken in order to disregard the directionality of the relation, which is irrelevant in this context).



LOW INTERACTION

HIGH INTERACTION

Figure 4.12. The temporal dynamics of the shift of the CA 1 gradient direction between the diagonals and the side of the rectangle as measured by the absolute value of Pearson's linear correlation coefficient between the major spatial direction (the diagonal) and the CA axis 1 for the neutral transmission model. The upper panel is for the low interaction scenario (Experiment 4.1), the low panel is for the high interaction scenario (Experiment 4.2).

4.3. THE CONFORMIST MODEL

The conformist model is one of the frequency dependent models of cultural transmission (Boyd & Richerson 1985; Lycett 2015a). Unlike the neutral transmission model, in which the probability of copying a trait is proportional to its frequency, the conformist transmission model assumes that the most common variants are more likely to be copied than their frequency would suggest. This model is inherently social, as individuals are making their choices in reference to the choice made by the majority of the population. Conformist transmission can be illustrated by many examples where people show a tendency to conform by choosing the most common cultural trait in the population (cultural practices, fashion choices, social attitudes etc.) The degree of conformism in the population can be conceptualized as the probability that an individual will behave in a conformist manner and copy the most frequent variant. This allows us to explore the implications of different degrees of conformism.

The conformist model can be derived from the neutral transmission model setup by specifying that a certain proportion of individuals will choose the most frequent variant in the systemic population, rather than randomly choosing on the basis of the variant frequency structure. The technical implementation is identical to the way that conformist transmission is simulated in Porčić (2015), except for the fact that the simulations in this book do not assume non-overlapping cultural generations. Namely, in the simulation of the conformist model, each agent has four options when it has to decide about the variant of the item: 1) copy the most frequent variant from the current set of variants, with probability equal to *conf* (probability or degree of conformism); if there are two or more modal variants, the choice between them will be random; 2) introduce a completely new variant (mutation) with probability equal to *v;* 3) copy a variant from another cell with probability equal to *m;* 4) randomly copy a variant from another individual from the same cell with probability 1 – *v* – *m* – *conf*. It should be emphasized that there are other possibilities for modeling the conformist transmission (e.g. Crema et al. 2016), and the results may be different for other conceptualizations of this model.

The initial setup is the same as for the first simulation experiment with the neutral transmission (population size = 100, mutation rate (*v*) = 0.005, probability of interaction (*m*) = 0.1, average item use-life = 2 iterations, with initial systemic assemblages for each cell being created by randomly sampling 100 items from a uniform distribution of 10 variants). In this configuration all cells start with similar assemblages, with only stochastic differences due to sampling. This initial moment would be equivalent to an anthropological situation where a migration has just occurred and the population is still not yet culturally structured. Again, I will simulate time-averaging by aggregating cell assemblages from 50 consecutive iterations into a single assemblage from each cell, and use the same statistical tools to analyze the patterns. I will experiment with two scenarios. In both scenarios the degree of conformism is set to 20%. The first scenario is a low interaction scenario (m = 0.1), where in each transmission episode the probability of copying a variant from a different cell is 10%. The second scenario is a high interaction scenario where this probability is raised to 30% (m = 0.3).

4.3.1. Low interaction conformist model scenario with 20% degree of conformism (Experiment 4.4)

Figure 4.13 shows the configuration of the typological space after 50 iterations based on the first two CA axes, which account for 9.6% of inertia, as well as the CA axis 1 and 2 scores plotted in space. The results of the CA analysis suggest that there are four groups of cells which are typologically similar, but that their distribution in space is random – there is no clear tendency for typologically similar cells to create clearly delineated spatial blocks.

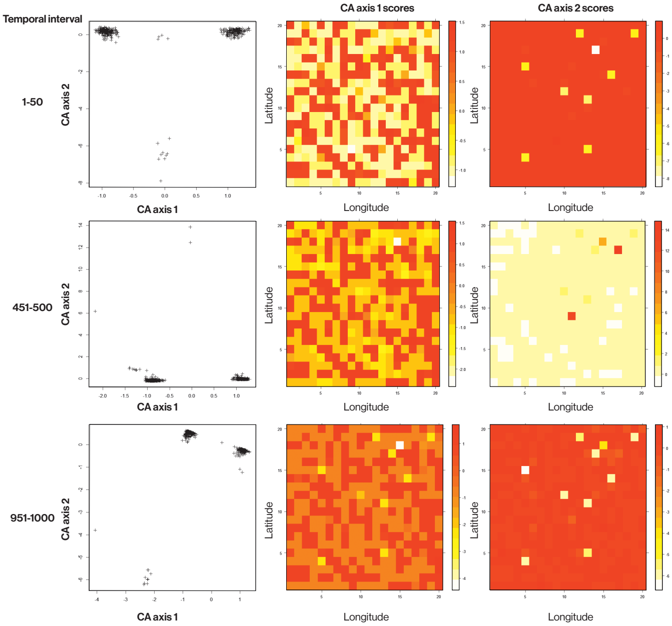


Figure 4.13. The configuration of the cell assemblages in the typological space defined by the first two CA axes (the first column of panels), and the plot of CA 1 and CA 2 scores for each cell in space (the second and third column) at different time points, with time-averaging, for the low interaction conformist transmission scenario (Experiment 4.4).

The lack of spatial patterning is also suggested by the low values of the correlation between the typological BR distances and spatial distances (Table 4.2, Figure 4.14). However, the correlation between Jaccard and spatial distances is by an order of magnitude higher, suggesting that there is a low correlation between typological distances (based on the presence and absence of types) and spatial distances, over short range (Table 4.2, Figure 4.14).

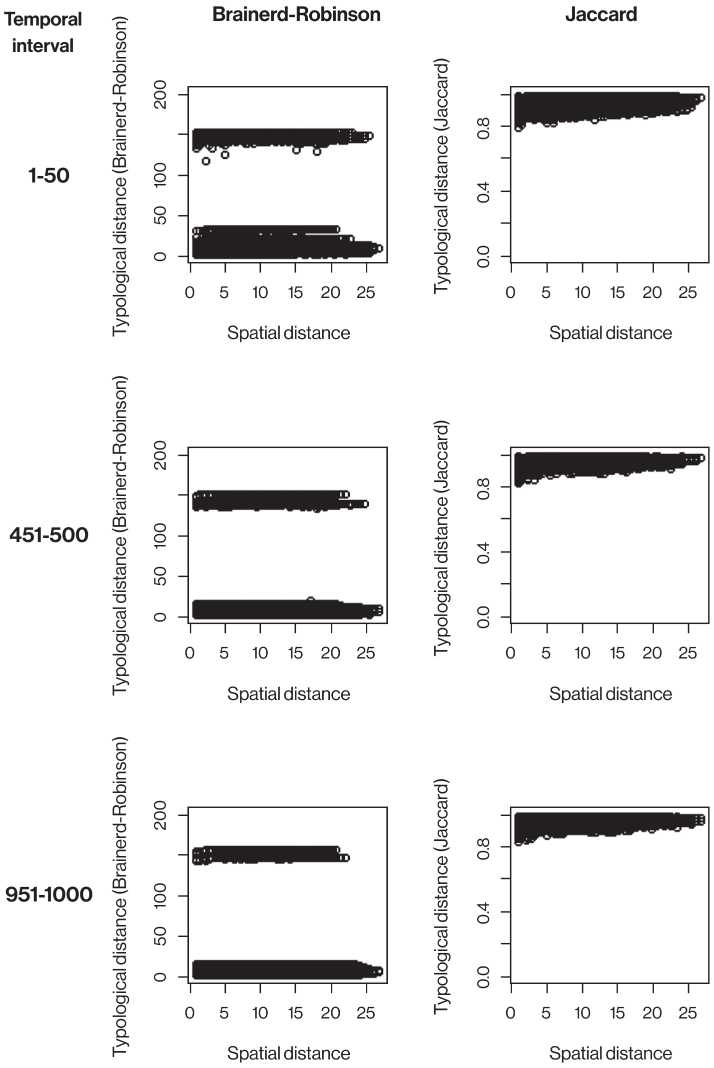


Figure 4.14. The typological (as measured by BR or Jaccard distance) vs. spatial distance between time-averaged cell assemblages at different times, for the low interaction conformist transmission scenario (Experiment 4.4).

We can see that there are now two main groups of typologically similar assemblages in the CA space (Figure 4.14). The assemblages are dominated, basically, by two variants with percentages of ~85%, and ~15%, whereas other variants are present with only one instance or a few instances. Therefore, we have a large group of assemblages where the ratio between the two of the original ten variants (variants 4 and 6 in this case[24] - but this is purely a result of chance) is approximately 85:15, and another group where this ratio is approximately 15:85. The distributions of relative frequencies of types 4 and 6 in space are almost mirror images of each other (Figure 4.15), and are remarkably similar after 500 and after 1000 years, suggesting that this is the equilibrium configuration. The spatial pattern of typological differences and similarities is the same as 450 iterations before. We can see that assemblages are either very similar or very different based on the bimodal distribution of BR distances (Figure 4.14). In order to check if the equilibrium with only two variants is the only one, I repeated this particular scenario 30 times, and I looked at the distribution of variant frequencies in the assemblage consisting of aggregated assemblages from the year 950 to the year 999. It turns out that two equilibrium states are most probable: 1) The one I have just described, where two variants stand out with large frequencies and most assemblages have ~85% and ~15% of these two dominant variants, accompanied by rare variants – 9 out of 30 simulations had this outcome; 2) The equilibrium state, where all simulated assemblages in the region are dominated by one variant (with ~97% on average) and accompanied by rare variants – 21 simulations were single-variant dominance outcomes.

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[24] There is nothing special about these particular variants. It was solely by chance they happen to be the ones that were increased to large frequencies. If we repeat this simulation scenario many times, other original variants will rise to high frequencies, but the general pattern will always be the same.

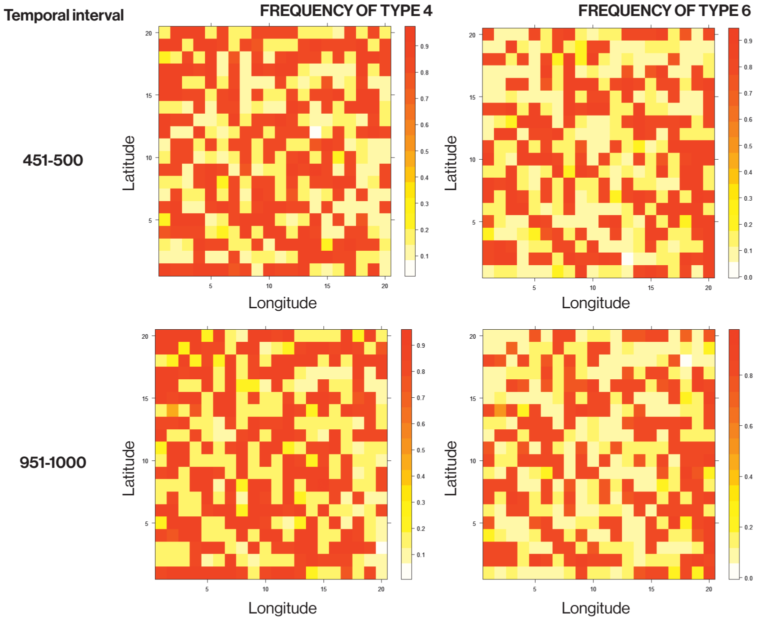

Figure 4.15. The relative frequency of two dominant types across the study region after 550 and 1000 iterations of the low interaction conformist model (Experiment 4.4).

4.3.2. High interaction conformist model scenario with 20% degree of conformism (Experiment 4.5)

In the high interaction scenario, the process always results (based on the 30 repetitions) in the dominance of one of the original variants. In the simulation outcome presented here, after 500 iterations, all assemblages are already dominated by a single type with frequency ~97%. This is the stable value which does not change through time, and the entire space is typologically uniform, dominated by the single type. The local differences are due to differences in rare types.

If we fast forward to 950-999, only one variant remains dominant in the entire region with ~97.5%, but the spatial structure of typological similarities and differences remains practically the same as 450 years before. The typological differences as measured by the BR coefficient are extremely small (the mean BR distance is 5.6), as all assemblages in the simulated study are dominated by the same type. The clear spatial structure deriving from the distribution of the rare types reflecting the isolation by distance process is detectable only with the Jaccard coefficient (the mean Mantel correlation between spatial and Jaccard distances is 0.36).

How can we interpret this result? As all assemblages start with the same spectrum of variants, the frequencies of a small number of the originally present variants are amplified by chance and conformist behavior in the first iterations. Solely by chance, the same variant can become dominant in several cells. Once a variant becomes dominant, its frequency will increase by the conformist process. Fixation will never occur, because of the mutations and some degree of spatial interaction that can introduce some other variant. The spatial structure reflecting the isolation by distance will be visible only in the spatial distribution of the rare variants. Alternatively, chance may have it that two variants rise to high frequencies in the region instead of only one.

In the more likely outcome of a single variant dominance, a researcher looking at the distribution of the artifact types would see incredible uniformity over a large area. In the less likely variant, a researcher would see two kinds of assemblages with a steady ratio of two dominant types. In a more realistic scenario, our hypothetical researcher would only have a small sample of each assemblage – even if he had a random sample of 5% for each assemblage, in most assemblages he would only find a single variant or two dominant variants; therefore the spatial structure arising from the rare variants would be lost – e.g. in one simulation we run, the Mantel correlation falls from 0.07 for a full population to 0.02 for a 5% sample.

The values of the Mantel correlation support this general picture of the weak spatial structure (Table 4.2). They are generally very low and not statistically significant. Only the correlations bases on the Jaccard distances are slightly higher, but still generally low compared to the neutral model.

Degree of interaction	Accumulation interval	Mantel correlation (BR distance vs. spatial distance)	Mantel correlation (Jaccard distance vs. spatial distance)	CA axis 1 inertia	CA axis 2 inertia
Low (m = 0.1)	1-50	0.004 (min = -0.04; max = 0.05)	0.03 (min = -0.01; max = 0.08)	6.5%	3.1%
	501-550	0.007 (min = - 0.03; max = 0.06)	0.2 (min = 0.08; max = 0.26)	5.9%	5.7%
	951-1000	0.0004 (min = -0.06; max = 0.05)	0.17 (min = 0.06; max = 0.25)	5.9%	5.7%
High (m = 0.3)	1-50	0.02 (min = -0.03; max = 0.05)	0.13 (min = 0.06; max = 0.23)	4.8%	2.%
	501-550	0.03 (min = -0.01; max = 0.18)	0.36 (min = 0.32; max = 0.38)	0.6%	0.6%
	951-1000	0.05 (min = -0.04; max = 0.41)	0.36 (min = 0.33; max = 0.38)	0.7%	0.6%

Table 4.2. The mean, minimum, and maximum Mantel correlations between typological and spatial distances for the high and low interaction scenarios of the conformist model (probability of conformism 0.2), based on the 30 simulation repetitions.

4.3.3. The conformist model scenario which starts with a spatial structure – space divided into two cultural regions (Experiment 4.6)

These observations and conclusions are only valid in respect to the initial conditions where all initial assemblages were identical. What would happen if we had a spatial structure to begin with? I will examine the case where a sharp cultural boundary (defined by the material culture) already exists from the beginning of the simulation. The initial situation is such that half of the cells in the region start with identical assemblages (a simple random sample from a set of ten equally probable variants), whereas the other half starts with identical assemblages with a different composition – the initial assemblage is randomly sampled from a set of nine variants different from the variants of the first group of cells, and one shared variant. The two groups are perfectly clustered spatially, with each group forming a spatial block that occupies exactly one half of the simulated space (Figure 4.18). The transmission setup is the same as in the Experiment 4.4, assuming a low interaction (m = 0.1) and degree of conformism of 0.2.

First, we can see that when we perform a CA analysis the two cultural regions are clearly distinguished on the first CA axis, and the cells have extreme scores on the CA axis 1 corresponding to their respective initial groups (Figure 4.16). 500 iterations of conformist transmission later, when we look at the cell assemblages from the time interval 501-550 years summarized by the CA, we can see that the original cultural boundary persists through time (Figure 4.16). Gradients are visible within blocks, and they are oriented towards the boundary line dividing the study region into subregions. The graph in Figure 4.16 suggests that there is some mixing in the boundary area, as the CA 1 scores are more similar to each other in the boundary regions compared to the hinterland regions, but the spatial boundary is clear and sharp. This boundary persists in an unchanged form even after 4000 years (Figure 4.16 shows the situation after 1500 iterations).

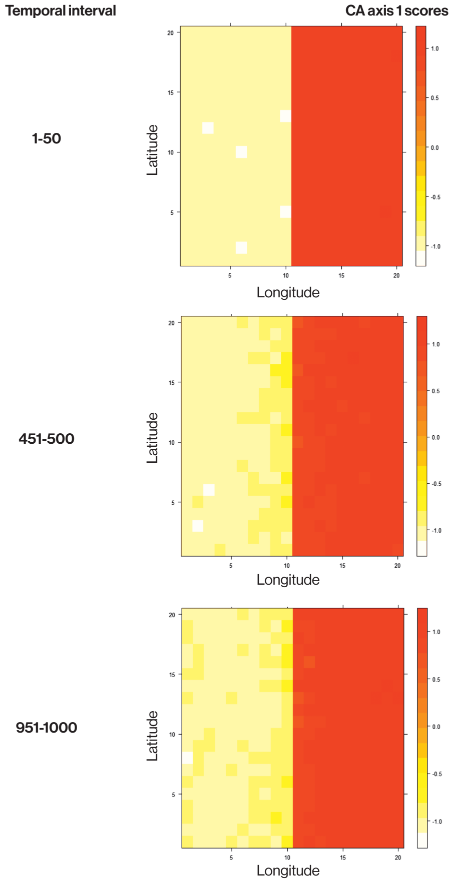

Figure 4.16. The CA axis 1 scores plotted in space for the low interaction conformist model transmission for the case in which there are two distinct cultural regions to begin with (Experiment 4.6).

4.3.4. *The conformist model scenario with initial population structure but lower degree of conformism (Experiment 4.7)*

What would happen if the degree of conformism was lower, e.g. 5%, and we started with two distinct cultural regions, as in the previous experiment? In Figure 4.17 we can see the situation as summarized by the CA analysis. The boundary between the two regions becomes less sharp as time goes by. It remains visible and it shifts towards one of the cultural regions as the variants from one cultural region are becoming dominant. After 2000 years (1951-2000 interval) the boundary disappears and the entire region is typologically uniform. Therefore, a lower degree of conformism does not allow the cultural boundary to persist for long, and it also amplifies the effect of drift, leading to the dominance of a small number of types. This is an intuitive result, because in each transmission event there are more agents who copy from other cells than agents who behave in a conformist manner, so the initial structure is destroyed quickly. This occurs because the probability of interaction between cells is greater than the probability of conformist behavior in this case.

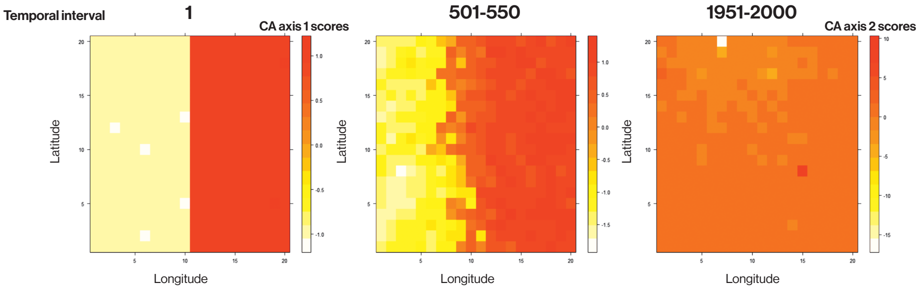

Figure 4.17. The CA axis 1 scores plotted in space for different temporal intervals for the low interaction conformist scenario with 5% degree of conformism (Experiment 4.7).

4.4. THE AXELROD MODEL

The main motivation for the research in this chapter was to explore the spatio-typological implications of cultural transmission models in order to understand better what can stand behind the phenomena of archaeological cultures. But in traditional archaeology, archaeological cultures are more than just patterns of material culture in space – they are thought of as reflections of some kind of population structure (e.g. reflecting group identities or political entities) (Shennan et al. 2015; Shennan 1994; Roberts & Vander Linden 2011). None of the models I have explored so far has this particular social ingredient. One may argue that the conformist model is inherently social, as the choice of conforming to the majority is *par excellence* a social act; but this has only a local effect, as the agents conform to the majority in their own cells, and there is nothing in the model that addresses group identity or structure.

The *Axelrod model* is a cultural transmission model that seems to fit some of the basic intuitions of cultural historians about group formation (or ethnogenesis) and persistence. The model was formulated and implemented as an agent-based computer simulation by Robert Axelrod, in order to explain several anthropological and political phenomena related to social cohesion and conflict, and the persistence of cultural boundaries (Axelrod 1997). The model is very simple. The cells are arranged into a grid. Each cell is equivalent to a local community (or homogenous village, as Axelrod calls it, since he assumes that all individuals in the cell have identical cultural traits); and each possesses its own cultural characteristics. The cultural characteristics of each cell are modeled as ordered vectors of integers. Each element of the vector represents a specific cultural dimension, e.g. the first element may be language, the second, marital residence pattern, the third, religion etc. Each of the vector elements can have one of the potential traits (values) associated with the particular cultural dimension. The cells are the basic units (agents) in the model. A cell picked at random chooses another cell to interact with within its radius of interaction (as limited to its immediate neighbors). The probability of choosing a cell is proportional to the current level of similarity between the two cells. When the two cells interact, the active cell will copy the value of one of the cultural dimensions from the chosen cell, making the two cells even more similar than before. If the similarity between two cells is below a certain threshold (e.g. if they are different in all or most dimensions), they will not interact at all.

The core principle of the model is that people preferentially interact with culturally similar people and tend not to interact with culturally different people. This is the concept of *homophily* which, it can be argued, is one of the major factors of group formation and maintenance, and which can lead to the formation of a population structure in space (Shennan et al. 2015). Axelrod demonstrated with simulations that this model produces a varying number of spatially bounded clusters of cells, cultural regions, which are discrete and have permanent boundaries (Axelrod 1997). A spatial mosaic of distinct and completely different cultural regions can emerge from a simple set of principles characterizing the Axelrod model, with the principle of homophily being the central one, as it models the essence of interactions driven by the group identity. This is why this model was quickly recognized as highly relevant for modeling ethnic structure and group formation in archaeology (Drost & Vander Linden 2018; Kovacevic et al. 2015)[25].

In this section I will present the Axelrod model that I adapted for the purposes of this study. The Axelrod model is implemented by modifying the neutral model of transmission in the following way. Individual cells are interpreted as local groups. When the individual agent from a cell chooses to copy the variant from another cell, the choice of the target cell will be influenced both by the geographic distance and the current level of cultural similarity between the two cells as measured by the Brainerd-Robinson coefficient. This is implemented by converting the geographic and typological similarity matrices for each pair of sites into probabilities of interactions, and multiplying them in order to obtain a new matrix of interaction probabilities. The choice of the target cell for each agent from each cell will be stochastically determined according to this matrix, which is updated in each iteration. Only the cells for which the similarity level with the focal cell is above 100, as measured by the rescaled Brainerd-Robinson similarity measure (which goes from 0 to 200), are included in the set from which the target cell is chosen. When the target cell is chosen, a random agent will be selected as a model from which to copy a variant, as in the simple neutral transmission setup. Therefore, in addition to the spatial distance, the individual also takes into account the current level of similarity between his own group and other groups when choosing the group (cell) from which to copy a variant. If this level of similarity is below a certain threshold, the interaction is not possible, regardless of the spatial distance between the groups.

This version of the Axelrod model includes drift into the model, as the process of neutral transmission is occurring within each cell. Axelrod (1997: 221) stated that to include the drift into the model would be an interesting extension, and this is precisely what I did here, primarily in order to model the transmission at the individual rather than the group level. I do not assume that cells are culturally homogenous villages, as each cell contains a population of items. Additionally, the version of the model in this study is different from the original model, because only one cultural dimension is modeled (e.g. the simulated pottery type), and we are not looking at the composition of the living

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[25] It should be emphasized, however, that the Axelrod model captures only one aspect of the complex process of group formation and collective identity (see Barth 1998). The process of group formation necessarily entails political integration, which has more to do with the socio-economic structure rather than the degree of shared stylistic features. In other words, political integration is certainly influenced by interactions between individuals and groups which may be initially driven by the principle of homophily (especially when it comes to language), but this is not sufficient to explain the group formation process. Therefore, when we use the Axelrod model as a model for group formation, the underlying political, social and economic process remains a black box.

assemblages, but at time-averaged assemblages in the simulated archaeological record where the deposition rate is governed by the average use-lives of objects.

4.4.1. The Axelrod model with all assemblages being identical at the start and the homophily threshold set to 50%, low interaction (Experiment 4.8)

I will start exploring the Axelrod model with the standard simulation setup used for the neutral model low interaction scenario (for the parameter setup see Table 4.3). I only show the typological vs. spatial distance graph here (Figure 4.18), as the CA plots are not so useful in this case, for reasons that will soon become clear. After 100 years (time-averaged assemblages from the interval between 51 and 100 iterations), the situation is such that approximately half of the cells cannot interact with each other, as the pairwise BR distances are above 100[26] (Figure 4.18). After 500 years, the number of pairs which can interact is even smaller – we can clearly see how the cells are divided into two groups below and above the interaction threshold (100 BR distance). The trend of typological divergence is evident from Figure 4.18, which shows that as time goes by, more and more of the pairwise distances go beyond the interaction threshold (the BR similarity/distance of 100). After 1000 iterations (aggregated assemblages from iterations 951-1000), the situation is such that the distance between a majority of pairs of cells is maximal or almost maximal, regardless of the spatial distance. The pairwise typological distances below the interaction threshold still keep the weak correlation with the spatial distance, but their number decreases as more and more cells diverge beyond the interaction threshold. The initial situation of uniformity of assemblages is destroyed quickly by drift within cell assemblages. The cells share so few variants that the variation cannot be successfully represented in the lower dimensional space. The weak spatial structure which emerges is quickly destroyed by the divergence of cell assemblages.

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[26] It should be noted that the current level of similarity/distance between cells is based on living (systemic assemblages), whereas the graphs presented in the figures refer to archaeological assemblages. But as the archaeological assemblages from each iteration are random samples of systemic assemblages, the BR similarity/distance coefficients based on the archaeological assemblages are a reasonable proxy for the same variable in the systemic assemblages.

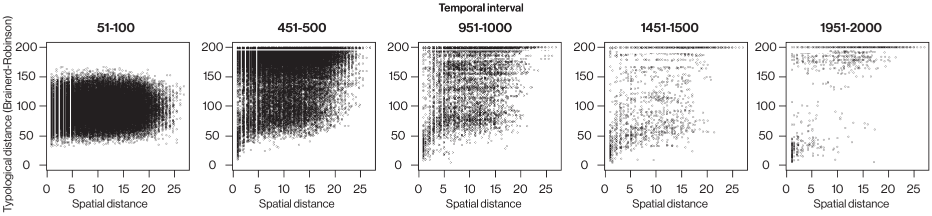

Figure 4.18. Typological (Brainerd-Robinson) vs. spatial distances in different time intervals for Experiment 4.8

4.4.2. *The Axelrod model with all assemblages being identical at the start and the homophily threshold set to 50%, high interaction (Experiment 4.9)*

In this experiment, the simulation setup is the same except for the degree of interactions between cells. In this experiment, I explore what happens if the interaction is higher, i.e. if the probability of interaction is increased to 30% (Table 4.3). The evolution of the spatial patterns is complex in this case, as two processes seem to be running in parallel, with one being dominant in the long run (Figure 4.19). The first process leads to the standard isolation by distance pattern, as seen in the experiments with the neutral model. The gradient of typological similarity forms along the diagonals of the square grid. But this is only pertains to the cell pairs which are above the similarity threshold necessary for the interaction. At first, all of the cell pairs can interact with each other, as their assemblages are all identical to begin with; but as time goes by, more and more cell pairs "leave" this block of interacting cell pairs, as their assemblages drift away from each other. We can see how isolation by distance loses importance by looking at the distribution of the different CA axes scores in space. For example, after 50 years, the CA axis 1, which captures the largest percent of variance, forms a gradient in space along the diagonal (Figure 4.20). However, after 500 years, this spatial pattern is captured by the second CA axis, which captures less variance than the first (Figure 4.20). This is so because the dominant dimension of variability becomes the one which separates the non-interacting cells from each other.

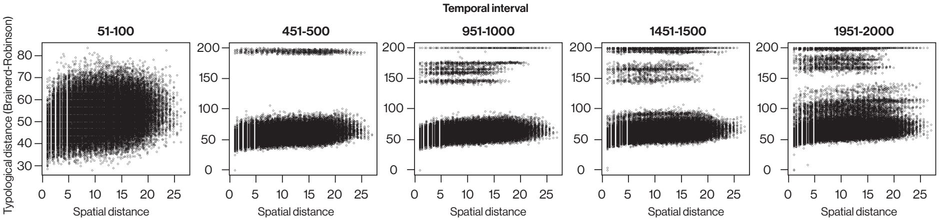

Figure 4.19. Typological (Brainerd-Robinson) vs. spatial distances in different time intervals for Experiment 4.9.

Therefore, in the long run, the behavior of the system is such that it will eventually lead to the same outcome as in the previous experiment – the correlation between typological and spatial distances will disappear as cells diverge to the degree that they cannot interact any more. In the high interaction scenario, it takes more time for this to happen, so the isolation by distance pattern is present for a long period of time, although it slowly vanishes. Here, we can see that even after 2000 years, there is a spatial structure in the form of the isolation by distance pattern for a subset of cell pairs.

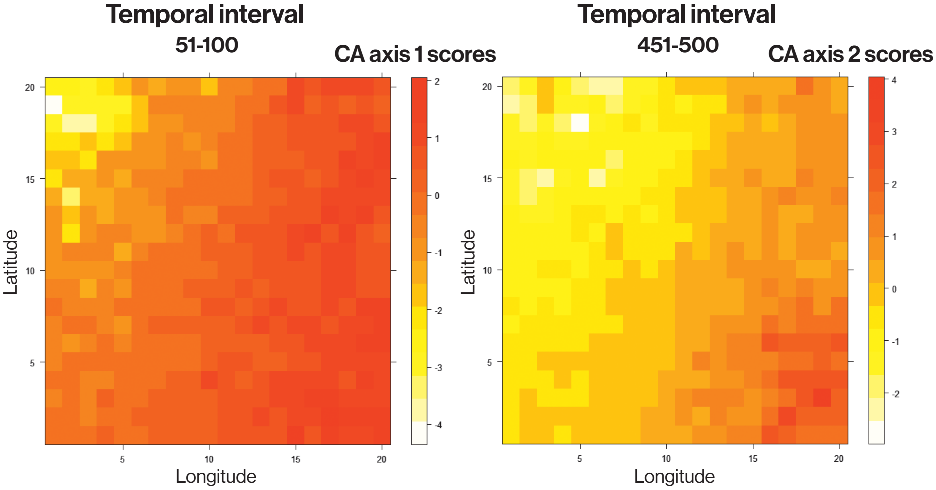

Figure 4.20. The plot of CA 1 scores for each cell in space after 100 iterations (left panel), and the plot of CA2 scores for each cell after 500 iterations (right panel) of the Axelrod model Experiment 4.9.

4.4.3. The Axelrod model with two cultural regions at the beginning, and the homophily threshold set to 50%, low interaction (Experiment 4.10)

In this experiment I explore the low interaction Axelrod model scenario (parameters as in Experiment 4.8) but with different initial conditions (Table 4.3). In this scenario the population structure is present from the very beginning – the region is divided into two halves, in two distinct cultural regions. The cells in both regions start with identical assemblages (a simple random sample from a set of ten equally probable variants). The initial assemblages from the two regions have only one variant in common. In Figure 4.21, we see that after 100 years the population structure is still intact – the two cultural regions are clearly discernible in both the typological and geographical spaces. However, after 500 iterations, the evolution of the system is similar to the case when all cells start with identical assemblages (Figure 4.21). Intuitively, one would expect the Axelrod model to conserve the initial situation with two distinct stylistic regions, just as the conformist model does; but what happens is the same as in the case of the Axelrod model scenario, when all cells start with different assemblages. The drift causes cell assemblages to diverge rapidly, and when the similarity falls below the threshold, no further interaction is possible. The same process which unfolded in the previous experiments unfolds in this case as well, and the result is a mosaic of different cell assemblages in space with no clear population structure at all.

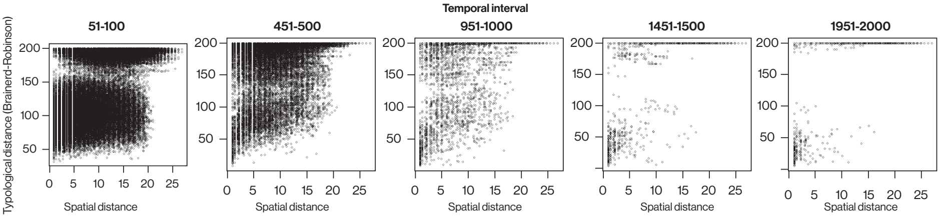

Figure 4.21. Typological (Brainerd-Robinson) vs. spatial distances in different time intervals for Experiment 4.10.

4.4.4. *The Axelrod model with two cultural regions at the beginning, and the homophily threshold set to 50%, high interaction (Experiment 4.11)*

In the next experiment, I start with the same setup as in the previous one, with two distinct cultural regions in the beginning, but I increase the degree of intercommunity interaction to 0.3 (see Table 4.3). The resulting patterns are more complex than in the previous experiments, but the main evolutionary trend is basically the same – the divergence of cell assemblages until they cannot interact any more. Figure 4.22 suggests that cell pairs cluster in two main groups – those which can and those which cannot interact. But we can see that the distribution of the typological distances is actually multimodal – there are many cell pairs which have BR distances above the interaction threshold (i.e. they cannot interact any more), but are not at the extreme end of the scale. These are assemblages which are in the process of drifting away completely.

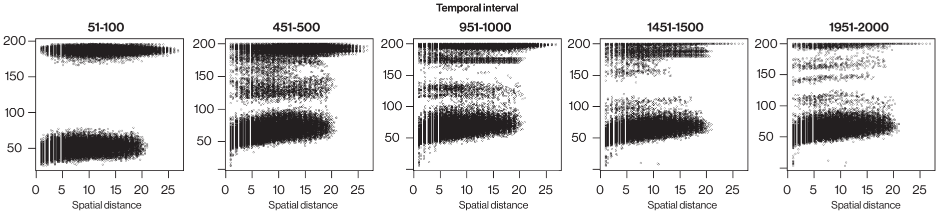

Figure 4.22. Typological (Brainerd-Robinson) vs. spatial distances in different time intervals for Experiment 4.11.

If we look more closely at what happens here, we will notice one major difference between this scenario and the previous ones – the initial spatial structure of material culture is preserved in the 2000 years/iterations of the simulation run. This may not be obvious from Figure 4.22, but it is clearly detectable if we look at the results of the CA (Figure 4.23) and especially the results of the cluster analysis (Figure 4.24). After the first 100 iterations, the first CA axis captures the distinction between the two original cultural regions (Figure 4.23). After 500 iterations, this structure is visible on CA axis 4, and after 1000 iterations on CA axis 10. As time goes by, the typological distinction between the two original cultural regions moves to higher CA dimensions. This is because the dominant axis of variance becomes one which separates the cells which drifted away completely from the rest of cells.

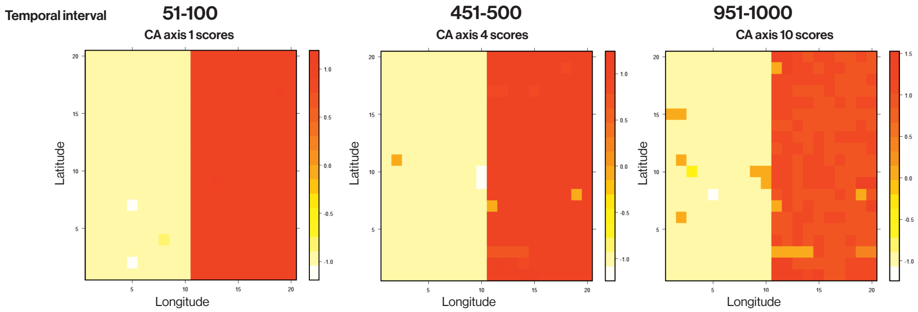

Figure 4.23. The plot of CA 1, CA 4, and CA 10 scores for each cell in space after 100, 500 and 100 iterations, respectively, of the Axelrod model Experiment 4.11.

The results of the cluster analysis show clearly how the spatio-cultural structure is preserved through time. Figure 4.24 shows the three-cluster solution which seems to make most sense based on the dendrogram. We can see that there are two clusters which contain most of the cells of each original cultural region, and the cells belonging to the third cluster are interspersed within the spatial boundaries of the two more numerous clusters. The third cluster consists of cells which diverged beyond the interaction threshold, and we can clearly see that their number increases through time. We can also see that the average distances at which the subclusters of the third cluster form are higher than the average distances within clusters 1 and 2, and this is because the cells which belong to this third cluster have diverged from each other. So, we have three clusters – two major clusters with truly similar cell assemblages corresponding to the initial cultural situation, and the third cluster with dissimilar assemblages, which belong to the same cluster only by virtue of being completely different from the cells of the first two clusters.

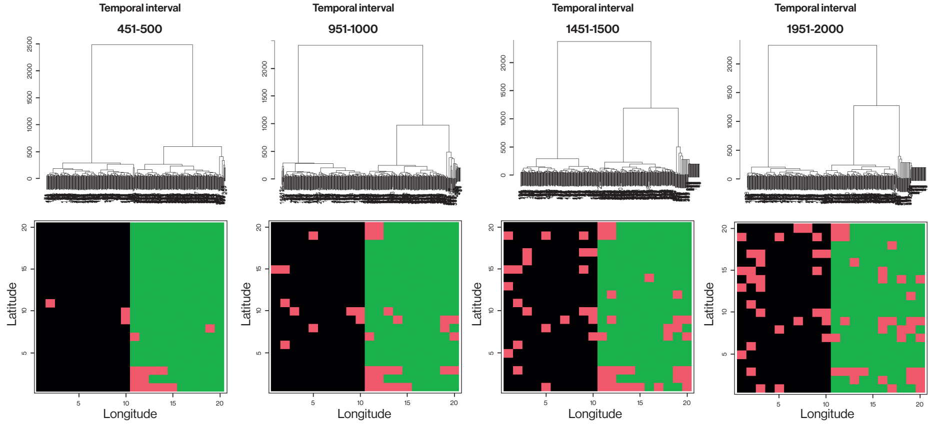

Figure 4.24. The results of the cluster analysis (Ward's method) performed on BR distances at different intervals in time for the Experiment 4.11.

So this scenario, although its results seem different, is basically just the slow motion version of the previous scenarios. The high level of interaction combined with the initial spatio-cultural structure only makes the process of divergence slower. However, in practice i.e. on a realistic time scale, this scenario preserves the initial cultural conditions in a recognizable form, at least for the first two thousand years.

4.4.5. The Axelrod model with two cultural regions at the beginning, and the homophily threshold set to 20%, low interaction (Experiment 4.12)

In this experiment, I explore the effect of decreasing the homophily threshold. The experimental setup is the same as in Experiment 4.10 (two distinct cultural regions), but the homophily threshold is set to the lower value – the two cells will not interact only if the BR similarity between them is lower than 20 (0.1 when rescaled to a zero-to-one scale) (Table 4.3).

In this scenario, the initial structure is destroyed quickly and after 500 years, isolation by distance pattern emerges (Figure 4.25-4.26). However, the divergence of cell assemblages due to drift takes over at some point, so we again have pairs of cells which cannot interact anymore and pairs of cells which can, and the spatial structure is the isolation by distance pattern – the gradient of typological distance along the diagonal. This is clearly reflected in the typological vs. spatial distances graph, as we can see this correlation pattern in the subset of pairs of assemblages which can interact.

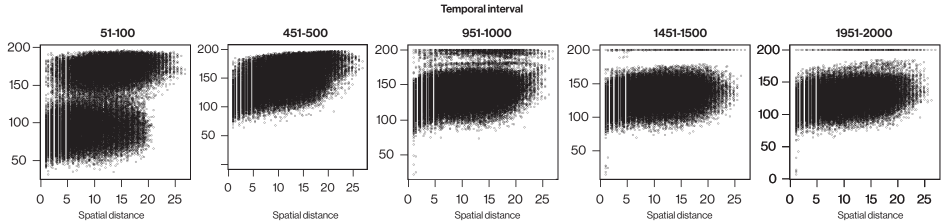

Figure 4.25. Typological (Brainerd-Robinson) vs. spatial distances in different time intervals for Experiment 4.12.

Decreasing the homophily threshold has the same effect as increasing the degree of interaction – it slows down the divergence of the cells. In addition, it works against preserving the initial structure. What would happen if the interaction threshold was set to extremely high values? With the benefit of hindsight from the previous experiments, we can easily deduce the consequences. The increase of the homophily interaction threshold would accelerate the divergence of the cells, as even small changes in the structure of assemblages would make further interaction between cells impossible.

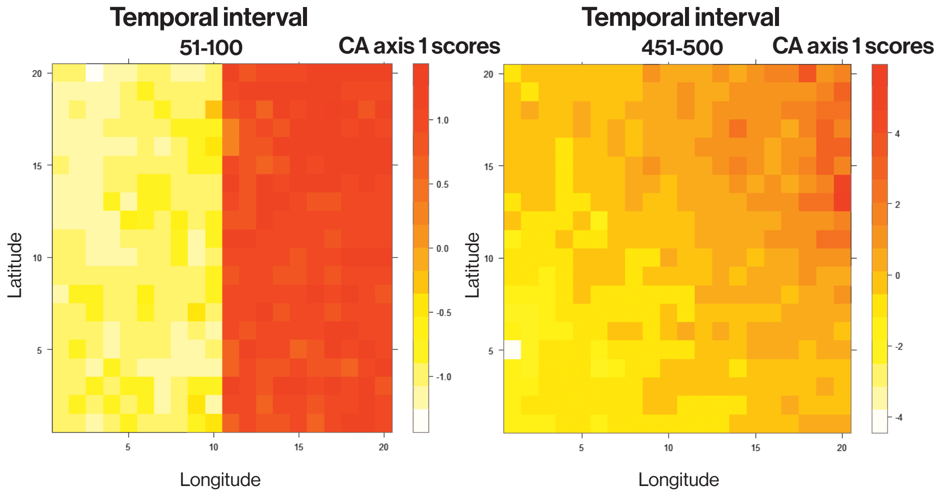

Figure 4.26 The plot of CA 1 scores for each cell in space after 100 iterations (left panel), and after 500 iterations (right panel) of the Axelrod model Experiment 4.12.

Experiment number	Grid dimensions	Item population size	Initial distribution of variants	Average item-use life	Mutation rate (ν)	Probability of interaction (m)	Homophily threshold (BR similarity scaled from 0 to 1)
4.8	20x20	100	All cells start with identical assemblages (randomly assigned one of 10 variants)	2 iterations	0.005	0.1	0.5
4.9	20x20	100	All cells start with identical assemblages (randomly assigned one of 10 variants)	2 iterations	0.005	0.3	0.5
4.10	20x20	100	Two culturally distinct regions. Within regions, assemblages are identical, as each item is randomly assigned to one of 10 variants. Only one variant is shared between the regions.	2 iterations	0.005	0.1	0.5
4.11	20x20	100	Two culturally distinct regions. Within regions, assemblages are identical, as each item is randomly assigned to one of 10 variants. Only one variant is shared between the regions.	2 iterations	0.005	0.3	0.5
4.12	20x20	100	Two culturally distinct regions. Within regions, assemblages are identical, as each item is randomly assigned to one of 10 variants. Only one variant is shared between the regions.	2 iterations	0.005	0.1	0.2

Table 4.3. Summary of the Axelrod model experiments.

4.5. THE EFFECTS OF SAMPLING

For all of the simulation experiments presented in this chapter the assumption was that the entire archaeological record – 100% of cells and 100% of assemblages - was available for analysis. This would correspond to a situation where every single site from a particular period and region was excavated entirely, and that all items of a particular artifact class were recovered and available for analysis. This is apparently an unrealistic assumption, but my primary aim has been to explore the spatial implications of cultural transmission at the theoretical level. However, the question related to the sampling effects is relevant for the practical applications of the theory. The main question is: would any of the presented patterns be detectable from samples, if only a fraction of cells and a fraction of cell assemblages were available for the analysis, as is the case in the real world? This question is easy to answer in general, but difficult to answer in particular. If the patterns are strong (e.g. clear spatial gradients, high correlation between spatial and typological distances), then we should be able to detect them from small samples. If not, then the small samples would only reveal noise from the sampling error – no spatial patterns would be discernible. This is the general answer to the question, and quite easy to deduce from the basic statistics – the stronger the effect size, the more likely it is to be detected from small samples. However, the particular question would be what is the sample size required to detect the patterns given the specific parameter combinations? This question can easily be answered by using the simulation framework presented in this book. It is not my intention to go in this direction, so I will only provide some illustrations for some of the scenarios that were presented earlier in this chapter.

For example, if we only had a sample of 10% of excavated cell sites (assuming that in the center of each cell is a single settlement) and 100% of each site was excavated, the gradient would still be detectable in some of the samples. Figure 4.27 shows the scores of the CA axis 1 plotted in space based on the aggregated assemblages from 751 to 800 iterations from the low interaction neutral model (with the standard setup of Experiment 4.1 described at the beginning of the chapter). The typological gradient is clear along one of the major diagonals of the study area.

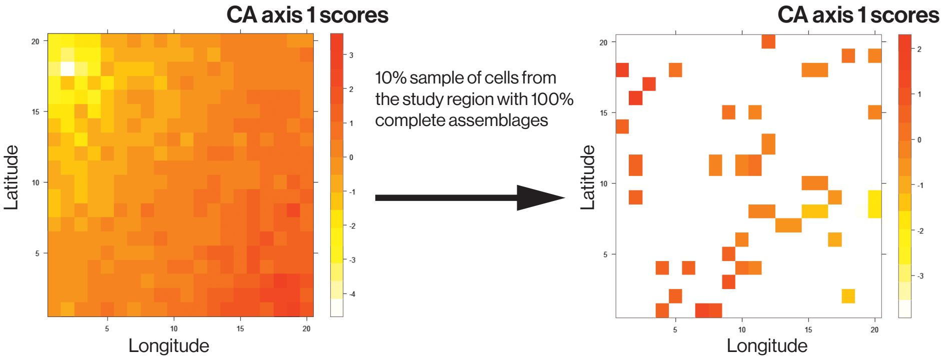

Figure 4.27. The effects of sampling on the detectability of the typological gradients in space. On the left, the plot of the CA axis 1 scores for the low interaction neutral model is presented for the aggregated assemblages from 751 to 800 iterations. The plot on the right shows the same thing for the random sample of 40 (10%) cells, but with complete (100%) assemblages.

When we take a 10 percent sample of the cells and perform CA on the entire assemblages from these cells, the gradient is still clearly visible. Even if we take random samples of only 10% from each of these assemblages and perform CA, the gradient is visible in most of the samples (2 out of 3 in this case, see Figure 4.28).

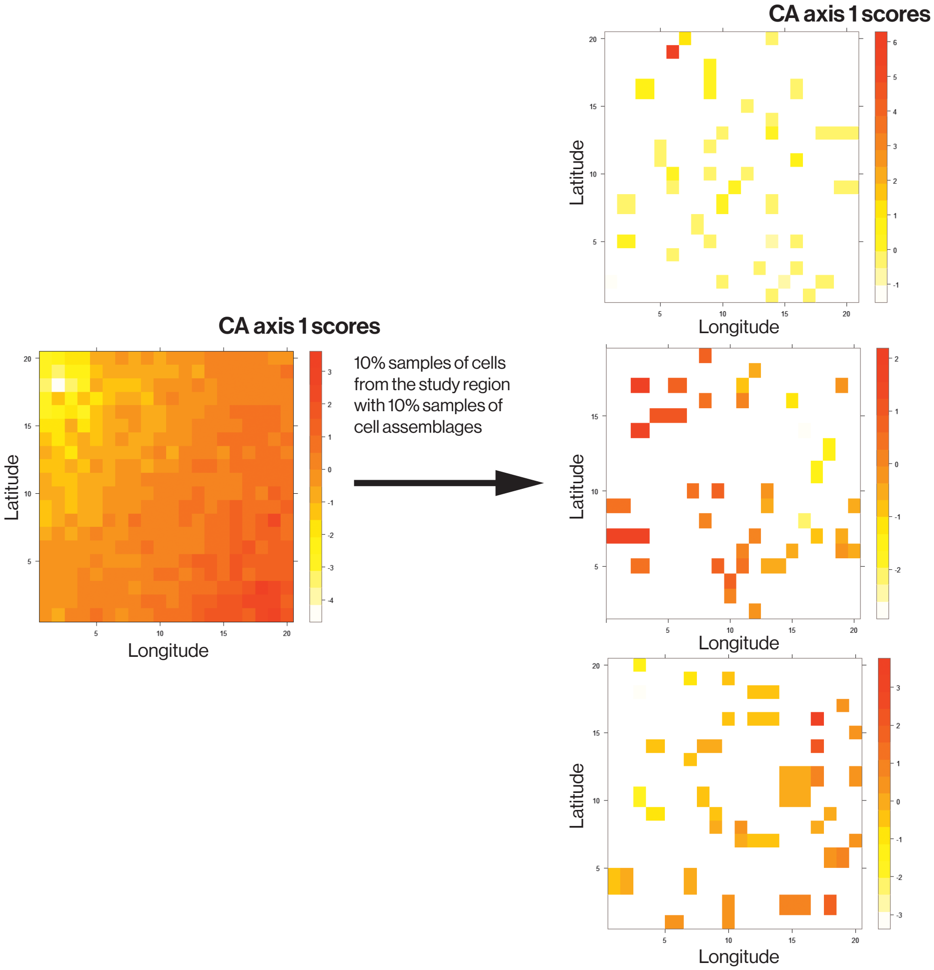

Figure 4.28. The effects of sampling on the detectability of the typological gradients in space. On the left, the plot of the CA axis 1 scores for the low interaction neutral model is presented for the aggregated assemblages from 751 to 800 iterations. The plot on the right shows the same thing for the three random samples of 40 (10%) cells, where each cell is represented by the 10% random sample of the assemblage.

4.6. DISCUSSION

More than 40 years ago, Stephen Shennan gave an impressive empirical demonstration of the inadequacy of the archaeological culture concept both as an observational and interpretational unit in prehistoric archaeology. He was able to show, by using quantified data on material culture traits of the Bell Beaker culture graves from Central Europe, that there was no homogenous

Bell Beaker culture[27], but an underlying complex spatial pattern of variability of different traits (Shennan 1978). However, there was a clear spatial pattern in this variation. Most of the trait frequencies studied by Shennan have a clinal distribution along the main spatial axis, just as we would expect from the isolation by distance model. These frequency clines are analogous to the typological gradients from the simulation results. Therefore, the patterns of Bell Beaker material culture variability closely resemble the patterns produced by the baseline neutral transmission model coupled with isolation by distance. But this is only one example.

The simulations presented in this chapter show that different models of cultural transmission may or may not produce spatial structuring of the formal variation of the material culture. Some of the simulation results were quite predictable, particularly for the neutral transmission, as this is the classic isolation by distance pattern which has been known in biology for decades. However, the results presented here are interesting because they represent illustrations for the specific parameterizations of the isolation by distance model chosen to reflect roughly the conditions of a generic preindustrial (prehistoric, to be more precise) demographic and cultural situation in realistic temporal and spatial frames. These simulations show that the neutral model, which assumes nothing but random (unbiased) copying and interactions conditioned exclusively by geographic distance, can produce very strong spatial patterns. The nature of typological variation in space produced by this model is continuous. The typological landscape gradually changes along the spatial dimensions. This means that there are no discrete spatio-typological groups and no clear boundaries between them. But if we look only at the extremes of the study area, and/or if we insist on imposing division into groups by applying some kind of formal or informal cluster analysis, we will see what we want to see – different groups. This picture would be objective in some sense (as assemblages from one part of the map may have little or nothing in common with assemblages from another part of the map), but it would be a great error to interpret such spatial clustering in the ways that archaeological cultures are often implicitly or explicitly interpreted – as reflections of discrete social, political or ethnic groups. The simulations clearly show that a model which assumes no group structure and localized interactions can give rise to such a pattern.

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[27] It is a Late Neolithic and Early Bronze Age phenomenon (depending on the area) dated broadly between 2900/2800 and 2000/1900 BC (Milisauskas & Kruk 2011). In traditional European prehistoric archaeology, the Bell Beaker phenomenon was seen as an archaeological megaculture.

Moreover, we can see that the spatial directions of typological gradients are arbitrary and dependent on the shape of the study area. The two main patterns indicative of this model are: 1) the presence of a typological gradient along the major spatial direction of the study area 2) the typological gradient changes directions when we change the shape of the study area (in practice, when we include more sites, or take a subsample of the original set of sites, in such a way that the direction of the longest spatial axis is changed).

Surprisingly, the Axelrod model, when coupled with drift and interactions determined by spatial distance, and quasi-realistic parametrization, does not produce spatially and typologically distinct groups of communities. The result is always a mosaic of different, usually one-cell, microcultures randomly scattered across the map. Moreover, simulations based on the Axelrod model cannot conserve the initial population structure in the long run. The process of divergence can be slowed down under certain circumstances, such as high intercommunity interaction and a low homophily threshold for interaction. When the degree of interaction is high, the initial spatio-cultural structure can be conserved for long periods of time (e.g. for at least 2000 years), so for all practical purposes the Axelrod model can conserve the initial cultural situation under such conditions.

The only model that produces clear typological boundaries and population structure in space is the conformist model, when space is partitioned into different cultures to begin with. If not, the conformist model also produces a mosaic of distinct cell assemblages dominated by one or two types, a situation that is rarely if ever encountered in reality. Some spatial structure is detectable, but only when rare types are included.

How do the results of the simulation compare with ethnographic and ethnoarchaeological studies that focus on the spatial patterns of material culture and the relation of the patterns to the social world? Perhaps the most famous case where isolation by distance is seen as the main factor that structures material culture variability in space is the study by Welsch et al. (1992). The statistical analysis of variability in assemblages of material culture obtained by ethnographers at different villages on the North Coast of New Guinea at the beginning of the 20th century indicated that similarities and differences among these assemblages are most strongly associated with geographic propinquity, irrespective of linguistic affinities. The author concluded that “the similarities and differences we find among these village assemblages are most strongly correlated with geographic propinquity, irrespective of linguistic affinities” (Welsch et al. 1992: 568). In a reanalysis of the Welsch et al. data, Moore and

Romney (1994) concluded that language had a significant role in the structuring of material culture variability. Similar conclusions were reached by Shennan and Collard (Shennan & Collard 2005). The conclusion of Terrel's (2010) recent re-analysis of the material culture of the northern coast of New Guinea is that isolation by distance is the main factor structuring the patterns of material culture variation in space (see also von Cramon-Taubadel & Lycett 2018). However, the data analyzed by these researchers are not data on stylistic variation – they are the data on presence and frequency of different classes of material culture, rather than data on the variation within a functional class. In order to further investigate these issues, Fyfe (2009) focused on the formal variability within the two classes, arrows and string bags. The results of Fyfe's analysis also suggest the main role of isolation by distance as the crucial factor behind the formal variability of material culture. The main dimension of typological variation is correlated with the principal spatial direction in the region. Therefore, in this case there is a correspondence between real world patterns and the simulations of the neutral model where isolation by distance is conditioning interactions between communities. There are many other studies based on ethnographic or archaeological data where isolation by distance patterns and typological gradients can be observed.

Jordan and Shennan analyzed the basketry made by different Indian groups in the late 19th and early 20th century in North California, and found that space is the major structuring factor in the variability of basketry attributes (Jordan & Shennan 2003). The typological gradient of the basketry closely follows the major spatial directions of the study area (NW-SE), and there is a high correlation between distances based on basketry attributes and spatial distances between different communities.

Lycett analyzed the parfleche characteristics and moccasin beadwork decoration of the Great Plains Indians, based on the ethnographic data (Lycett 2019; 2015b). The distribution of parfleche characteristics was not spatially structured, but the moccasin beadwork was, as both the Mantel correlation test and the principal coordinates analysis show. The ordination of the Great Plain Indian communities on the first principal coordinate axis (analogous to the first CA axis) resembles the north-south sequence of the communities in geographic space.

Schillinger and Lycett investigated the correlation between material culture traditions and geographical distance in the Upper Amazon region and found the same isolation by distance pattern, as in the examples described above

(Schillinger & Lycett 2019). The similarities in material culture were correlated to spatial distances between communities.

Mathew and Perreault (2015) performed a cross-cultural study on the dataset of 172 Native American small-scale societies, and found that variables related to cultural history, i.e. related to social learning and cultural transmission, had more impact on the behavioral variability between communities than ecological variables. However, the results of this study have shown that both spatial distance (cultural interactions) and cultural phylogeny (cultural descent) had impact, with the cultural phylogeny variables having larger impact on average than the spatial distance.

I mentioned only some of the many examples in the preceding paragraphs (for many more see Hodder 1978). The Mantel correlation coefficients from several studies are summarized in Table 4.4. It is difficult to make direct comparisons between the empirical and simulated correlation coefficient values, as there are many uncontrolled factors present in the real world data (sampling effects, temporal effects, demographic processes etc.), but it is interesting to note that most of the values of correlation coefficients between the material culture distances and spatial distances are not too far away from the simulated data.

Region	Material culture	Mantel correlation coefficient (absolute value) between geographic distances and material culture (dis)similarity	Reference
New Guinea (early 20th century)	Various classes	0.34-0.48 (depending on the interassemblage distance measure)	(Welsch et al. 1993)
North California (late 19th, early 20th century)	Basketry	0.627	(Jordan & Shennan 2003)
Upper Amazon (early 20th century)	Various classes	0.44	(Schillinger & Lycett 2019)
Great Plains (19th century AD)	Moccasin beadwork	0.43	(Lycett 2019)
North America, Northern Iroquoian (14th-17th century AD)	Pottery	0.43-0.53 (depending on the interassemblage distance measure)	(Hart 2012)
Western Mediterranean Neolithic, 6th millennium BC	Pottery	0.49	(Rigaud et al. 2018)
Western Mediterranean Neolithic, 6th millennium BC	Personal ornaments	0.39	(Rigaud et al. 2018)
Western Anatolia, Aegean, Balkans 6600-6100	Pottery	0.16	(de Groot 2019)
Western Anatolia, Aegean, Balkans 6200-5900	Pottery	0.3	(de Groot 2019)
Western Anatolia, Aegean, Balkans 6000-5700	Pottery	0.37	(de Groot 2019)
Western Anatolia, Aegean, Balkans 5800-5500	Pottery	0.43	(de Groot 2019)

Table 4.4. Mantel correlations between spatial and typological distances for the selected ethnographic and archaeological examples.

There is also one important point to be made about interpreting the Mantel matrix correlation between cultural and spatial distances. This correlation is dependent on the spatial scale of observation. For example, if we look at the Figure 4.3 which shows the plot of spatial vs. typological distances based on the results of Experiment 4.1 (neutral transmission with low interaction), we can see that the relationship between the two variables changes with distance. To demonstrate this, I will „zoom in“ at the scatter of points for the 951–1000 iterations interval shown in Figure 4.3, by looking at the shorter span of typological distances on the *y* axis (Figure 4.29). If we only look at the cells which are approximately 5 cell square side lengths (50km if we interpret the simulation setup in quasi-realistic terms) or less apart from each other, we would get a relatively high correlation of 0.47 for this spatial window (spatial window A in Figure 4.29). This is higher than the overall correlation when the spatial window includes all distances between cells, which is 0.42 (cf. Table 4.1). So, as we expand the spatial scale, the correlation decreases. This is so because after a certain spatial distance threshold is passed, it does not matter whether two cells are 15 or 25 distance units apart, their interaction is going to be extremely unlikely and the corresponding typological distances would be equally large (spatial window B in Figure 4.29). The net result is a loss of correlation. So, if we look at the pairs of cells which are more than 5 square side lengths apart, the Mantel correlation drops to 0.25. If the spatial scale was larger, the overall correlation would decrease even more.

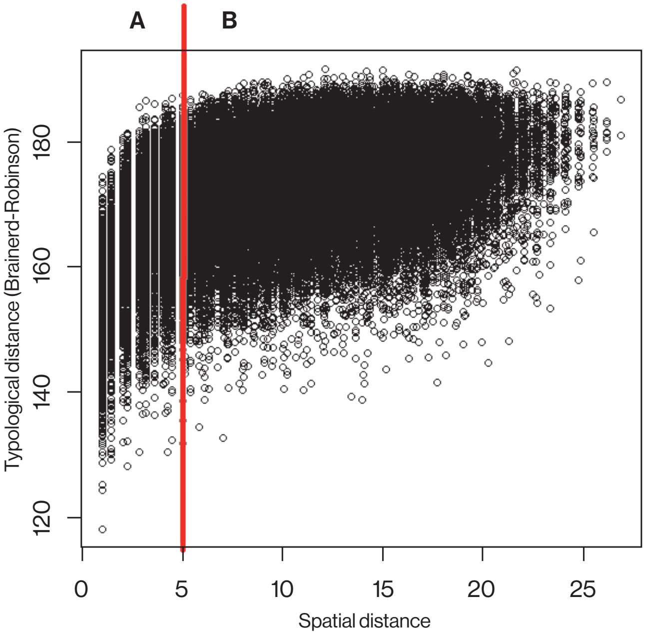

Figure 4.29. Typological vs. spatial distance graph for the low interaction neutral model (Experiment 4.1). The vertical line is drawn approximately at the threshold distance when the effect of spatial distance on typological distance becomes weaker. In area A, the correlation coefficient value is 0.47, in area B it is 0.25.

The strength of the distance matrix correlations depends also on the range of interaction. The range of interaction depends on how the probability of interaction is modeled in respect to spatial distance. In this book, I have modeled the probability of interaction to be proportional to the inverse of the squared distance between the cell communities. The exponent 2 (squared distance) was kept constant, as it was chosen as the „standard" way to model interaction between human communities in space (see Chapter 3, section 3.2.1, Eq. 3.1). However, there is nothing fixed about the inverse square. We could easily imagine other values of the exponent, such as inverse cube, or any other real number value, which would result in different shapes of typological vs. spatial distance curves, and subsequently in different patterns of correlation decay. The value of the exponent of the inverse distance determines the spatial range of interaction – the higher the exponent, the more localized are the interactions, as the probability of interaction decreases more quickly with spatial distance. Figure 4.30 compares exponents 1 and 5 to exponent 2 which was used in the simulations in this book. The exponent value of 5 leads to more localized interactions than the inverse squared distance, whereas exponent 1 results in a higher average range of interactions as probabilities of interaction.

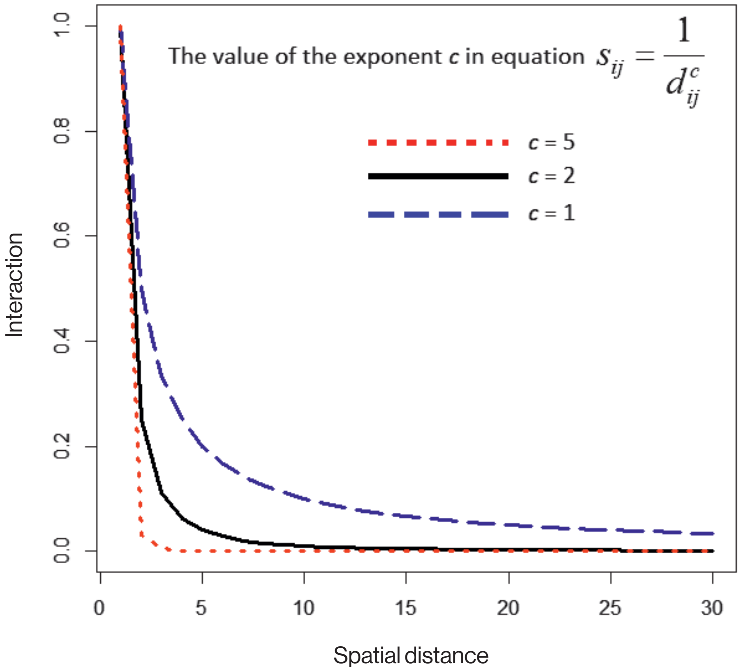

Figure 4.30. The function which represents the relationship between spatial distance and interaction between communities, parametrized with different values for the c exponent. Higher values of c lead to more localized interactions as the interaction likelihood drops quickly with increasing distance.

The ethnoarchaeological research shows that the formal attributes (morphological, technological, decorative and compositional) of material culture are spatially structured, sometimes coinciding with social boundaries as well (Stark et al. 2000; Graves 1994; Gosselain 1992; Hodder 1977; 1982; 1978). What was noted in some of these cases is that the ethnographically documented interaction between people across the boundaries of social groups was not reflected in the material culture. For example, Hodder concluded that in the Baringo District in Kenya there were discrete boundaries in the spatial distribution of material culture, coinciding with the boundaries of the Pokot, Tugen and Njemps tribes (Hodder 1977; 1982). Even though the interactions across the tribal boundaries were intensive, this was not reflected in the material culture, which was structured along tribal boundaries. In other words, no gradients or clines were observed, as each tribe had a distinct and spatially bounded material culture. Hodder suggested that this situation was the result of conformism – that there were strong pressures within each tribe to conform to the norms, which also included the production and use of material culture (Hodder 1977; 1982).

Hodder used this result to question the traditional archaeological assumption that interaction between groups will depend on spatial distance and will be reflected in the material culture, with (dis)similarities of material culture between communities as a measure of their interaction. This assumption was questioned by many others as well. Plog reviewed ethnographic and archaeological literature and concluded that stylistic similarity does not measure interaction, as in many cases there is no correlation between stylistic and spatial distances, or the correlations were low (Plog 1980). Jones also suggested that "archaeologists cannot then assume that degrees of similarity and difference in material culture provide a straightforward index of interaction" (Jones 1997: 115).

How do the results of the simulations presented in this chapter resonate with these observations and conclusions, as interaction determined by distance is assumed in each of the simulation? There is no single correct answer to this question. The simulations show that this will depend on the transmission model, its parameters, initial conditions, and the passage of time. There are several points to be made here:

1) The isolation by distance effect is expected to be most visible when communities are sedentary. Residential mobility may complicate the correlation between typological and spatial distances. However, at larger spatial scales, the isolation by distance effect can also be present in the case of mobile

communities, if the scale of observation is larger than the scale of mobility. But the simulations presented here are intended to be valid for the sedentary case, as no residential mobility is modeled in any of the scenarios.

2) The simulations in this chapter show that even when the interactions (transmission between cells) are structured by distance, the correlation coefficients will not be high, due to the effects of drift.

3) In archaeological cases, there is never a perfect contemporaneity between site assemblages (this is noted by Plog 1980: 16-17, 22-24). Therefore, typological distances between sites are always influenced by the temporal dimension as well (these effects are analyzed in Chapter 6).

4) Sampling effects can destroy the spatial pattern even if there was one – one of the three random samples presented in Figure 4.29 did not show the signal of spatial structuring that would have been detected if the entire population of cells and cell assemblages had been included into the analysis.

5) In all of the simulations presented in this chapter there are intercommunity interactions (copying variants from other cells) with the degree of interaction between cell communities determined by the spatial distance (proportional to the inversed squared distances between cells). However, these interactions are not necessarily reflected in the spatial pattern of formal variability, especially not in the conformist model, as there is a low chance that any imported type will increase in frequency in such scenarios[28]. This might resolve the paradox noted by Hodder (1982, 1979) in his ethnoarchaeological study that tribal boundaries were clearly reflected in the material culture despite the intensive interaction across tribal borders. The conformist transmission model, when the initial situation is such that there are distinct groups to begin with, predicts this kind of spatial distribution of material culture. It is interesting that Hodder did note that some of the metric attributes (e.g. the dimensions of the spears) were spatially autocorrelated within tribal areas, which is equivalent to a clinal distribution. In Wiessner's (Wiessner 1983; 1984) terms, artifact classes which have discrete distributions associated spatially and socially with different tribes would be examples of the emblemic style, where conformist transmission is the main mechanism of its persistence, whereas some of the

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[28] The spatial structure of interaction is captured only if the Jaccard distance/similarity metric is used for the cluster analysis. This would only be captured with entire populations or large samples, as instances of foreign variants are rare and almost never increase in frequency.

metric attributes that do show clinal distributions are manifestations of the assertive style, which can be transmitted according to the neutral model.

6) Rather than looking for a single general theory of style, cultural transmission theory circumvents the entire problem of defining style and its function by offering the opportunity to construct explicit models that may capture a wide variety of factors which cause and structure formal variations of material culture in time and space (Eerkens & Bettinger 2008). In the cultural transmission theory framework, the kind of style and its social function (if there is one in any particular case) will be reflected in the model of transmission. If we can capture the crucial aspects of how material culture is generated, by formulating a specific cultural transmission model, then we can use these models to evaluate their correspondence with the empirical data, as researchers such as Kovacevic et al. (2015) and Crema et al. have done (Crema et al. 2014a). Different concepts and functions of style can be implemented in different models. For example, the assertive style can be modeled by neutral or anti-conformist transmission; the important features of the emblemic style can be related to the conformist or Axelrod model. However, the correspondence is only partial, as models of cultural transmission cannot capture the intentionality of using a certain variant as a social signaling vehicle.

This short exercise in cultural transmission in space shows that the issue of material culture variation in space is quite complex, as the quite limited range of scenarios explored here can generate different and interesting patterns. We can summarize and analyze these patterns using our statistical lenses for viewing formal variations in space. The neutral model seems to generate the clearest patterns of all the models explored here. It should be emphasized that this is only a small fraction of the possible models. For example, I did not explore the anticonformist model at all. Therefore, the results presented here only scratch the surface of potential variation.

5

PATTERNS IN TIME

Chapter 5

PATTERNS IN TIME

5.1. INTRODUCTION

In the previous chapter, I explored how different parameters and models of cultural transmission generate the patterns of material culture variability in space. In this chapter, I will shift the focus to the temporal patterns. We will see how another fundamental aspect of archaeology, the construction of relative chronology, has deep connections with cultural transmission theory. This theory can help us to better understand the patterns that we observe and to use this knowledge to improve and extend the traditional archaeological method of establishing relative chronology – the seriation method. I will focus in particular on the patterns related to the dynamics of type-frequencies in time, upon which the seriation method is based. The experiments in this chapter will show how these patterns can arise from cultural transmission and the properties of the archaeological record. In addition to studying the theoretical basis of seriation, I will explore the temporal signatures of the neutral, conformist and anti-conformist models. I will also use cultural transmission theory to investigate another theoretical problem – the remarkable chronological patterns associated with archaeological cultures which were revealed in a study by Manning et al. (2014).

5.2. SERIATION

The temporal patterns of material culture variability have always been in the focus of the archaeological research. Being able to tell which artifact/assemblage belongs to which period, or which artifact/assemblage is older or more recent than some other, is fundamental for the archaeological study of the past. The establishment of chronology comes first in the order of archaeological business. Today, archaeologists mostly rely on methods of absolute dating such as radiocarbon for acquiring both absolute and relative chronological information, but constructing chronologies was a serious methodological challenge in the pre-radiocarbon era (O'Brien & Lyman 1999).

In situations where assemblages come from stratified layers, the geological law of superposition enables archaeologists to determine the relative chronology by analyzing the stratigraphy. In the absence of depositional disturbances, the assemblages and artifacts from the top layers are more recent than the assemblages from the bottom of the sequence. But the task of establishing the relative chronology of non-stratified artifacts or assemblages is particularly difficult. For example, if we have a set of one-layered sites or a set of pits with no mutual stratigraphic links within a site, and we have pottery assemblages associated with each of these entities, how do we reconstruct a relative chronological sequence?

Archaeologists of the late 19th and early 20th century were quick to discover the answer to this question, as they invented seriation as a method of relative dating (O'Brien & Lyman 1999; Lyman et al. 1998). This is one of the few methods in archaeology which is authentically archaeological, meaning that it was not borrowed from other disciplines, as is often the case in archaeology, but was invented by archaeologists in order to solve a specifically archaeological problem. Flinders Petrie and Alfred Kroeber are usually credited with being the founders of the method (O'Brien & Lyman 1999; Lyman et al. 1998).

The general principle of seriation is that the archaeological entities or units should be rearranged in such a manner as to minimize the dissimilarity between adjacent pairs of entities in the sequence, i.e. that the most similar entities are next to each other. The underlying logic is that the units which are most similar to each other in their formal properties (on the basis of the attributes of individual artifacts, or presence/absence or frequency distribution of types in assemblages) are most likely to be close in time (Dunnell 1970).The temporal direction of the sequence (which end of the sequence is the earliest/latest) must be established independently. Seriation can be performed on attributes of artifacts, individual objects or assemblages of artifacts. O'Brien and Lyman (1999) defined three kinds of seriation (summarized here from Porčić 2018):

Phyletic seriation. In phyletic seriation, attributes, individual objects (artifacts) or object types are seriated based on their overall similarity. In most applications, phyletic seriation is based on the subjective judgment of similarity, but it can be made formal by quantifying the features of analytical units, e.g. by recording metric data or calculating similarity indexes between objects based on their attribute states, if the attributes are nominal or ordinal scale variables.

Occurrence seriation. This is based on the (dis)similarity between units (usually assemblages), based on the presences or absences of elements. The main principle behind the method was formulated by Flinders Petrie (Petrie 1899), who invented the method, and this principle has later been referred to as the *concentration principle* (Kendall 1963). The concentration principle states that archaeological units should be arranged in such a way that the spans of the characteristics that describe them (e.g. the span of presence of each attribute of the artifacts, or the span of presence of each type within assemblages) should be the shortest possible across the seriation sequence.

Frequency seriation. This is usually applied to assemblages characterized by frequencies of types, as this kind of data contains extra information on the frequencies of types or attributes in addition to the mere presence/absence data used for the occurrence seriation. The aim of the frequency seriation is to order the units in such a fashion that the relative frequencies of attributes/types follow a unimodal curve across units. This means that the relative frequency of each attribute/type should display monotonical increase followed by decrease in relative frequency, after reaching a maximal relative frequency for a given set of assemblages (it is also allowed for attributes/types to have truncated sequences, in the sense that the relative frequency of an attribute/type may only increase or decrease across the sequence) (Dunnell 1970; Lipo et al. 1997; Ford 1962; O’Brien & Lyman 1999; Porčić 2018; 2013a). Ford invented a manual technique of seriation based on visual patterns (O’Brien & Lyman 1999: 124-125; Lyman et al. 1997: 128; Ford 1962). The first step was to graphically represent the frequency distribution of types for each assemblage on individual narrow paper strips. The percentage of each type in each assemblage was represented by the width of a horizontal bar on the strip. The analyst would then rearrange the paper strips until the sequence was such that the relative frequencies of all or at least most of the types were approximately unimodal. The visual patterns resulting from successful seriations were named *battleship curves*, as they resembled a bird’s eye view of the silhouette of a battleship (Figure 5.1). If this can be done, the resulting sequence is interpreted as a relative chronological sequence. Therefore, in addition to the concentration principle, frequency seriation also includes the *unimodality principle* or *popularity principle*, which was based on the empirical generalization that things slowly come into fashion, reach a peak of popularity, and then slowly go out of fashion (e.g. different hair styles, clothes designs, architecture styles etc.). It was noted in many cases where the relative chronology is known (e.g.

from stratified deposits) that frequencies of certain attributes/types of a certain class of material culture change according to or approximating the popularity principle.

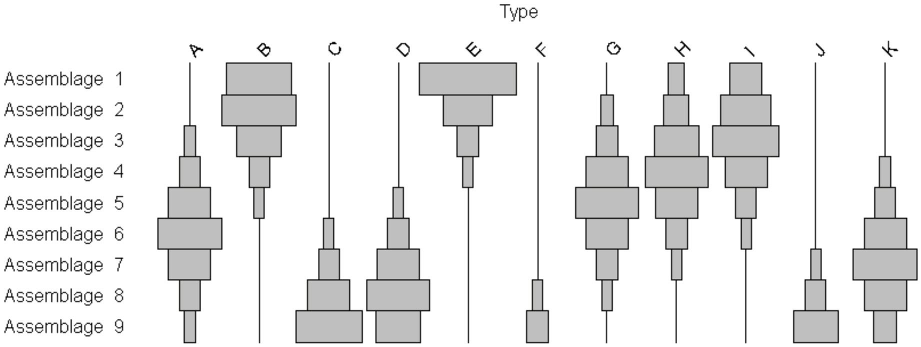

Figure 5.1. The hypothetical and ideal "battleship" patterns, with types having perfectly unimodal distributions (from Porčić 2018: Figure 2).

5.3. WHY DOES SERIATION WORK?

The seriation method was based on fact that there are recurring and consistent patterns of change of material culture through time. From the perspective of archaeological theory, the key question is: what is the explanation for these patterns? Why are the distributions of the relative frequencies of types unimodal rather than bimodal, uniform or approximating some other shape? As already noted, this was explained away by invoking the popularity principle and the analogy with changing fashions. But this is not an explanation, because we may rightly ask why are fashions changing in this way?

The answer to this question came almost a century after seriation was first invented. The first cultural evolutionary formulations of the seriation phenomenon were made by Robert Dunnell (Dunnell 1970; 1978; 1980). The theoretical contribution is related to Dunnell's specific definition of style. Unlike others who looked for the intrinsic stylistic component of objects and the function of style (see Chapter 1), Dunnell defined the style in a manner that linked it to cultural transmission and cultural evolution. For Dunnell, "Style denotes those forms that do not have detectable selective values", as opposed to functional traits that must have selective values (Dunnell 1978: 199). In terms of modern cultural transmission theory, this can be rephrased as: the attributes or types are stylistic if the change in their frequencies is consistent with the neutral (unbiased) model of cultural transmission. This was an important step, because stylistic temporal dynamics were conceptualized as the outcome of the neutral evolutionary process acting on a population of attributes and types as a consequence of cultural transmission.

The key step in linking seriation and the popularity principle with cultural transmission theory was made by Fraser Neiman (1995) in his seminal paper "Stylistic Variation in Evolutionary Perspective: Inferences from Decorative Diversity and Interassemblage Distance in Illinois Woodland Ceramic Assemblages" (see also Teltser 1995a). Neiman simulated the outcomes of simple unbiased (neutral) transmission with mutations. He demonstrated that the temporal dynamics of variant frequencies closely resembled the "battleship" patterns expected from successful seriations (Neiman's simulation setup has been replicated in this book, see below). In other words, the relative frequencies of simulated variants behaved in time similarly to the relative frequencies of real types and attributes – after the first appearance by mutation (innovation), their frequencies increased, reached a peak, and then gradually decreased. It should be noted, however, that neither the simulated nor the real world types were in perfect correspondence with unimodal distribution. This means that small fluctuations in frequencies, departing from the strict unimodality principle, always occur. This is an issue which we will return to soon in this chapter.

The results of Neiman's simulations have clearly shown that cultural transmission theory offers a good explanation for cultural patterns that were observed to occur in all times and places[29]. The neutral model of cultural transmission was the potential mechanism behind the popularity principle. This realization opened up new possibilities for theorizing seriation and extending its epistemic potential beyond the reconstruction of relative chronologies. The most notable achievement in this area was that of Lipo et al. (1997), who demonstrated that seriation can be used to identify cultural lineages in space and time. The spatial scale of cultural transmission is closely linked to temporal patterns.

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[29] The seriation of coin assemblages is the major exception to the interpretation of seriation patterns in terms of cultural transmission theory and the neutral transmission model. It is possible to establish the relative chronology of coin assemblages by seriation even though the dynamics of change in coin type frequencies have nothing to do with cultural transmission and the neutral transmission model (see Lockyear 2000a; 2000b; 2022). In the ideal case, the relative frequency of a coin type is greatest at the moment of its first emission, although in practice there is a lag until the coins are distributed; so the first half of the battleship curve (before the peak) is expected to be much shorter than the second half (after the peak) (Lockyear 1993; 1999). The decrease of a coin type is not due to differential copying but to coin decay rates and the fact that new issues appear all the time (Lockyear 1993; 1999). Therefore, even though unimodality is expected in coin assemblages, as well as ordination by similarity, these patterns are not generated by the process of cultural transmission.

Archaeologists have always been aware of the fact that the success of a seriation depends on choosing the assemblages from a limited spatial area (Dunnell 1970). Lipo et al. (1997) used cultural transmission theory to model the effects of space on the temporal patterns of the simulated material culture. They demonstrated that if there is little interaction between the two microregions within a region, it will not be possible to successfully seriate assemblages from the region as a whole. This result has important methodological implications: if a criterion for a successful seriation can be established, then it should be possible to define the spatial areas of intensive social interaction based on the subsets of assemblages that can be seriated successfully. This can also be used to detect important historical changes such as the splitting or merging of communities – or, more precisely, of cultural lineages. Building upon the main results of the Lipo et al. (1997) paper, Lipo et al. (2015) presented a method that can create branching or merging seriation sequences that resemble phylogenetic trees. But unlike the classic phylogenetic graphs, where the end nodes are, at least in theory, contemporary entities whose phylogeny is modeled by the tree, branching seriation sequences explicitly represent ancestral assemblages in the sequence. The importance of these results cannot be overestimated, as they represent a tool for identifying community structure in space and time on the basis of stylistic data.

5.4. THE ISSUE OF UNIMODALITY

For almost a century, unimodality has been the gold standard for successful seriation[30], and the degree of conformance to the unimodality ideal was taken as the measure of the fit (Lipo et al. 1997). Deviations from ideal unimodality, which were regularly present both in the most successful seriations as well as in the stratified sequences, were thought primarily to reflect sampling errors and the effects of the formation processes. But Neiman's simulation results clearly suggested that the perfect unimodality was not present in the simulated sequences where there was no sampling error or taphonomic factors affecting the loss or distortion of the original chronological signal. This was indeed an interesting situation. The fact that Neiman's results strongly resembled

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[30] In the meantime, Lipo et al. (2015) have shown there is a much better criterion for constructing seriation – the continuity principle. A successful seriation sequence generated by the process of cultural transmission will be such that typological distances in terms of attribute states or variant frequencies between artifacts or assemblages, respectively, will be the least possible, because the evolution of artifacts and assemblages proceeds gradually. The outcome of this process is continuity in the sequence. This is basically the rationale behind the concentration principle and the most general principle of seriation that applies to all kinds of seriations, whereas unimodality only applies to frequency seriation (and in some sense to occurrence seriation). Lipo et al. (2015) and Madsen (2020) suggest that it is more practical to look for seriation solutions that minimize distances between entities than to look for the best approximations of unimodal solutions.

empirical patterns was persuasive evidence that the neutral model of cultural transmission was an excellent explanation for the popularity principle, yet perfect unimodality was not observed in the simulation data where it could not be explained away by different sources of error.

But what causes unimodality in the first place? Let us start with the most recent work by Madsen, who addressed this issue in his PhD thesis. Madsen (2020) concluded that there is nothing special about unimodality when it comes to seriations:

> *"...there is nothing necessary about unimodality given cultural transmission. Instead, culture-historical classifications and typologies were constructed such that they produced compact spatiotemporal distributions and generally followed unimodal histories. This is precisely what Krieger's (1944) "test of historical significance" yields when applied to a candidate typology. This is accomplished by ensuring that types are composed of multiple dimensions of variation which co-occur on artifacts identified to that type. Each dimension of variation (e.g., surface treatment) may have complex histories, like those seen in Figure 5.2, but when we combine several dimensions into a class, the history of the co-occurrence of each combination of attributes becomes smoother and more localized in time and space. This process of class construction necessarily results in a more compact spatiotemporal distribution for the class than for any of its constituent attributes."*
>
> *(Madsen 2020: 118-119)*

Therefore, Madsen suggests that the fact that in the real world types often conform very well to the unimodality ideal can be explained by the fact that types constructed by paradigmatic classification (such as the intersections of all possible attribute states) (Dunnell, 1971; O'Brien & Lyman 2000) represent averaged and smoothed histories of individual attributes that are less unimodal when taken individually. In this chapter, I will test this hypothesis.

In addition to this, Madsen suggests that the fact that relative frequencies are closed scales (they must add up to 1 or 100, for proportions or percentages, respectively) also contributes to the appearance of unimodality. Madsen then concludes:

> *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. From the perspective of culture historians, unimodality was a sufficient criteria for recognizing patterns that were likely chronological from those that were likely not. While focusing on only those classes that produced unimodal distributions in class frequencies might have ignored other potentially historical significant classes, without any other means of identifying chronological patterns, culture historians were satisfied with the subset that worked.*
>
> *(Madsen 2020: 119-120)*

I will start investigating these issues by proposing, as an additional hypothesis for the explanation of unimodality, *that the level of time-averaging (aggregation) increases the level of unimodality in the data.* This hypothesis has already been anticipated by Neiman in his doctoral dissertation:

> *"Clearly this implies that chronological variability among assemblages characterized in terms of style would most closely approximate the monotonic frequency seriation model when those assemblages were derived from communities of multiple individuals, or were the result of large amounts of time averaging, or both".*
>
> *(Neiman 1990: 197)*

Intuitively, this proposition makes sense. If the process is such that variant frequencies change by drift, decreasing temporal frequency should highlight the wax-and-wane patterns, as the stochasticity of individual transmission events will become more patterned when averaged over multiple transmission episodes. Likewise, assemblages from stratified deposits, where the unimodal pattern was observed and inspired the formulation of the frequency seriation method, are not snapshots of systemic assemblages, but accumulations of objects from wide intervals of time (usually tens or hundreds of years).

5.5. QUANTIFYING UNIMODALITY

5.5.1. *The seriation coefficient*

Before I proceed with the investigation, a technical digression is needed in order to find a way to quantify the degree of unimodality in a particular sequence of assemblages. In an attempt to construct a goodness of fit measure for seriation solutions, several years ago I introduced the *seriation coefficient* (Porčić 2013a):

$$S = (Max - O) / (Max - E) \quad \text{(Eq. 5.1)}$$

where O is the observed total number of modes, E is the expected total number of modes if all types had unimodal distributions (E is therefore equal to the number of types), and Max is the maximum total number of modes, depending on the number of assemblages in the data matrix. The data matrix is conceptualized in such a way that the rows correspond to different assemblages and the columns correspond to different types. For an even number of assemblages, the maximum total number of modes is equal to the number of types multiplied by the number of assemblages divided by 2. For an odd number of assemblages, the maximum total number of modes is equal to the product of the number of types on one side, and the number of assemblages plus 1 divided by 2 on the other. The number of assemblages had to be taken into account because data matrices with a low number of rows can have fewer potential departures from unimodality than matrices with a greater number of rows. In its essence, the seriation coefficient measures how well the empirical data approximate the ideal unimodal seriation model (it can take values between 0 and 1 – values close to 1 indicate a strong fit to the seriation model, while values close to 0 indicate a poor fit). Therefore, *unimodality coefficient* would be the more accurate name for this indicator.

However, there is a problem with this measure – in its original form (Porčić 2013a), it overestimates the magnitude of unimodality of sequences. The procedure for calculating the maximal number of modes needed for the calculation of the seriation coefficient may sometimes grossly overestimate the true maximum and thus inflate the value of the coefficient. For this reason, I use a modified version of the seriation coefficient which is not inflated. I present a better way for estimating the maximum number of modes, which removes the inflation problem. The technical details related to the modification of the seriation coefficient and the associated R code are presented in Appendix 4.

5.5.2. *The absolute coefficient of unimodality*

In addition to fixing the problem with the original seriation coefficient, I would also like to introduce here an additional goodness of fit measure for seriation solutions. The seriation coefficient as defined in Porčić (2013a), and modified in this book, can be interpreted as a *relative coefficient of unimodality*. It is relative because it compares the empirical number of modes to the potential maximum number of modes, taking into account the number of assemblages and types. We could also define a simpler measure – a ratio of the number of types to the observed number of modes. If all types have only a single mode along the seriation sequence, then the value of this coefficient is equal to one, which is exactly what we would want from a measure of unimodality in the case of a perfect fit. As the empirical number of modes increases, the value of such a coefficient would decrease. I will call this coefficient an *absolute coefficient of unimodality,* as it does not take into account the potential for the number of modes of the data matrix; it is only based on the observed number of modes and the number of types (the expected number of modes for the ideal unimodal sequence). In order to make the text easier to follow, I will henceforth refer to the relative coefficient of unimodality (the modified seriation coefficient) as S1, and to the absolute coefficient of unimodality, as defined here, as S2.

The S2 coefficient is a non-linear function of the observed number of modes, as it decreases faster with the increasing empirical number of modes (Figure 5.2), unlike S1, which is a linear function of the observed number of modes (Appendix 4, Figure A4.1). For example, when the number of modes reaches 5 modes per type, the S2 value falls to ~0.2. Given that it does not take into account the number of assemblages and, by implication, the potential for the deviations from unimodality, it is best to use it to compare seriations with data sets of similar dimensions in terms of the number of assemblages and types.

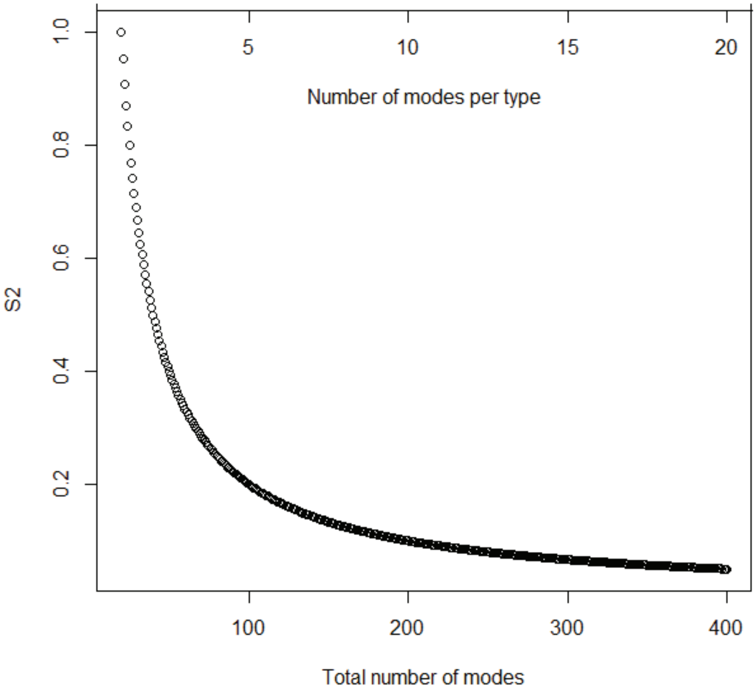

Figure 5.2. The S2 (absolute coefficient of unimodality) for the hypothetical data set containing 40 assemblages and 20 types changes linearly as a function of the total number and the number of modes per type.

5.5.3. Neiman's example (Experiment 5.1)

Let us start with Neiman's (1995) seminal example. A neutral model of cultural transmission is simulated for 400 time-steps, with population size of 50, mutation rate equal to 0.01, all agents starting with the same variant, and use-life of objects being equal to one simulation time-step. Therefore, in each time-step an assemblage of size 50 items is produced. If we look at the relative frequency of variants for assemblages in their true temporal sequence, we can see that the overall pattern only approximates to the unimodal pattern, and that it is far from perfect (i.e. many variants having two or more modes) (Figure 5.3). This is confirmed by the values of the seriation coefficients: S1 is equal to 0.82 and S2 is equal to 0.37.

If we did not know the true order of the assemblages and performed the seriation using correspondence analysis (CA), we would get seriation solutions like those in Figure 5.3. These solutions also approximate to the unimodal model, but not perfectly. Moreover, they have lower unimodality than the true sequence (S1 = 0.61, S2 = 0.21), even though the accuracy of the seriation solution is very high (Spearman's rho between the true and reconstructed orders of assemblages is 0.98). Even though the value of Spearman's rho suggests an extremely high correlation between the true and reconstructed orders, looking at Figure 5.3 shows that there are many reversals present in the reconstructed sequence even though it is correct in general. Comparing the sequences from Figure 5.3 leads to the impression that CA tends to increase the unimodality of variants with higher overall frequencies, while decreasing it for the less numerous variants – it makes the temporal distributions of the most frequent variants more unimodal at the expense of the less frequent variants, thus lowering the overall unimodality of the sequence.

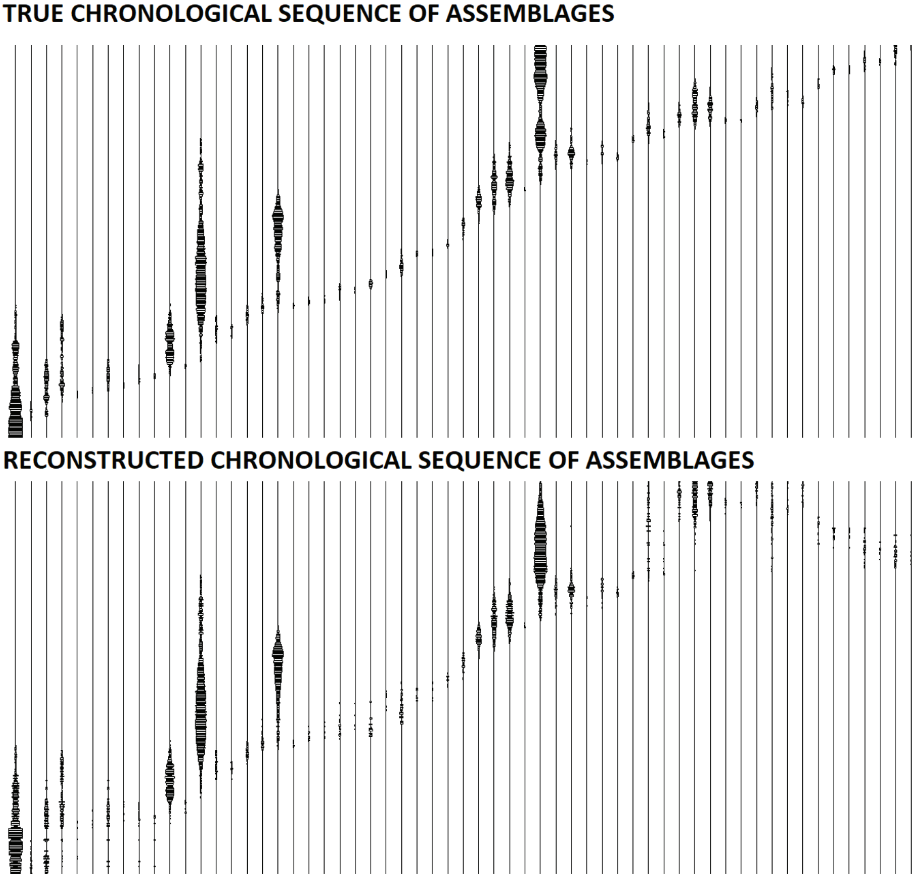

Figure 5.3. The battleship plot showing the true sequence of assemblages in the upper panel; the reconstructed sequence of assemblages by seriation using CA in the lower panel. There are 204 variants in total, but for clarity only variants with total frequencies greater than 10 are shown in the graph. Time flows from bottom to top.

5.6. TESTING THE TIME-AVERAGING HYPOTHESIS

5.6.1. Testing the overall effect of time-averaging on unimodality (Experiment 5.2)

In order to fully investigate this issue, I made a series of 111,607 simulations, each having a particular combination of simulation parameters. For each simulation run of 1000 iterations, a single value is generated by randomly sampling from a set of discrete values defined for each simulation parameter: 1) Population size: 25, 50, 100, 200, 500, 1000; 2) Mutation rate: 0.0005, 0.001, 0.01; 3) Initial diversity of variants: 10, 30, 50; 4) Item use-life: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10; 5) Degree of time-averaging (accumulation interval width): 1, 10, 20, 50, 100, 200. Therefore, there are potentially 3240 distinct and equally probable combinations of parameter values, with 30.45 observations for each combination of parameters on average, given the 111,607 simulation runs. In this way, I generated a large amount of cultural transmission sequences, each one subjected to seriation analysis by CA. For each simulated sequence, unimodality coefficients S1 and S2 were calculated for the true sequence of assemblages, as well as for the reconstructed sequences. Seriation accuracy for each sequence was calculated as a Spearman's rho coefficient between the true and reconstructed orders of units. This allows us to systematically explore the influence of different parameters of transmission and time-averaging on the unimodality and accuracy of seriation solutions, and to make more general statements based on the wider range of transmission and archaeological parameter values and their combinations.

The first step will be to explore the distribution of seriation accuracy coefficients, as well as the unimodality of the true and reconstructed sequences, in order to see how well the seriation with this particular technique is successful, and how close these sequences are to the unimodal ideal. In general, CA does a relatively good job in reconstructing the correct order (Table 5.2). The mean seriation accuracy (correlation between the true and reconstructed sequence) is 0.853, the median is 0.95, while 75% of sequences have a seriation accuracy of over 0.802, with distribution strongly skewed to the left as the greatest number of cases cluster in the upper end of the range (Figure 5.4).

	Seriation accuracy	S1 (true sequence)	S2 (true sequence)	S1 (reconstructed sequence)	S2 (reconstructed sequence)
Mean	0.85	0.80	0.70	0.78	0.69
Median	0.95	0.82	0.85	0.79	0.83
Std. Deviation	0.21	0.143	0.33	0.16	0.33

Table 5.2. Descriptive statistics for the coefficients of unimodality and seriation accuracy based on the 111607 results of Experiment 5.2.

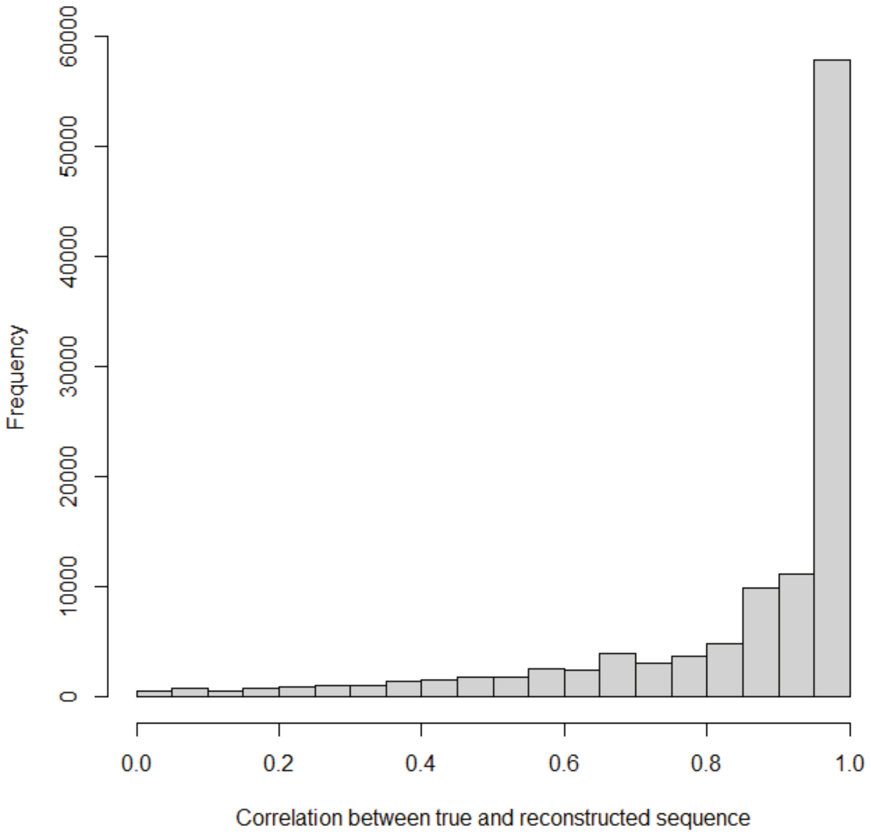

Figure 5.4. The distribution of correlation coefficients measuring seriation accuracy based on the results of Experiment 5.2.

As for the unimodality of true sequences, the mean for the S1 coefficient is 0.803, the median is 0.82, and 75% of cases have values greater than 0.718. Distribution is slightly skewed to the right (Figure 5.5), with 1 being the modal value. For S2, mean is 0.703, median is 0.854 and 75% cases have values greater than 0.48. Distribution seems to be bimodal, but the great majority of cases cluster around the high values, with 1 again being the modal value. Therefore, most true sequences are highly unimodal.

Similar results are obtained for the reconstructed sequences (Figure 5.5). For S1, the mean is 0.782, the median is 0.794, and the value of the 25th percentile is 0.655. The shape of the distribution is similar to S1 for true sequences. For S2, the mean is 0.688. the median is 0.829, and 75% of cases have values greater than 0.422. The distribution is slightly bimodal. Therefore, reconstructed sequences are also highly unimodal. The mean S1 and S2 values for reconstructed sequences are only slightly lower than the corresponding means of the true sequences.

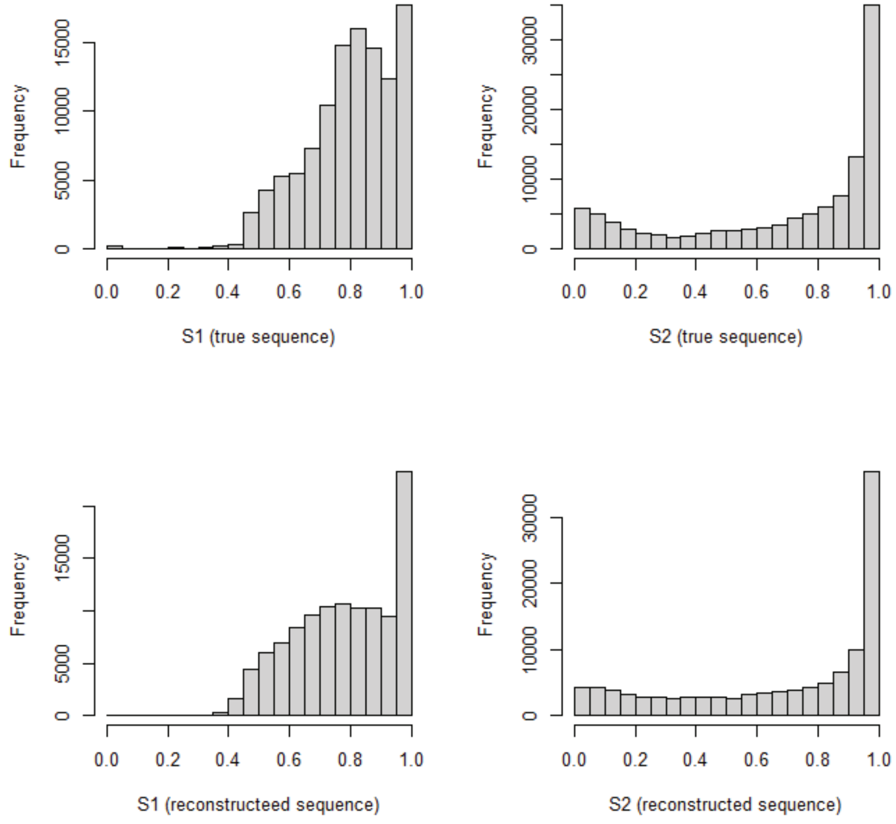

Figure 5.5. The distributions of the S1 and S2 coefficients for the true and reconstructed sequences based on the results of Experiment 5.2.

The second step of the analysis is to explore the influence of the transmission parameters and time-averaging on the unimodality of the true assemblage sequences. I performed a multiple regression analysis with the S1 unimodality of the true sequence coefficient as dependent, and degree of time-averaging, population size, mutation rate, average use-life, and initial diversity of variants as independent variables. The regression model has a moderate effect size (R^2 = 0.386; 38.6% of the variance of the S1 unimodality coefficient is explained by the independent variables). The regression parameters are summarized in Table 5.3. As the individual parameter values were sampled independently from one another, the parameters are not correlated, so we can interpret the standardized beta coefficients as closely approximating the zero order linear correlations between the dependent and individual independent variables. All independent variables are statistically significant predictors, but this is to be expected, given the large sample size, so I will focus on the standardized slope coefficients as measures of effects size for each variable. As predicted by the main hypothesis in this chapter, the time-averaging does indeed have the highest relative impact on the true unimodality as measured by the S1 coefficient, as its standardized beta coefficient is the highest (0.524). The next variable that also positively correlates with S1 is the mutation rate, but its influence is twice as low (standardized beta = 0.262) compared to the influence of time-averaging. The average use-life is negatively correlated with the unimodality, meaning that items with longer use-lives are less likely to have unimodal variant frequencies under the neutral transmission model. This effect of use-life is somewhat lower than the effect of the mutation rate and it is negative (standardized beta = -0.195), indicating that lower use-life leads to higher unimodality. Population size and the initial diversity of variants are positively correlated with S1 very weakly, therefore this relationship, although statistically significant, has no practical implications.

	Unstandardized Coefficients		Standardized Coefficients	p
	b	Std. Error	Beta	
Degree of time-averaging	0.001	0.000	0.524	0.000
Population size	0.0000036	0.000	0.009	0.000
Mutation rate	8.624	0.077	0.262	0.000
Use-life	-0.010	0.000	-0.195	0.000
Initial diversity of variants	0.000	0.000	0.048	0.000

Table 5.3. Results of the multiple linear regression based on the results of Experiment 5.4, with the S1 of true sequences as the dependent variable.

As the relations between variables are not always linear, I also calculated the Spearman correlation matrix between all pairs of the extended set of variables (which includes seriation accuracy, S2 for true sequences, as well as S1 and S2 for the reconstructed sequences) based on the 111,607 individual simulation results (Table 5.4). The results show that the degree of unimodality of both true and reconstructed sequences is indeed positively and relatively strongly correlated with time-averaging. Time-averaging is also significantly, if weakly correlated with seriation accuracy (rho = 0.282).

	S1 (true)	S2 (true)	S1 (reconstructed)	S2 (reconstructed)	Seriation accuracy	Degree of time-averaging	Population size	Mutation rate	Use-life	Initial diversity of variants
S1 (true)	1.000	0.861	0.528	0.715	0.429	0.679	0.031	0.267	-0.203	0.056
S2 (true)		1.000	0.650	0.932	0.309	0.895	-0.055	0.204	-0.230	0.053
S1 (reconstructed)			1.000	0.817	0.077	0.620	-0.382	-0.037	-0.103	0.068
S2 (reconstructed)				1.000	0.164	0.882	-0.209	0.082	-0.199	0.048
Seriation accuracy					1.000	0.282	0.570	0.328	0.026	0.043
Degree of time-averaging						1.000	0.003	0.001	-0.002	0.006
Population size							1.000	-0.001	0.001	0.002
Mutation rate								1.000	-0.004	0.001
Use-life									1.000	-0.004
Initial diversity of variants										1.000

Table 5.4. Spearman's rho correlation matrix between simulation parameters based on the results of Experiment 5.2. Correlations significant at the 0.05 level in boldface.

The relationship between the degree of unimodality of true sequences, reconstructed sequences and seriation accuracy is complex. We can see that there is a moderate correlation between the unimodality of true sequences and the seriation accuracy (for S1 rho is 0.429, for S2 rho is 0.309), but only a very weak, yet statistically significant, correlation between unimodality of reconstructed sequences and seriation accuracy (for S1 rho = 0.077, for S2 rho = 0.164). This means that sequences for which the true order of assemblages is closer to the unimodal ideal are more likely to be correctly reconstructed by seriation, although the effect size for such a tendency is moderate, given the correlation coefficient values. There is also the same tendency for the reconstructed sequences – those which are more unimodal are also more accurately reconstructed and vice-versa – but this tendency is very weak and practically insignificant given the low correlation coefficient values.

In order to explore this issue in more detail, I discretized the S1 values for the true and reconstructed sequences, as well as Spearman's rho values which measure the seriation accuracy (Tables 5.5 and 5.6). The results presented in the form of a contingency table clearly show that unimodality has the highest impact on accuracy only when the S1 for both true and reconstructed sequences is low. This means that true sequences which have low unimodality are less likely to be correctly reconstructed ($P(\text{Accuracy} > 0.66 \mid \text{S1 true} < 0.33) = 0.043$; $P(\text{Accuracy}) > 0.66 = 0.84$), and it also means that reconstructed sequences with low unimodality are less likely to be accurate ($P(\text{Accuracy} > 0.66 \mid \text{S1 reconstructed} < 0.33) = 0.275$; $P(\text{Accuracy}) > 0.66 = 0.84$). At high levels of unimodality, the relative frequency structure is approximately equal to the marginal relative frequencies of the seriation accuracy indicator. The relevant probabilities based on the contingency table are $P(\text{Accuracy} > 0.66 \mid \text{S1 true} > 0.66) = 0.862$ and $P(\text{Accuracy} > 0.66 \mid \text{S1 reconstructed} > 0.66) = 0.807$. Even though highly accurate sequences are dominant when the unimodality of either true or reconstructed sequences is high (~0.8), this is essentially the same proportion as the general proportion of accurate seriations in the results ($P(\text{Accurate}) = 0.84$). Therefore, the information that unimodality is high, whether true or reconstructed, does not reveal much about the seriation accuracy.

			Seriation accuracy			Total
			< 0.33	0.33-0.66	> 0.66	
S1 (true sequence)	< 0.33	N	115	115	14	244
		% of S1 (true sequence)	47.1%	47.1%	5.7%	
	0.33 - 0.66	N	1590	3359	14272	19221
		% of S1 (true sequence)	8.3%	17.5%	74.3%	
	> 0.66	N	3437	9288	79417	92142
		% of S1 (true sequence)	3.7%	10.1%	86.2%	
Total		N	5142	12762	93703	111607
		% of S1 (true sequence)	4.6%	11.4%	84.0%	

Table 5.5. Contingency table showing cross-tabulation of discretized seriation accuracy and discretized S1 (true sequence) for Experiment 5.4.

			Seriation accuracy			Total
			< 0.33	0.33-0.66	> 0.66	
S1 (reconstructed sequence)	< 0.33	N	17	39	15	71
		% of S1 (reconstructed sequence)	23.9%	54.9%	21.1%	
	0.33-0.66	N	546	1502	27592	29640
		% of S1 (reconstructed sequence)	1.8%	5.1%	93.1%	
	> 0.66	N	4579	11221	66096	81896
		% of S1 (reconstructed sequence)	5.6%	13.7%	80.7%	
Total		N	5142	12762	93703	111607
		% of S1 (reconstructed sequence)	4.6%	11.4%	84.0%	

Table 5.6. Contingency table showing cross-tabulation of discretized seriation accuracy and discretized S1 (reconstructed sequence) for Experiment 5.2.

Population size and mutation rate are positively correlated to seriation accuracy – higher population and mutation rate moderately increase the probability that the sequence will be correctly reconstructed. Additionally, population size is negatively correlated to the unimodality of reconstructed assemblages. Use-life is weakly negatively correlated to unimodality of both reconstructed and true sequences. The initial diversity of types has no practically significant effect either on seriation accuracy or on unimodality.

5.6.2. *Time-averaging, unimodality and seriation accuracy – controlling the number of assemblages (Experiment 5.3)*

Finally, I conducted one more simulation experiment in order to eliminate the potential effect of different numbers of assemblages on unimodality and accuracy of seriation (e.g. it is more likely to obtain the correct solution by chance with a smaller number of assemblages due to the smaller number of permutations). In previous experiments, increasing the degree of time-averaging implied decrease in the number of assemblages as the total simulation time was fixed. In this experiment, I vary the degree of time-averaging, but I keep the number of assemblages constant by adjusting the total simulation time. The number of assemblages for the analysis is fixed at 20. If the degree of accumulation is such that items from 50 individual iterations are aggregated into one assemblage, the total simulation duration is 1000 steps. If the degree of accumulation is such that items from 100 individuals iterations are aggregated into one assemblage, the total simulation duration is 2000 steps. The population size was fixed to 100, the mutation rate was set to 0.01, the average uselife was set to 2 steps, and the initial diversity of variants was 10. The degree of time-averaging is the only variable that was allowed to vary, by the choice of one of the following values that indicates the number of successive assemblages that were aggregated for each of 1019 simulations: 5, 10, 25, 50, 75, 100.

The results of this experiment are summarized in Table 5.7, where Spearman's correlation coefficients between the key variables are shown. Time-averaging is strongly correlated to the unimodality of the true sequence as measured by the S1 coefficient – increasing time-averaging increases the unimodality of a true sequence. The degree of time-averaging is also moderately correlated to the seriation accuracy. It is also interesting to note that the correlation between the unimodality of reconstructed sequences and the seriation accuracy is strong, implying that sequences with higher unimodality are more likely to be correct.

	Degree of time-averaging	Seriation accuracy	S1 (true sequence)	S1 (reconstructed sequence)
Degree of time-averaging	1.000	0.475	0.906	0.644
Seriation accuracy		1	0.548	0.860
S1 (true sequence)			1	0.751
S1 (reconstructed sequence)				1

Table 5.7. Spearman's rho correlations between unimodality and seriation accuracy for Experiment 5.3.

5.7. PATTERNS IN TIME GENERATED BY OTHER MODELS OF CULTURAL TRANSMISSION

As mentioned in Chapter 2, there are other models of cultural transmission which can generate unimodal or approximately unimodal distributions of cultural variant frequencies in time (Acerbi et al. 2012; Klimek et al. 2019; Newberry & Plotkin 2022). This implies that the neutral model is a sufficient, but not a necessary condition for this pattern to arise. In this section, I will address this issue explicitly, and explore whether the other two most commonly used models in evolutionary archaeology, the conformist and anticonformist models, can also produce unimodal patterns. I will compare the three models (neutral, conformist and anti-conformist) to see how they affect the degree of unimodality of temporal sequences.

The implementation of the neutral and conformist models in simulations has already been described in Chapters 3 and 4, but a short digression needs to be made to describe the implementation of the anti-conformist model. To reiterate, the anti-conformist model is a model of cultural transmission where there is a positive bias towards rare cultural variants in the population. There are several ways to interpret anti-conformist bias, and so, as for the conformist model, other formulations are also possible for the anti-conformist model (e.g. Kandler & Crema 2019; Crema et al. 2016). In this study, I interpret anti-conformist bias as a pro-novelty bias, meaning that anti-conformist behavior will consist of favouring new variants (the ones generated by mutations), since they are the least frequent in any time step. The likelihood of copying the new variant will depend on the degree of anti-conformism in the population, conceptualized as the probability that an individual will behave in an anti-conformist manner, i.e. copy the least frequent variant. Therefore, in the simulation of the anti-conformist model, each agent has three options when it has to decide about the variant of the item: 1) copy the least frequent variant from the current set of variants with probability equal to *anticonf* (probability or degree of anti-conformism) - if there are two or more such variants with equal frequencies, the choice between them will be random; 2) introduce a completely new variant (mutation) with probability equal to μ; 3) randomly copy a variant from another agent from the same cell with probability $1 - \mu - anticonf$.

How would the temporal pattern of type frequencies look, if we added a degree of conformist or anti-conformist bias? Let us set up an experiment (*Experiment 5.4*) with an (item/agent) population size of 100, mutation rate equal to 0.01 (1%), starting with an initial assemblage in which each of the 10 initial variants has the same frequency (10). The average item use-life is set to 2 iterations and the simulations will run for 2000 iterations. The time-averaging interval is set to 25 iterations (or 25 years, approximating one generation, which is a reasonable generic value for the duration of a building horizon), which means that there will be 80 assemblages in a sequence for each simulation run. I try out nine simulation scenarios: the first scenario will be the pure neutral model; the following four scenarios will implement the conformist model with increasing probability of conformist behavior (*conf*), set to 5%, 10%, 20%, and 50%, sequentially; and the final four simulation scenarios will implement the anti-conformist model with the probability of anti-conformist behavior (*anticonf*) set to 5%, 10%, 20%, and 50%, sequentially. Each scenario is run for 50 times. I calculate the seriation coefficient S1 for each simulation run.

Figure 5.6 shows distributions of S1 for different transmission models. It is apparent from this graph that all three models are capable of generating sequences with high levels of unimodality, but there are systematic differences between the models – the anti-conformist model generates slightly higher unimodality values than the neutral model, whereas the conformist model generates lower S1 values than both the neutral and anti-conformist models. This pattern is even sharper when the degree of (anti)conformity is plotted against S1 (Figure 5.7).

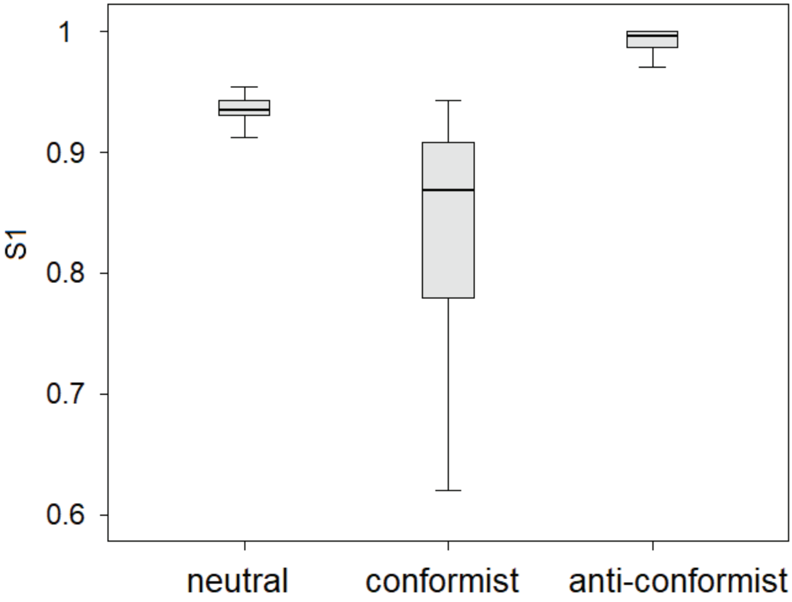

Figure 5.6. Boxplots showing the distributions of the S1 coefficient based on the sequences generated by the neutral, conformist and anti-conformist models (Experiment 5.4).

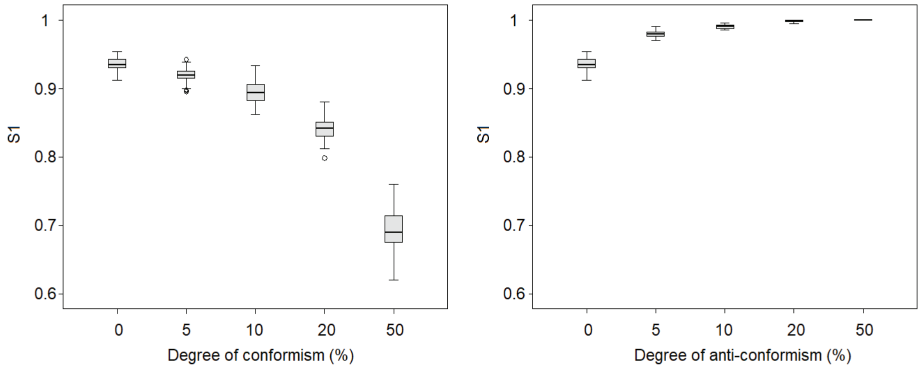

Figure 5.7. Left: The decrease of unimodality with increasing conformism (based only on the neutral and conformist scenarios of Experiment 5.4). Right: The increase of unimodality with increasing anti-conformism (based only the on neutral and anti-conformist scenarios of Experiment 5.4).

To see why is this so, I present three typical battleship plots for the neutral, conformist (*conf* = 10%) and anti-conformist (*anti-conf* = 10%) transmission scenarios based on the simulations in this experiment (Figure 5.8). The reduced degree of unimodality in the conformist transmission compared to the neutral model is a reflection of a drastically different dynamics of change in type frequencies. A type which by chance becomes the most frequent is the one which is always present, but its frequency oscillates owing to constant mutations, thus decreasing the unimodality of its frequency distribution in time. On the other hand, the dynamics of the anti-conformist model is such that, as soon as the new mutation appears, it becomes transmitted, leading to the increase of its frequency, and the decrease in the frequency of older variants. This kind of dynamics makes it less likely that the older variants will increase in frequency once they have passed their peak; so the result is perfect or almost perfect unimodality in anti-conformist transmission.

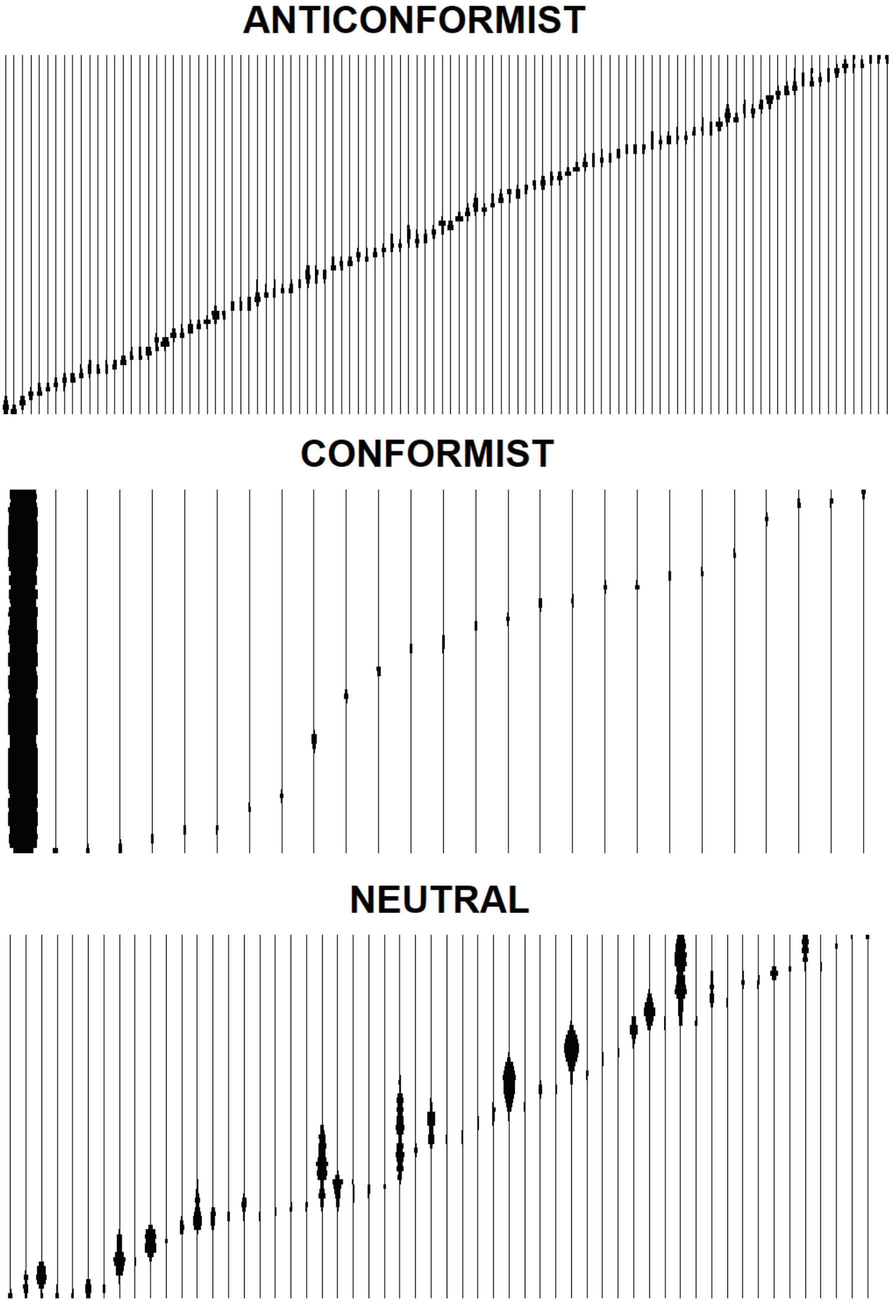

Figure 5.8. The battleship plots for the typical neutral, conformist and anti-conformist transmission scenarios from Experiment 5.4. For the neutral and conformist simulation runs, only types which have frequency greater than 100 are shown; whereas for the anti-conformist simulation, only types which have frequency greater than 200 are shown. Time runs from bottom to top.

It should be noted that the battleship plots in Figure 5.8 reveal something potentially more important than differences in unimodality between transmission models. What this graph also suggests is that the three models produce drastically different distributions of type durations (i.e. how much time passes between the first appearance and disappearance of a type). I collected type duration data for the simulations in Experiment 5.4 and calculated the coefficients of variation and maximum type duration for each run (Figure 5.9). The highest maximum duration of types is associated with the conformist model, and the lowest with the anti-conformist model, with the neutral model in between. The coefficient of variation of type duration is the lowest for the anti-conformist model and highest for the conformist model, again with the neutral model between. It is remarkable that the distributions are almost non-overlapping; but it should be noted that the simulations in Experiment 5.4 did not include mixed conformist and anti-conformist models, where a fraction of the population copies according to conformist bias, whereas another fraction copies according to an anti-conformist bias. The mixing of biases within a single experiment might blur the picture (cf. Kandler & Crema 2019: Figure 3).

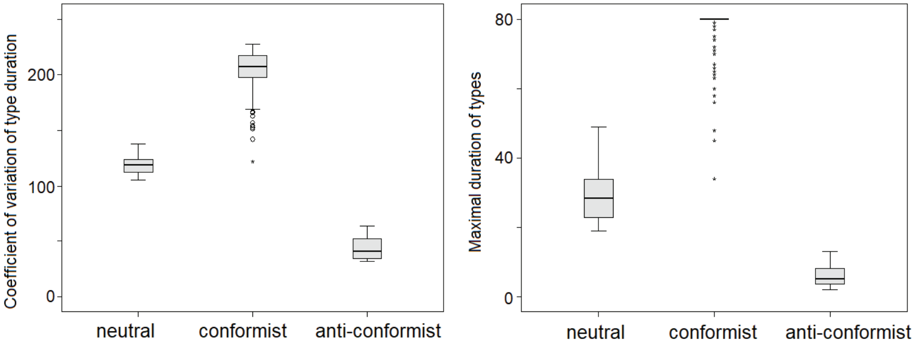

Figure 5.9. Left: Distribution of coefficient of variation of type durations in individual simulation runs in Experiment 5.4 for each model of transmission.

Right: Distribution of maximal type durations (in time steps of 25 iterations) in individual simulation runs in Experiment 5.4 for each model of transmission.

5.8. EMPIRICAL ILLUSTRATIONS OF THE RELATIONSHIP BETWEEN TIME-AVERAGING AND UNIMODALITY

5.8.1. The empirical demonstration

I anticipate that many archaeologists would now stop me and ask a commonsense question: are these effects purely statistical artifacts of the models and simulations, or do they have grounding in the empirical reality of the archaeological record? This is a perfectly legitimate question. If the models and simulations presented in this chapter do manage to capture important aspects of the social and cultural dynamics that produced the archaeological record, then we should observe the same effects in the real data. The theoretical issues that I explored throughout this chapter have clear empirical implications, especially when it comes to the effects of time-averaging on the unimodality and accuracy of seriation solutions. The main issue that was explored in this chapter was unimodality, and there is a clear prediction that follows from the theoretical explorations presented here: the unimodality of temporal sequences should increase with time-averaging. I have managed to show that this is the case with simulated data, but now it is time to demonstrate this with the real-world archaeological data.

In order to test this prediction empirically, I will use the data from several stratified sites where the relative chronological sequence of the assemblages is known. I will artificially create time-averaged assemblages by merging the original assemblages coming from the successive stratified horizons. Then, I will calculate the unimodality as well as the seriation accuracy coefficient (Spearman's rho between true and reconstructed sequence) for the different levels of time-averaging. I apply this procedure to three independent data sets from the Balkans.

5.8.2. Case study 1: Ezero

Ezero is an Early Bronze Age site in Bulgaria (~3100-2800 BC) (Weninger 1995; Георгиев et al. 1979). It is a stratified tell site with 12 building horizons of similar duration (Weninger 1995). I will use the published data on the frequencies of relief decoration motifs in each of the 12 stratified building horizons in Ezero (Георгиев et al. 1979:Table 200) (Table 5.8). Therefore, the original number of assemblages is 12, and I will emulate time-averaging by merging assemblages from the adjacent building levels. I will explore two levels of time-averaging (Table 5.9). The first level is based on merging pairs of adjacent assemblages (II & III; IV & V; VI & VII; VIII & IX; X & XI; XII & XIII), whereas the second level is based on merging triplets of continuous assemblages (II & III & IV; V & VI & VII; VII& IX & X; XI & XII & XIII).

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
II	1	7	6	4	2	0	0	1	1	0	0	0	0	0	3	0	0	0	6	0	1	0
III	2	4	7	4	2	1	0	7	0	4	2	0	3	0	3	0	0	0	18	0	4	2
IV	5	10	3	8	4	3	0	5	1	5	4	0	3	1	5	0	0	0	14	0	5	3
V	0	3	2	15	7	1	0	5	1	3	5	0	3	0	6	0	0	0	11	1	5	3
VI	8	1	0	6	3	4	1	10	7	5	7	0	0	0	2	1	0	0	15	0	6	6
VII	24	5	1	1	3	16	0	14	9	2	6	0	0	0	2	0	0	0	18	1	12	12
VIII	11	0	0	0	0	6	0	7	4	0	2	0	0	0	6	0	0	0	8	1	0	3
IX	7	3	0	0	0	7	1	4	4	1	2	1	0	0	5	0	0	0	2	2	4	1
X	14	2	0	0	0	7	0	8	6	0	0	0	0	0	7	0	1	3	9	2	4	4
XI	32	3	0	0	0	11	0	8	0	1	0	0	0	0	0	0	5	3	12	6	6	5
XII	36	2	0	0	0	2	1	9	2	0	0	2	0	0	0	1	6	5	6	2	2	0
XIII	20	0	0	0	0	5	0	0	15	0	0	0	0	0	0	0	2	9	5	0	2	3

Table 5.8. Ezero vertical handle data set (data from Георгиев et al. 1979:Table 200). Building horizons in rows, type codes in columns.

For the Ezero data, the unimodality coefficients S1 and S2 for the true sequence of assemblages increase from 0.49 and 0.39, to 0.7 and 0.67, respectively, as the accumulation interval width increases from one horizon to two horizons, and to 0.9 and 0.92 for the accumulation interval width of 3 assemblages (Table 5.9). The correlation between the true and reconstructed sequence is very high to begin with (rho = 0.97), with the reconstructed sequence being closer to the unimodal ideal than the true sequence. With the first aggregation (increase of the accumulation interval width to 2 horizons), the seriation accuracy becomes perfect – the order of the true sequence and the sequence reconstructed by CA become identical. Further time-averaging increases S1 and S2, but leaves the accuracy unchanged, as it has already reached its maximum.

Aggregation interval width	S1 true	S2 true	Seriation accuracy (Spearman's rho)
1	0.49	0.33	0.97
2	0.7	0.67	1
3	0.9	0.92	1

Table 5.9. The influence of time-averaging on unimodality and accuracy of seriation for the reconstructed and true sequences of stratified building horizons based on pottery decoration motifs at the Early Bronze Age site of Ezero in Bulgaria.

5.8.3. Case study 2: Selevac

Selevac – Staro selo is a Late Neolithic multiphase site in Serbia with an archaeological record spanning several centuries, from the last quarter of the 6th to the first half of the 5th millennium BC, as suggested by the radiocarbon data (Tringham & Krstić 1990). In the 1977-78 campaigns, nine building horizons (BH) were defined: I, II, III, IV, V, VI, VII, VIII, XIX (Tringham & Krstić 1990). In order to test the hypothesis that the unimodality increases with time-averaging, I used the published data on the typology of the shouldered bowls, i.e. the frequencies of the 86 shouldered bowl types in different building horizons in Selevac (Vukmanović & Radojčić 1990). Sherds were assigned into types based on the profile shapes, and the total of 86 shouldered bowl types was defined by Vukmanović and Radojčić (1990). These are all extensionally defined types (*sensu* Dunnell 1971; O'Brien & Lyman 2000). It is a reasonable assumption that all variants within a single class such as shoulder bowls are analogous in function and therefore have similar use-lives and fragmentation rates.

Again, the results are in agreement with the predictions of the time-averaging hypothesis, although the increase in unimodality is more modest than in the previous case study (Table 5.10). When the assemblages from the originally defined 9 stratigraphic horizons (1977-1978 campaigns) are artificially time-averaged by merging the assemblages from horizons II and III, IV and IV-VI, VII and VIII, the S1 and S2 for the true sequence increase from 0.47 and 0.65, to 0.53 and 0.79, respectively. The seriation accuracy becomes perfect after time-averaging, although it was very high to begin with.

Degree of time-averaging	S1 true	S2 true	Seriation accuracy (Spearman's rho)
No artificial aggregation (original stratigraphic units)	0.47	0.65	0.89
Artificially time-averaged assemblages	0.53	0.79	1

Table 5.10. The influence of time-averaging on unimodality and accuracy of seriation for the reconstructed and true sequences of stratified building horizons based on the shouldered bowl form types at the Late Neolithic site of Selevac in Serbia.

5.8.4. Case study 3: Vinča – Belo brdo

Vinča – Belo brdo is the eponymous site of the Late Neolithic Vinča culture situated in the vicinity of Belgrade (Serbia), where the Late Neolithic horizons are dated between 5300 and 4500 BC (Tasić et al. 2015b; Tasić et al. 2015a). Amongst other things, the site is famous for its large collection ($N > 1000$) of clay anthropomorphic figurines from the Late Neolithic period (Лазић 2015; Срејовић 1968; Тасић 2008; Hansen 2007: 203-221). I have made an extensional classification (*sensu* Dunnell 1971; O'Brien and Lyman 2000) of the anthropomorphic figurine eye types (Figure 5.10) based on the photo archive of the Archaeological Collection of the Faculty of Philosophy, University of Belgrade. The archive contains photographs of the figurines excavated in the digs before the World War II (Васић 1932; 1936a; b; c). For each figurine fragment, the relative depth at which it was found is known, so the assemblages were created by grouping all figurines found at the same relative depth as they were recorded by their mechanical excavation spit of 10cm by the original excavator of the site M. Vasić (for details about the methods used to record the stratigraphic position of artifacts in the pre-World War II excavations in Vinča, as well as their validity, see Palavestra 2020; Schier 2000). I have recorded the figurine eye types on 389 figurine fragments or complete figurines where this attribute was observable. In total, 39 figurine eye types were defined.

Figure 5.10. The examples of the figurine eye types (meme variants) from Vinča – Belo brdo (photos by A. Radoman and V. Miladinović, published in Николић 2008: catalogue numbers 11, 12, 21, 22, 16, 20, 43, 44, 45).

There were four degrees of time-averaging in this exercise. The first degree was the lowest possible time-averaging level, when the original 10cm excavation spit units were used to group specimens into assemblages. The second and third degrees were generated by artificially merging the pairs of adjacent assemblages from the previous level of time-averaging. The fourth degree of time-averaging was made by grouping the analyzed figurines into 1 metre-thick deposits based on their relative depth. The results of the analysis are summarized in Table 5.11. The unimodality increases with increasing time-averaging as predicted by the main hypothesis (for visual assessment see Figures 5.11 and 5.12). The S1 and S2 coefficients are initially low (below 0.5), but they almost double when the time-averaging reaches the highest degree. Unsurprisingly, the accuracy of the seriation increases as well.

Aggregation interval width	S1 true	S2 true	Seriation accuracy (Spearman's rho)
1	0.358	0.291	0.557
2	0.383	0.371	0.763
3	0.483	0.565	0.8
7 assemblages by meters	0.767	0.796	0.964

Table 5.11. Time-averaging intervals and S1, S2, and seriation accuracy, Vinča – Belo brdo.

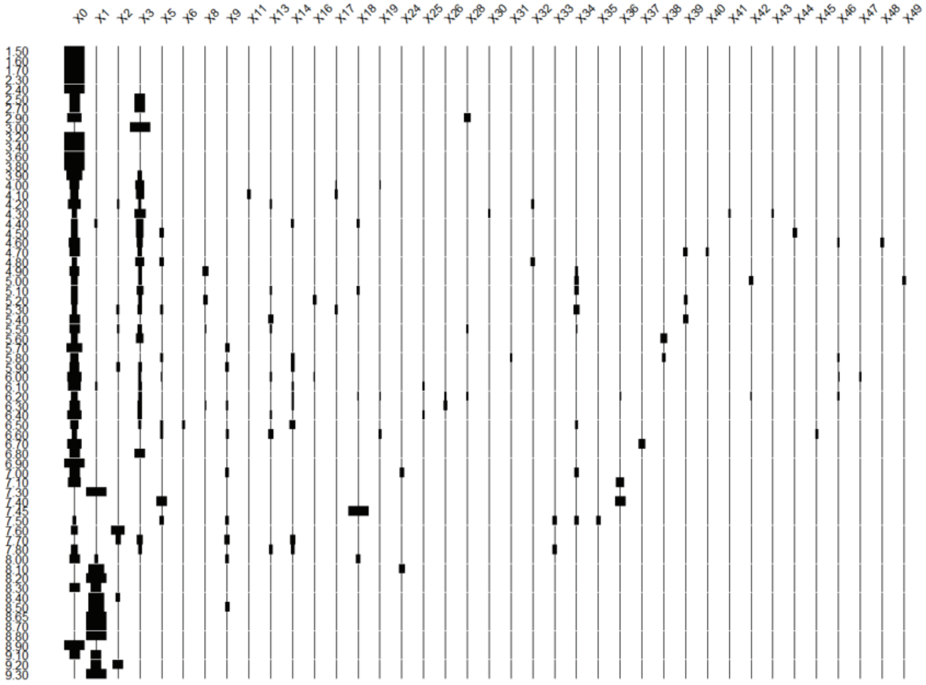

Figure 5.11. The battleship plot for the first degree of time-averaging based on the true stratigraphic sequence of anthropomorphic figurine types at Vinča – Belo brdo.

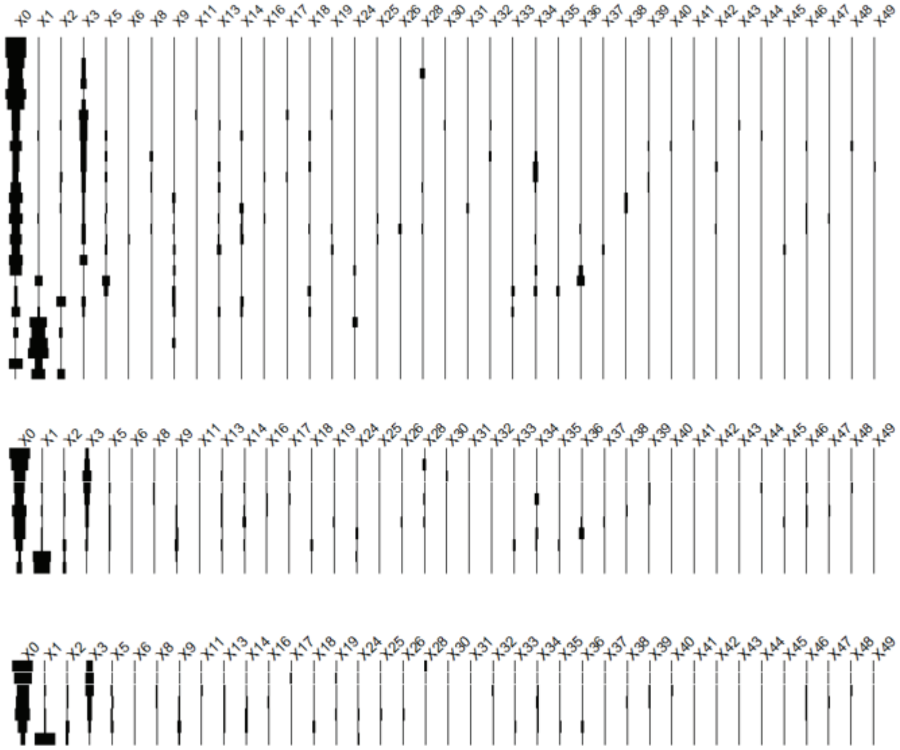

Figure 5.12. The battleship plot for the second, third and fourth (from top to bottom panel) degree of artificial time-averaging based on the true stratigraphic sequence of anthropomorphic figurine types at Vinča – Belo brdo.

5.9. THE NUMBER OF ATTRIBUTES AND UNIMODALITY

I now return to Madsen's (2020) hypothesis, that the number of attributes used to construct types is related to the unimodality in such a way that the increase in the number of attributes also increases the unimodality. In this section I am moving deeper, from the level of types and assemblages to the level of attributes and types. I will be looking at the change of frequencies of types in assemblages, but in this case the types will be paradigmatically constructed (see Dunnell 1971; O'Brien & Lyman 2000) from attributes, and the cultural transmission will be modeled at the attribute scale. Attributes will be transmitted independently of each other, but I will still track the frequency of types by constructing them as combinations of attribute variants.

We can already anticipate that Madsen's hypothesis will be supported, based on the results of the experiments presented earlier in this chapter, which suggest that mutation rate is an important predictor of unimodality (cf. Table 5.4). If each attribute is transmitted independently (in the neutral transmission mode), and if each attribute has the same mutation rate, then the compound mutation rate for the types constructed paradigmatically from these attributes will have a greater mutation rate than types based on single attributes[31], and therefore by implication, the unimodality of the temporal sequence of assemblages should be higher.

In order to explicitly test this hypothesis, I conducted a new experiment (*Experiment 5.5*) where types/variants are defined on the basis of a single attribute in contrast to three, six and twelve attributes. In each scenario, the population size (N = 100), the mutation rate (μ = 0.001), the average item use-life (L = 2), initial diversity (D = 10), the simulation run duration (t = 1000), and the degree of time-averaging (20 iterations) are the same for each attribute. This means that there are as many transmission chains as there are attributes, but attributes are not analyzed separately, they are combined into types and the frequency of types created in such way is counted in each assemblage in the sequence. For each scenario, the experiment is repeated a thousand times, and the S1 coefficient is calculated for each run. If Madsen's hypothesis is true, we should see an increase in the mean S1 value as we move from the one-attribute scenario to the multiple-attribute scenario.

The results partially support this hypothesis (Figure 5.13). The mean S1 is indeed greater when the number of attributes is greater than one. It is interesting to note that the seriation accuracy also increases with the increasing number of attributes used to define the types. However, the situation is more complicated than a simple monotonic positive correlation, as the average unimodality decreases with the increasing number of attributes used to define a type. More research is needed to systematically explore this issue, but I would speculate that this effect is due to the large number of attribute combinations which are possible with higher attribute numbers, and the possibility that some of their combinations will fluctuate at low frequencies in the sequence, thus violating the principle of unimodality.

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[31] It will be higher than the simple combination of individual attribute mutation rates, as the combination of the already existing attribute values will produce novel types even in the absence of the novel attribute values.

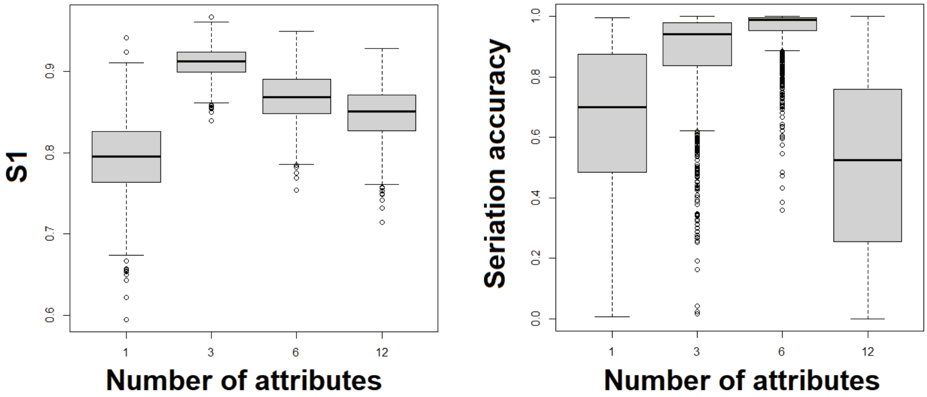

Figure 5.13. Left panel: The distribution of the S1 of the true sequences for types paradigmatically defined with increasing number of attributes. Right panel: The distribution of seriation accuracy sequences for types paradigmatically defined with increasing number of attributes; Experiment 5.5.

5.10. THE TEMPORAL DISTRIBUTIONS OF ARCHAEOLOGICAL CULTURES

5.10.1. The unimodality of archaeological cultures

Manning et al. (2014) discovered an interesting pattern when they studied the temporal distributions of archaeological cultures from the Neolithic period in Europe. The temporal distribution of an archaeological culture, or the intensity of an archaeological culture in Manning's et al. (2014) terms, refers to the summed probability distribution (SPD) curve[32] based on the calibrated radiocarbon dates assigned to a particular culture. For example, if all available calibrated probability distributions of the radiocarbon dates, based on the samples which are identified as belonging to the LBK culture, are summed the resulting curve would measure the intensity of the LBK culture in time. The curve would represent a proxy for the frequency of LBK artifacts or sites for different periods of time. When Manning et al. generated SPDs for 22 archaeological cultures, the shape of the SPD for each individual culture was very similar to the normal distribution curve (Manning et al. 2014: Figures 5-6). The intensity of a culture would gradually increase in time, reach the maximum, and then slowly decrease:

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[32] The construction and exploration of SPD curves is a popular method used to reconstruct and analyze population dynamics in archaeological demography (for general reviews see Crema & Bevan 2021; Williams 2012).

> *"Finally, it is worth pointing out that the characteristic normal distribution we have identified bears a striking resemblance to the so-called 'battleship curves' produced when frequency seriations are carried out on individual artefact types that are chronologically sensitive. When cultures are taken as entities they seem to mirror this effect. In essence, the number of dated events that archaeologists are prepared to label, for example as Horgen or Michelsberg, starts small, increases to a peak and then declines again. The pattern could arise because of the waxing and waning popularity of temporally correlated styles across a geographical region. Another possibility, supported by demographic proxies in some cases (Shennan et al. 2013), is that they reflect fluctuations in local populations; at some periods there are simply more people in the region, so the number of dated events characterised by the styles of the period is also bound to be greater. Of course, these two possibilities are not mutually exclusive, and in some cases it could be that new cultural innovations themselves result in periods of population increase. These questions remain open for subsequent analysis."*
>
> *(Manning et al. 2014: 1078)*

Therefore, one potential explanation for this phenomenon is demographic, and the pattern itself was anticipated by Shennan. According to Shennan (2000; 2013), the fluctuations in population size would have implications for the temporal variability of material culture. The population bottlenecks would create drift-like patterns in the domain of material culture. For example, the decrease in population size would also lead to the decrease of cultural diversity (e.g. diversity of pottery types). Variants that were rare before the bottleneck may become dominant afterwards simply by chance, when the population starts to grow again. This might be perceived as the end of one archaeological culture and the beginning of a new one.

In this section, I will explore the potential explanation for this phenomenon which excludes population dynamics (i.e. it assumes no changes in the population size). I will show that the pattern revealed by Manning et al. (2014) can also be predicted as a consequence of applying the traditional culture-historical principles of the construction of archaeological cultures to the variability of material culture generated by the simple neutral model of cultural transmission in space and time.

5.10.2. Simulating the temporal distribution of an archaeological culture (Experiment 5.6)

Let us run the low interaction neutral model simulation (with modeled space as in Chapter 4) with the following setup for 3000 iterations: population size, 100 (the number of items/artifacts); probability of inter-community interaction, 0.1; mutation rate, 0.001; average item use-life, 2 iterations; all cells start with the same assemblage with 30 types sampled with equal probability. In the next step, we will generate archaeological assemblages for each cell for every 100-year interval by aggregating the individual iteration assemblages.

How do we define the archaeological cultures based on the simulated assemblages? In the traditional culture-historical approach, archaeological cultures are usually defined - or “discovered” - in the following way (*cf.* Ford 1954b). In a region that has not been explored archaeologically, an archaeologist starts to excavate a site. Even though the choice of a site to be excavated first is usually a product of particular historical contingencies and idiosyncratic reasons from the perspective of our imagined archaeologist, this selection can be considered as random for all practical purposes in most situations. The formal characteristics of the material culture discovered at this site are used to define the new archeological culture - let us call it the X culture. As more sites are excavated in this region, they will be assigned to the X culture if they are sufficiently similar to the original type site, or they will be assigned to some other newly defined archaeological culture.

Now let us try to emulate this traditional algorithm for the definition of archaeological cultures with the simulated data. I will randomly choose a cell from the simulation grid (say 116), and I will randomly choose a temporal interval (say 1901-2000) of the assemblage. This will be equivalent to the fortuitously discovered type site of the archaeological culture X. I will call this cell the type site cell for the culture X. Next, I will calculate the Jaccard similarity coefficient[33] between the type site cell assemblage and all other cell assemblages within the same temporal interval, as well as between the type site cell assemblage and each cell assemblage from all the earlier and later temporal intervals (including the assemblages from different times coming the same type cell[34]). Next, I will determine the cut-off value for the Jaccard similarity coefficient – I will set it at 0.5. I cannot be certain what the right cut-off value

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[33] It seems to me that the Jaccard coefficient better reflects the subjective process of similarity evaluation, as in most cases the archaeologists have relied more on the presence of key types rather than their frequency, for the cultural assignment of the assemblage.

[34] We should imagine that the sites from the same cell but different times are not located in exactly the same spot within a cell.

is, because in the traditional approach, the similarities are based upon subjective judgments, and therefore the result will be qualitatively similar for the range of reasonably chosen cut-off values. The cells which have a similarity coefficient higher than the cut-off will be classified as belonging to the same culture X as the type cell. In the final step, I will count the number of cells belonging to our hypothetical culture on the basis of the randomly selected type cell assemblage for each temporal interval, and plot this count in time. Given the arbitrariness of the Jaccard similarity coefficient cut-off value, I will also track the mean value of Jaccard similarity between the type site cell assemblage and all other cell assemblages from all temporal intervals. So, the intensity of the simulated culture X will be tracked in two ways: 1) as the frequency of cells in each time interval which have a value of the Jaccard similarity coefficient greater than 0.5, and 2) as the mean value of the Jaccard similarity between the type site cell and all other cells in the different time intervals.

As apparent from the graphs (Figure 5.14), the resulting pattern is qualitatively the same as the one observed by Manning et al. (2014) in their empirical study. The intensity of the simulated culture increases as one approaches the temporal position of the type cell assemblage (iteration 1901-2000, or temporal interval 11), reaches its maximum in the temporal interval from which the type cell assemblage comes from, and decreases afterwards.

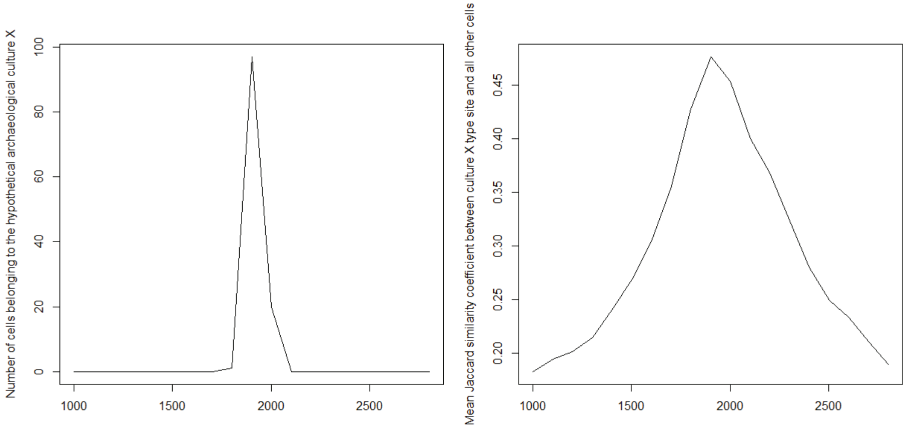

Figure 5.14. Results of Experiment 5.6. Left: the intensity of the simulated archaeological culture X in time, the y axis showing the number of cells in each 100 years-long temporal interval belonging to archaeological culture X (the frequency of cells in each time interval which have a value of the Jaccard similarity between themselves and the culture X type cell coefficient greater than 0.5); Right: the y axis showing the mean value of the Jaccard similarity coefficient to the X culture type cell in a 100-years-long temporal interval.

In addition to temporal clustering, the traditional algorithm for the discovery and construction of archaeological cultures will also produce spatially coherent entities. My emulation of this algorithm does the same. The plots in Figure 5.15 show the spatial position of the cells which have similarity values to the type site cell above the similarity threshold of 0.5 in the time interval to which the archaeological culture X type site belongs (iterations 1901–2000), and the intervals right before (1801–1900) and after this one (2101–2200). The plots in Figure 5.16 show the entirety of the grid where each cell is color-coded in respect to its Jaccard similarity value to the focal (type) cell in the time interval to which the focal cell belongs and the ones immediately before and after. The cells which are typologically similar are clustered in space as well, so these plots demonstrate the spatial coherence of archaeological cultures constructed in this way.

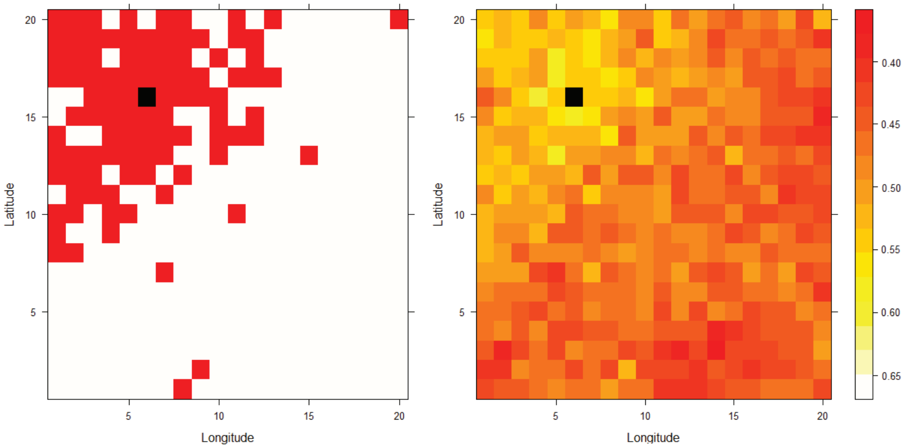

Figure 5.15. Results of Experiment 5.6. Left: the spatial position of cells (red) which have Jaccard similarity coefficient to the X culture type site cell (black) greater than 0.5 in the 1901-2000 iteration time interval; Right: The spatial distribution of Jaccard similarity values to the X culture type site cell (black) in the 1901-2000 iteration time interval.

This exercise shows how the continuous flow of culture, where no "natural" breaks exist, can be forced into discrete temporal (and spatial) entities by applying the traditional algorithm for the definition of archaeological cultures. The temporal center of such a distribution is a product of chance, as the conditions for assemblages to be associated with an archaeological culture depend on the characteristics of the site assemblage that happened to be discovered first.

It is important to emphasize that I do not argue that there are no true typological discontinuities and “natural” breaks in the temporal distributions of style in the archaeological record, or that the temporal distributions of cultures do not reflect changes in population size. My only intention with this exercise was to show that it is not necessary to assume such things in order to explain the chronological patterns of culture that we observe in the archaeological record. It is an empirical problem to determine in each particular case if the archaeological cultures as temporal entities are simply mirages emerging from the combination of the traditional archaeological culture construction algorithm applied to the continuous flow of style (e.g. resulting from unbiased cultural transmission), or if they represent true discontinuities in the typological space or reflect the underlying population dynamics.

5.11. DISCUSSION

In this chapter I tested the hypotheses about the unimodality of temporal sequences and explored the patterns in time generated by cultural transmission. First, I assumed that the neutral model is a good representation of the reality behind the generation of the variability of material culture through time. Under this assumption, I explored how different factors of transmission in combination with time-averaging influence the temporal patterns of material culture variability in the archaeological record. The simulation results clearly show that time-averaging is a major factor behind unimodality. It is encouraging to see that this prediction is also supported by the empirical case studies. The battleship pattern is intrinsic to the process of unbiased cultural transmission, but it does not create perfect unimodal patterns. The lack of perfect unimodality is not the consequence of the sampling size or noise in the data generated by various processes, but intrinsic to the neutral transmission process. The results show that low unimodality usually implies low seriation accuracy, but the opposite does not apply. If the unimodality of the original sequence is high, this does not necessarily imply that the seriation will be accurate. Likewise, if the reconstructed sequence has a high degree of unimodality this also does not mean that it is necessarily correct. On the other hand, sequences with low unimodality are almost certainly inaccurate. Therefore, unimodality seems to be the necessary, but not the sufficient condition for accurate seriation. However, these conclusions need to be qualified in two ways. First, these conclusions are limited to the CA as the seriation technique. Second, it is possible that some of the highly unimodal sequences for which the correct order was not reconstructed are generated by unrealistic parameter combinations.

Predictions of the simulations regarding the increase of unimodality due to time-averaging were empirically tested and found to be supported by the evidence, giving additional support for the basic theoretical premise of using the neutral model of cultural transmission as a potential explanation for the commonly observed temporal patterns in the archaeological record. This conclusion is further strengthened by the demonstration that other phenomena, such as the empirically discovered pattern pertaining to the temporal distributions of archaeological cultures, can also be accounted for by the neutral model in combination with the traditional logic of culture-historical archaeology.

However, we have also seen in this chapter that neutral transmission is a sufficient, but not necessary condition for unimodality. Other models of transmission, such as conformist or anti-conformist transmission, may also produce approximately unimodal sequences. As a matter of fact, if we are to look for the perfect unimodality, we are more likely to find it with the anti-conformist than the neutral model of transmission, as the average degree of unimodality is actually higher in the sequences produced by the anti-conformist model. So, when we use the neutral model as an explanation or a general model for stylistic patterns in time, we should be aware that we are using it as an approximation.

The results of the simulations also show that Madsen's (2020) hypothesis, that the number of attributes used to construct types via paradigmatic classification contributes to the unimodality of sequences of assemblages, is partially supported. Unimodality increases when more than one attribute is used to construct types, but it seems to decrease afterwards when the number of attributes increases furthers. Whether this phenomenon is the consequence of the model assumptions (e.g. the assumption that each attribute of an artifact is copied independently) remains to be explored in the future.

What are the practical implications of these results? If unimodality is a necessary condition for accurate seriation, then it might be a criterion to filter out seriation solutions with low unimodality as being bad candidates. Unfortunately, the high unimodality of a sequence does not guarantee that the particular seriation solution is accurate. We could perhaps do even more – we could artificially induce time-averaging, as I did in this chapter by merging stratigraphically adjacent assemblages. We would be sacrificing precision for accuracy, but this may be justified, especially when individual assemblages are too small for frequency seriation.

This approach would be particularly useful for seriating the grave goods assemblages. For example, if the individual graves usually have one or two ceramic vessels as grave goods, it will be difficult for the seriation method to capture the precise chronological sequence due to low assemblage size. If we aggregate assemblages from individual graves we will increase the assemblage size, but at the cost of decreasing the temporal resolution by time averaging. The reader has probably noticed that in order to perform artificial time-averaging we must know the relative chronology of individual graves, which is exactly what we wish to reconstruct. This is apparently not possible in the case of non-stratified graves. But if there are specific hypotheses about the spatio-temporal structure of a cemetery (e.g. which graves come from the same phase), this approach can be used at least to eliminate some of them, i.e. those with low unimodality.

Experiment 5.4, in which other models of cultural transmission such as the conformist and anti-conformist models were explored, revealed that although approximately unimodal sequences can be generated by any of these models, their signatures in the overall pattern of type duration distributions are different. These differences may have important consequences for the efforts to reconstruct the models of cultural transmission based on the empirical data. The distributions of the relative measures of variability of type durations, as well as their maximum values, are almost non-overlapping between the models, which suggests that these aspects of the data can be harnessed to the methods which aim to discriminate between different models.

6

PATTERNS IN SPACE AND TIME

CHAPTER 6

PATTERNS IN SPACE AND TIME

6.1. INTRODUCTION

In the previous two chapters I looked at the spatial and temporal effects of cultural transmission separately. In practice, temporal variation can be studied in isolation from spatial variation by looking at the stratified assemblages from a single site. But it is usually not possible to exercise control for the temporal dimension at the regional level in the same way, for at least two reasons. First, there is no ideal contemporaneity in the real world – it would be very difficult, if not impossible, to find sites and assemblages in a region that were occupied in the exact same temporal interval. Second, even if such situation existed, most of the time we would not be able to know that this was the case due to uncertainties related to conventional absolute dating methods such as radiocarbon dating (Bevan & Crema 2021). Therefore, most of the time, most of the assemblages that we analyze will more or less overlap temporally, except for the assemblages coming from the very extremes of the temporal interval, provided that the duration of the temporal interval under study (the temporal window) is longer than the duration of time-averaging of a typical assemblage (Figure 6.1).

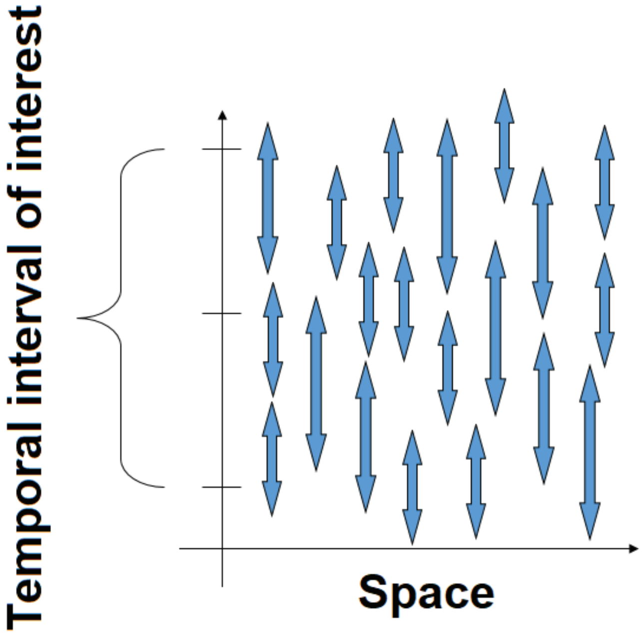

Figure 6.1. The variable durations and temporal spans of different assemblages. Each arrow represents a single assemblage, where the arrow length corresponds to the assemblage duration (temporal span of time-averaging).

For this reason, in this chapter I look at assemblages that reflect both spatial and temporal variations. This is a realistic situation faced by most archaeologists when they analyze the formal variability of assemblages coming from different sites in a certain region over a certain temporal interval – e.g. if one studies the variability of anthropomorphic figurine assemblages from the Late Neolithic in the Central Balkans which lasted between 5300 and 4500 BC. In the first part of this chapter, I look at simulated data from this perspective. The aim is to identify which aspects of the transmission process and the scale of analysis determine whether space or time will structure the formal variability of assemblages. In the second part of the chapter, I use the same analytical instruments to look at the empirical archaeological data from different regional, temporal, and cultural contexts, to illustrate that the patterns found in the simulated data can be identified in the real-world data.

6.2. THE SIMULATED PATTERNS

6.2.1. The general setup of the simulation experiments and data collection

For the purposes of this chapter, I will only explore the neutral model of cultural transmission as a baseline model. Again, we can interpret the spatial and temporal scale in the same way as in the previous chapter – the dimensions of each cell as 10x10km squares, and one simulation iteration as one year. In each experiment presented in this chapter, each simulation was run for 1000 iterations, corresponding to one thousand years of cultural evolution. Two sets of parameters will be explored: the observational and transmission parameters.

The width of the temporal window, the degree of time-averaging and the spatial scale are the observational parameters that will be varied in order to explore their influence on the patterns. Therefore, the simulated data will be collected in different spatial and temporal windows, as well as with different levels of time-averaging. The temporal window refers to the interval of iterations from which the assemblages may be formed by time-averaging. It is equivalent to the temporal frame of study (e.g. one may study assemblages from the period between 5400 and 4900 BC). For example, if I set the temporal window to between 500 and 1000 iterations, the cell assemblages used in the analysis can only consist of assemblages coming from within these boundaries. The degree of time-averaging is simply the number of single-iteration assemblages which are aggregated to create a cell assemblage. In the previous chapter, all assemblages from all cells had exactly the same temporal boundaries (in terms of the single-iteration assemblages that were aggregated), so I could completely control the temporal dimension and look at perfectly synchronous assemblages. In this chapter, the positions of the mid-points of assemblage temporal intervals will be randomly sampled for each cell within the temporal interval, with the constraint that the entire assemblage duration interval must be within the temporal window.

The width of the assemblage duration interval reflects the degree of time-averaging and it will be the same for all cell assemblages. It is not realistic for all assemblages to have equal durations, as the assemblage durations will inevitably vary in practice; but this kind of variation is not in the focus of this chapter, so I proceed with making this simplification. Therefore, the data will consist of cell assemblages which may or may not overlap in their temporal duration (the degree of overlap will depend on the degree of time-averaging and the width of the temporal window) as in Figure 6.1, with the difference that all cell assemblages will have identical durations (i.e. equal arrow lengths in terms of Figure 6.1). For example, if the temporal window is set to between 500 and 1000 iterations, and if the degree of time averaging is set to 100 iterations, one cell assemblage may be formed by aggregating iterations from 500 to 599, another one may span iterations 513-612, a third one 580-679, a fourth, 745-844, and so on. Note that despite the temporal overlap, we can still talk about the sequence of assemblages in terms of their aggregation interval midpoints (or start- and endpoints). The width of the temporal window and the degree of time-averaging are determinants of the temporal scale of the analysis.

The shape of the hypothetical region is rectangular in order to have a clear spatial direction in the study region. The default is the 10x40 cells grid (400 cells), unless stated otherwise. The spatial scale can be easily manipulated by simply reducing the number of cells in the analysis or by making the simulated grid larger. For example, we can implement a computer simulation in the entire virtual space (e.g. including all of the cells in the virtual space), but we can then restrict the analysis only to an arbitrary subset of this space.

I will also vary the transmission parameters such as the frequency of inter-community interaction, mutation rate and population size. The spatial interaction is governed by the spatial interaction model introduced in Chapter 3, and we explore two interaction levels, as in the previous chapter: the high interaction ($m = 0.4$[35] and the low interaction ($m = 0.1$) scenarios. All cells start with the same initial assemblages (sampled from a uniform distribution of 10 variants), and the average use-life of items is 2 iterations (years). The default population size in each cell is 100, and the default mutation rate is set at 0.005 – these values are assumed as default unless stated otherwise.

6.2.2. *The outline of the experiments*

As stated above, the idea is to explore how changes in the observational and transmission parameters of the neutral model influence the patterns of simulated material culture in space and time. I have conducted eight computer simulation experiments in order to investigate this (Table 6.1). In the first two experiments (6.1 and 6.2), I explore the influence of the degree of interaction, which is a transmission parameter. Experiment 6.1 is a low interaction scenario, and Experiment 6.2 a high interaction scenario. In the next three experiments,

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[35] Unlike Chapter 4, where the high interaction scenarios had the degree of interaction set to 30%, in this chapter I set it to 40%, to increase the contrast between high and low interactions, and demonstrate the effects of this parameter more clearly.

I change the observational parameters, and the temporal and spatial scales, in order to demonstrate their effects. In Experiment 6.3, I increase the width of the temporal window to show how it can amplify the temporal patterning, whereas in Experiment 6.4, I increase the level of time-averaging to achieve the opposite effect. Experiment 6.5 explores the effects of changing the spatial scale of observation – in this experiment, the size of the grid is reduced relative to the "default" grid size of 10x40 cells used in this chapter. Next, I move on to investigate the influence of the remaining transmission parameters. In experiments 6.6, 6.7, and 6.8, I show how changes in population size, mutation rate and average object use-life, respectively, can increase or decrease the correlations between space, time, and typological variation.

The number of iterations in each simulation run is 1000, and each experiment is repeated 30 times (30 simulation runs per experiment). The mean, minimum, and maximum are reported for each parameter of interest. The results of typical experiment outcomes are presented graphically as illustrations. For each experiment I look at two sets of correlations. The first set are the correlations between the major dimensions of typological variability represented by the CA axes 1 and 2, on one side, and on the other, the major spatial and temporal dimensions, represented by the x coordinates of the cells (as this is the major direction of spatial variation) and the midpoints of the time-averaging intervals, respectively. The second set of correlations are (Mantel) correlations between distance matrices – between Brainerd-Robinson typological distances on one side, and the spatial and temporal distances, on the other.

Exp. Number	Width of the temporal window	Degree of time-averaging (the duration of assemblage accumulation)	Spatial scale (size of the grid)	Interaction	Mutation rate	Item population size	Use life
6.1	200	50	10x40	Low (0.1)	0.005	100	2
6.2	200	50	10x40	High (0.4)	0.005	100	2
6.3	500	50	10x40	Low (0.1)	0.005	100	2
6.4	500	200	10x40	Low (0.1)	0.005	100	2
6.5	200	50	4x8	Low (0.1)	0.005	100	2
6.6	200	50	10x40	High (0.4)	0.0001	100	2
6.7	200	50	10x40	High (0.4)	0.005	20	2
6.8	200	50	10x40	High (0.4)	0.005	100	30

Table 6.1. The setup of the simulation experiments in Chapter 6.

6.2.3. *The low interaction neutral model scenario – setting up the baseline for testing the effects of degrees of interaction (Experiment 6.1)*

First, we will look at the results of the low interaction scenario within the temporal window between 600 and 800 iterations after the start of the simulation. The width of the accumulation interval is 50 iterations, and we are looking at all of the 400 cells in the simulated space. When the CA axis 1 scores are plotted in space, the familiar typological cline emerges along the major spatial direction (Figure 6.2; Table 6.2). The mean absolute[36] correlation between the cell coordinates along the major spatial direction and their CA axis 1 scores is 0.96. The CA axis 2 also reflects space but in a more complicated way – as a gradient away from the regional center (Figure 6.2). When we look only at the shape of the assemblage point cloud in the CA space, we will see the arch (horseshoe) pattern (Figure 6.3), but the signal here is primarily spatial. The first two CA axes reflect spatial components of typological variation. Therefore, even though there are temporal differences between assemblages, at this temporal and spatial scale, with a given level of interaction, most of the typological variance between assemblages is spatial rather than temporal. The temporal component of variability is usually captured by the CA axis 3 which correlates with time (mean absolute r = 0.68, min = 0.17, max = 0.86) (Figure 6.4).

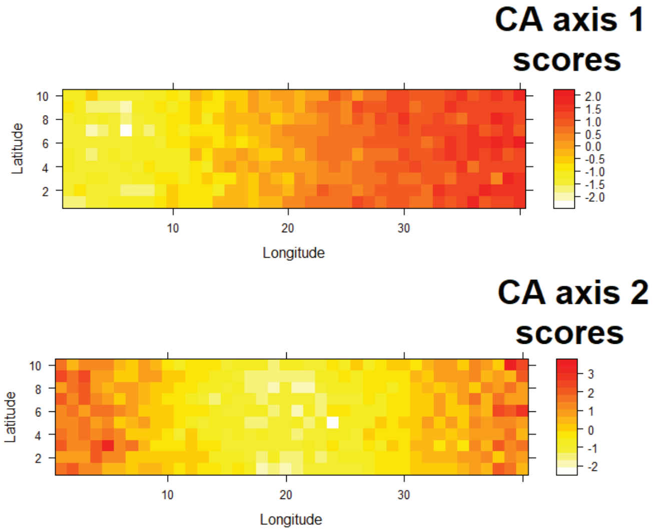

Figure 6.2. The plot of the CA axis 1 and CA axis 2 scores in space (based on a randomly chosen simulation run of Experiment 6.1).

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[36] The direction of the correlation is not important in this case as it is entirely contingent on the results of the CA analysis, and this particular aspect of the CA has no relevance for the interpretation.

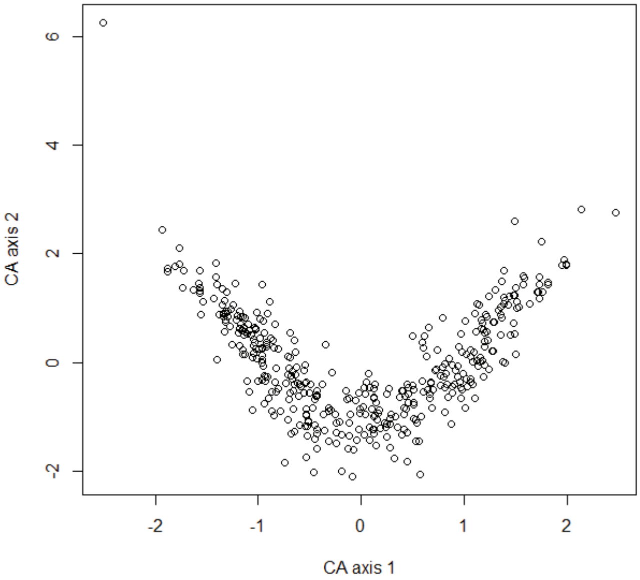


Figure 6.3. The configuration of cell assemblages in the typological space defined by the first two CA axes (based on a randomly chosen simulation run of Experiment 6.1).

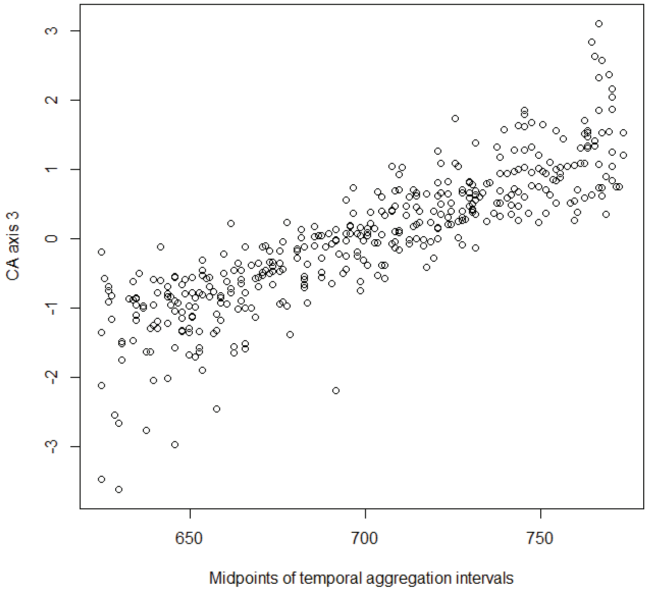


Figure 6.4. The correlation between the time and the CA axis 3 in Experiment 6.1.

This is also reflected in the Mantel correlation between typological, spatial and temporal distances. The mean correlation between spatial (Euclidean distances between cell coordinates) and typological distances (BR distances) is 0.5, whereas the mean correlation between temporal (Euclidean distances between midpoints of assemblage temporal spans) and typological distances is only 0.16 (Figure 6.5). It should be noted that the correlations between the summary typological dimensions (the CA axes) and space and time expressed as single variables (the major spatial direction and the midpoint of a temporal interval) are much higher than the direct correlations between distance matrices. This is so because correlations between matrices include all the noise of the raw inter-assemblage typological distances coming from the drift, as well as variation that is structured by space and time, whereas the CA axes capture the trends.

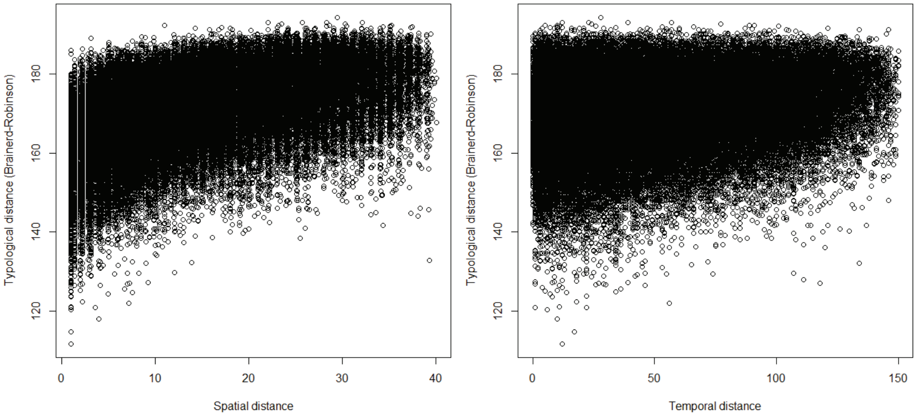
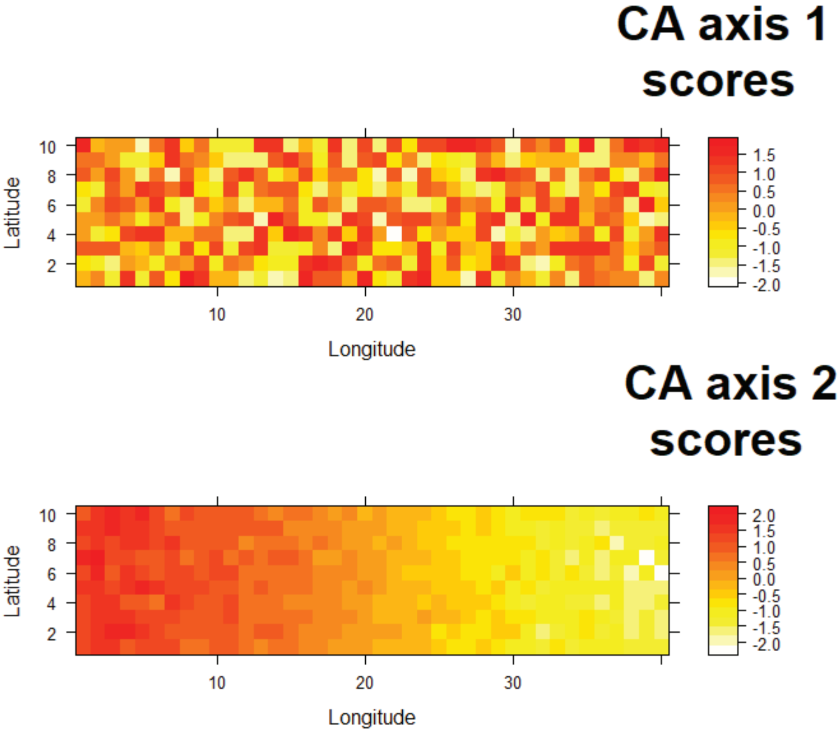


Figure 6.5. The correlation between typological (Brainerd-Robinson) distances, spatial distances (left) and temporal (right) distances (based on a randomly chosen simulation run of Experiment 6.1).

6.2.4. The high interaction neutral model scenario (Experiment 6.2)

But let us now look at the same spatio-temporal setup for the high interaction scenario. The temporal window is again between 600 and 800 iterations, and the width of the aggregation interval is 50 iterations. When we plot the CA axis 1 scores in space, no particular pattern can be observed – no spatial clines or gradients of typological variability (Figure 6.6). This is confirmed by the low of correlation between the major spatial direction and the CA axis 1 scores (mean absolute r = 0.07) and a relatively low correlation between spatial and typological distances (mean r = 0.46). In this case, it is time that correlates almost perfectly with the CA axis 1 (mean absolute r = 0.99, Figure 6.7). The mean correlation between temporal and typological distances is 0.7 (Figure 6.8).

The major dimension of inter-assemblage typological variability reflects time rather than space. This does not mean that space is not reflected in typological variation. The major spatial direction is almost perfectly correlated with CA axis 2 (mean absolute r = 0.96, min = 0.92, max = 0.98; Figure 6.9), and the mean correlation between spatial and typological BR distances is 0.46 (Figure 6.9). Therefore, in the high interaction scenario, typological variability between assemblages in mostly structured by the temporal dimension (Table 6.2). In other words, the sequence of cell assemblages along the CA axis 1 is the chronological seriation sequence, whereas the sequence on the CA axis 2 reflects the "East"-to-"West" spatial cline. It is interesting to note that, even though the CA axis 1 is almost perfectly correlated with time, the pattern of assemblages in the CA space defined by the first two axes does not resemble the arch shape characteristic of the chronological signal (Figure 6.10)



CA axis 1 scores

CA axis 2 scores

Figure 6.6. The plot of the CA axis 1 and CA axis 2 scores in space (based on a randomly chosen simulation run of Experiment 6.2).

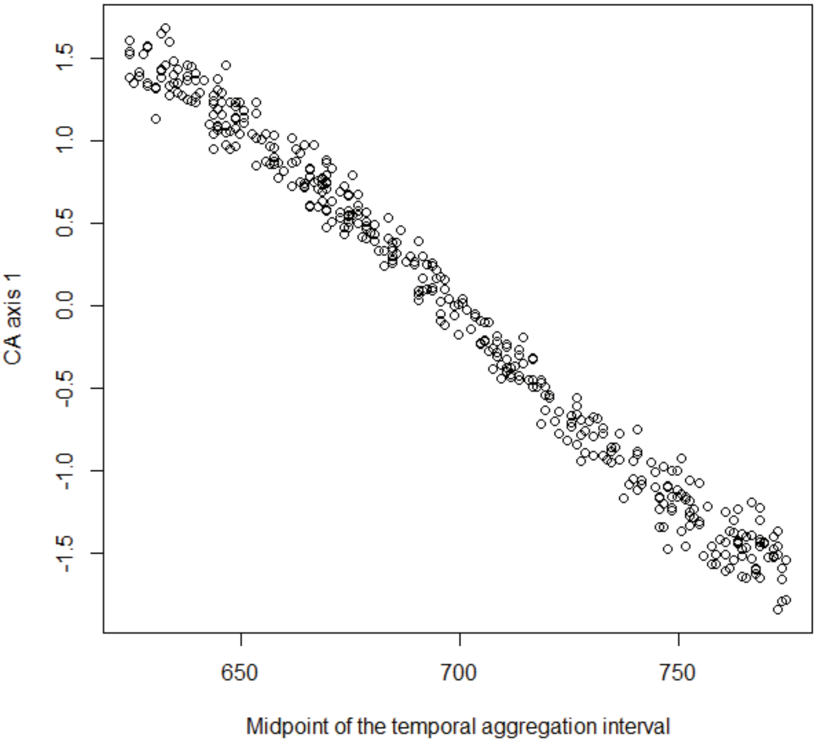


Figure 6.7. The correlation between time and the major typological dimension (CA axis 1) (based on a randomly chosen simulation run of Experiment 6.2).

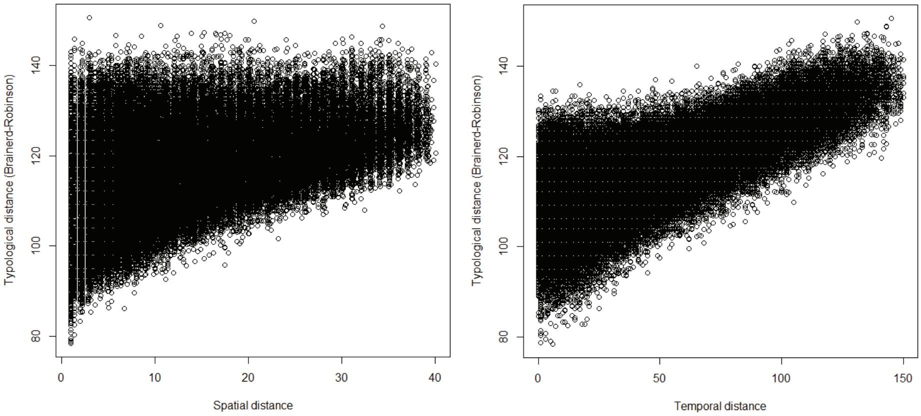


Figure 6.8. The correlation between typological (Brainerd-Robinson) distances, spatial distances (left) and temporal (right) distances (based on a randomly chosen simulation run of Experiment 6.2).

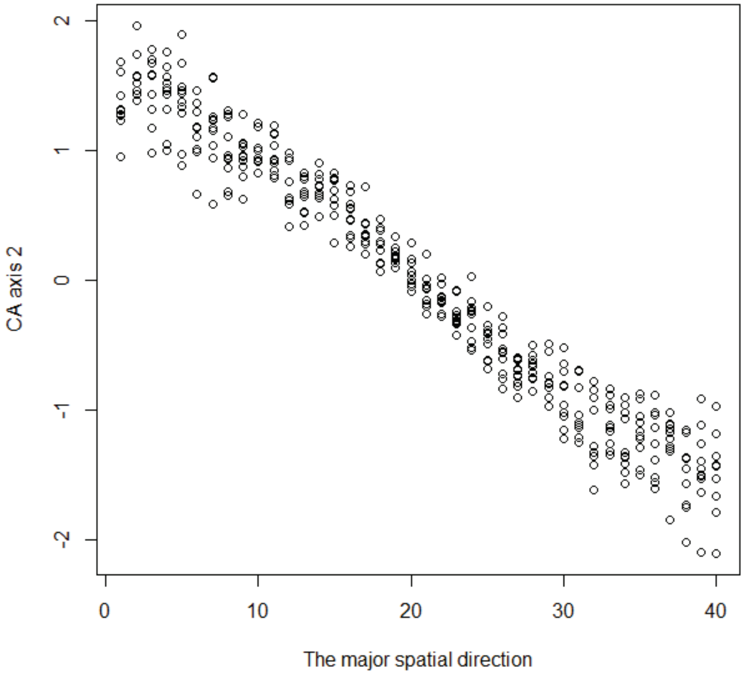


Figure 6.9. The correlation between the major spatial direction and the CA axis 2 (based on a randomly chosen simulation run of Experiment 6.2).

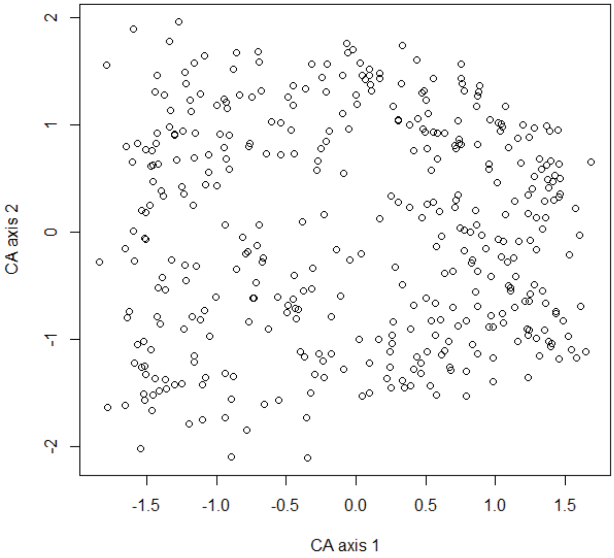


Figure 6.10. The configuration of cell assemblages in the typological space defined by the first two CA axes (based on a randomly chosen simulation run of Experiment 6.2).

6.2.5. *Changing the temporal scale by increasing the width of the temporal window of analysis (Experiment 6.3)*

Let us now explore how changing one aspect of the temporal scale, the width of the temporal window of analysis, can change the patterns. In this experiment, the width of the temporal scale is increased to include iterations from 500 to 1000 iterations from the same simulation reported in Experiment 6.1 (see above). To remind the reader, this was the low interaction scenario where the major typological dimension was strongly correlated with the major spatial dimension, when we looked at the time window spanning iterations 600-800. When we expand the time window, the pattern changes (Table 6.2). The CA axis 1 scores, which reflect the typological dimension, do not correlate strongly with the major spatial direction any more (mean absolute r = 0.09), but with time (mean absolute r = 0.96). Therefore, when the size of temporal window was increased, with everything else being the same as in Experiment 6.1, the temporal dimension became more important than the spatial dimension. The space is still significantly reflected in the typological variation, as the CA axis 2 which explains only slightly less typological variance than the CA axis 1 correlates with the major spatial direction (mean absolute r = 0.87, min = 0.52, max = 0.93).

The correlations between distance matrices also reflect this. The mean correlation between the BR distances with temporal distances is 0.44, whereas the mean correlation between typological distances and spatial distances is 0.29 (Figure 6.11).

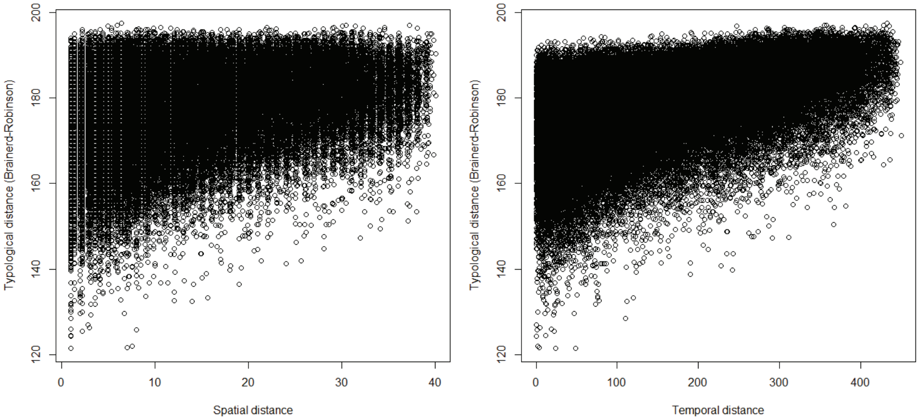


Figure 6.11. The correlation between typological (Brainerd-Robinson) distances, spatial distances (left) and temporal (right) distances (based on a randomly chosen simulation run of Experiment 6.3).

6.2.6. *Changing the temporal scale by increasing the degree of time-averaging (Experiment 6.4)*

The pattern from the previous experiment can easily be reversed to the original pattern from Experiment 6.1, where space was the dominant structuring factor. This can be achieved by changing the other aspect of the time scale – by increasing the aggregation interval. In this experiment, the width of the temporal window is the same as in Experiment 6.3 (500-1000 iterations), the basic simulation setup is also the same (the low interaction scenario), but the width of the aggregation interval is 200 iterations instead of 50. In this experiment, we are assuming that we have a lower temporal resolution and that the assemblages have accumulated over a longer time period, i.e. to include sites or site-phases that lasted 200 rather than 50 years.

When the CA axis 1 scores are plotted in space, the typological gradient along the major spatial direction emerges again (Figure 6.12) and the mean absolute value of the correlation is 0.97. This result makes perfect sense – the increased time-averaging leads to increased overlap between assemblages, which reduces the temporal variation. Again, this does not mean that the temporal signal is lost, as there is a strong correlation between the CA axis 2 with time (mean absolute r = 0.96, min = 0.86, max = 0.98). This is also reflected in the Mantel correlation coefficients between distance matrices. The mean correlation between the typological and spatial distances is 0.62, and between typological and temporal distances 0.43 (Figure 6.13).

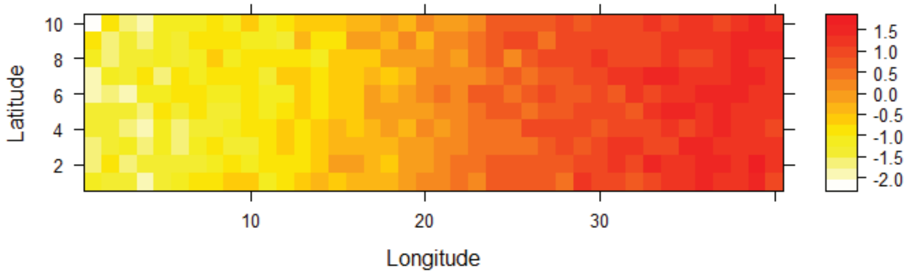


Figure 6.12. The plot of the CA axis 1 scores in space (based on a randomly chosen simulation run of Experiment 6.4).

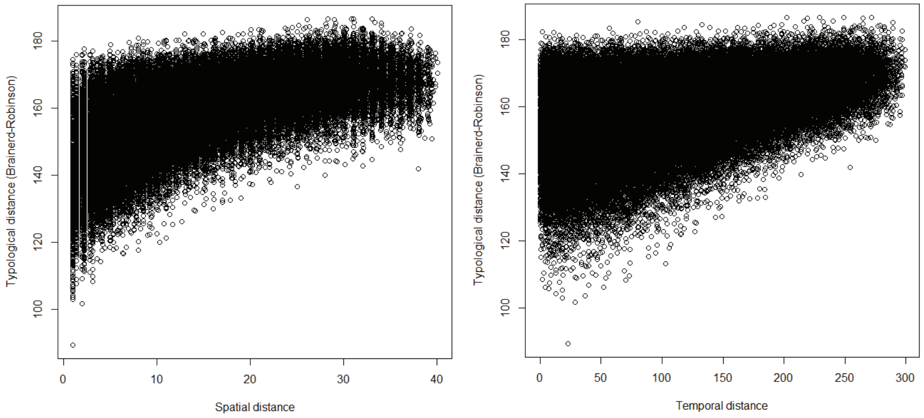


Figure 6.13. The correlation between typological (Brainerd-Robinson) distances, spatial distances (left) and temporal (right) distances (based on a randomly chosen simulation run of Experiment 6.4).

6.2.7. The effect of the spatial scale (Experiment 6.5)

The spatial scale can also influence the patterns of correlation between space, time and typology. In this experiment we start with the results of the low interaction scenario with data accumulated in 50 iteration intervals within the 200 iteration wide temporal window (as in Experiment 6.1). The resulting pattern is the typological gradient following the major spatial direction of the study area. But if we reduce the spatial scale and perform the CA only on the section of the study area, and plot the CA axis 1 scores in space, the spatial gradient becomes less clear (Figure 6.14; Table 6.2). This is so because the CA axis 1 is now more correlated with time (mean absolute r = 0.83) than space (mean absolute r = 0.3). Again, this is to be expected, as the reduced spatial variation brings to the front temporal differences between the cell assemblages. The mean correlation between the typological and spatial distances is 0.33, and between typological and temporal distances is 0.47 (Figure 6.15).

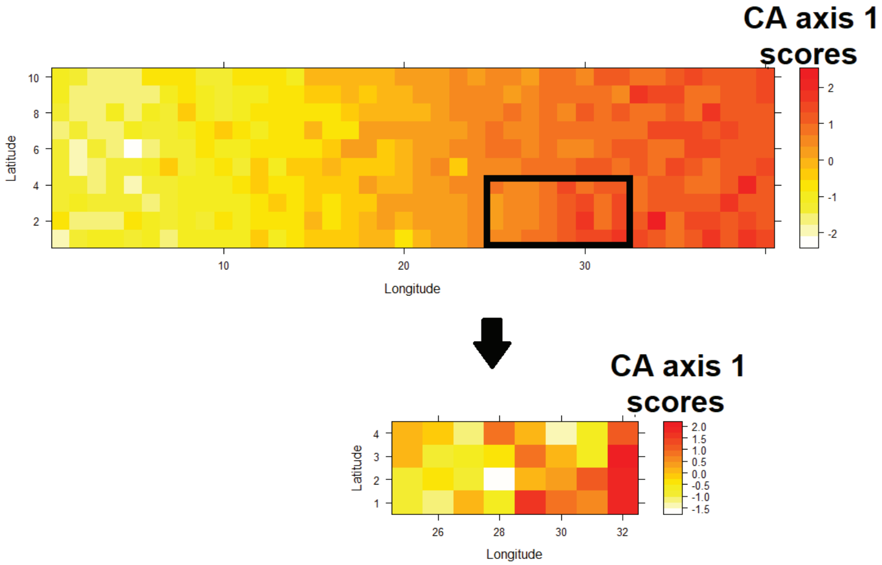


Figure 6.14. Above: the plot of the CA axis 1 scores in space when the CA is performed on all cell assemblages; below: the plot of the CA axis 1 scores based on the CA performed only on the cells belonging to the subspace of the original simulated grid (based on a randomly chosen simulation run of Experiment 6.5).

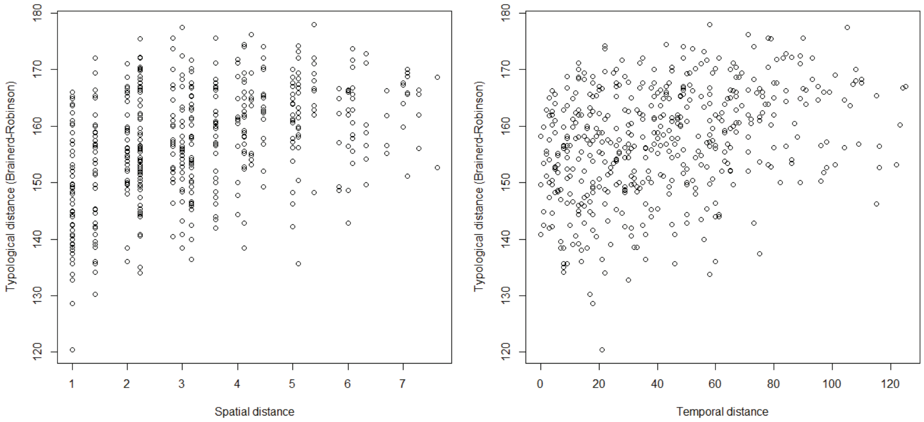


Figure 6.15. The correlation between typological (Brainerd-Robinson) distances, spatial distances (left) and temporal (right) distances (based on a randomly chosen simulation run of Experiment 6.5).

6.2.8. The effect of mutation rate (Experiment 6.6)

In the experiments presented so far, I have explored how the observational parameters combined with only one transmission parameter – the probability of intercommunity interaction – produced different patterns. In this experiment and in the experiments that follow, I will focus on transmission parameters such as the mutation rate, population size, and the average use-life. The hypothesis is that *the change in the parameters that increase or decrease the rate of cultural evolution, i.e. the change of variant frequencies in time, will also increase or decrease the importance of the temporal dimension in relation to the spatial dimensions in structuring the variability of material culture*.

In this experiment, I demonstrate how the decrease in the mutation rate weakens the temporal structuring that we observed in Experiment 6.2, which will serve as a comparison baseline for this experiment. The setup of the experiment is the same as for Experiment 6.2 (the high interaction scenario), with the difference that the mutation rate is reduced from 0.005 to 0.0001, i.e. it is lower by an order of magnitude. The results show that the space becomes more important when the mutation rate is low, as the correlation between the CA axis 1 and the major spatial direction increases substantially (mean absolute r = 0.23) compared to Experiment 2, where the corresponding value was 0.07. The mean absolute correlation between the CA axis 1 and time is 0.71, which is lower than in Experiment 6.2, where it was 0.99 (Figure 6.18, Table 6.2). The mean correlation coefficient between the typological distances and spatial distances is 0.17, whereas the mean correlation is 0.20 for the correlation between the typological and temporal distances, the former being higher, and the latter lower, in relation to the corresponding values in Experiment 2 (Figures 6.16, 6.18-19; Table 6.2).

As predicted, the decrease of the mutation rate also decreased the importance of the temporal dimension in the structuring of the material culture, and so in this case, the main axis of typological variability reflects both time and space (which are not correlated), even though the degree of interaction is high.

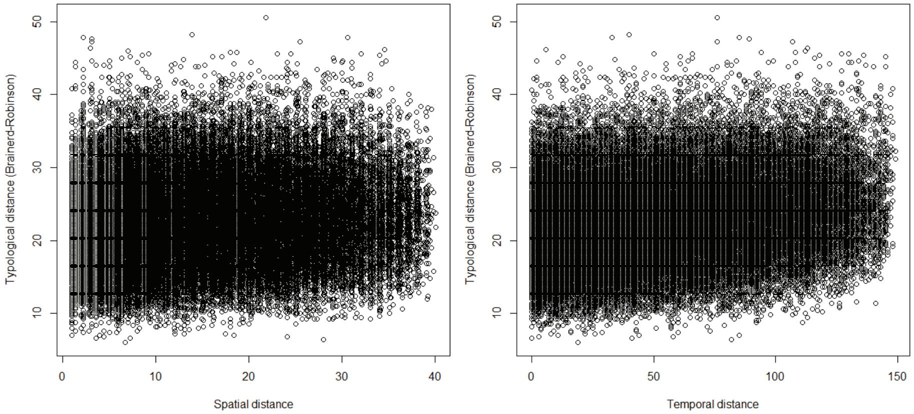


Figure 6.16. The correlation between typological (Brainerd-Robinson) distances, spatial distances (left) and temporal (right) distances (based on a randomly chosen simulation run of Experiment 6.6).

6.2.9. The effect of population size (Experiment 6.7)

In order to demonstrate the effect of the population size, and to see if it matches the predictions of the hypothesis stated above, I start from the setup of Experiment 6.2 (the high interaction scenario),with the difference that the item population size in this experiment is reduced from 100 to 20.

The results show that the mean absolute correlation between CA axis 1 and the major spatial direction is 0.15, and the mean absolute correlation between CA axis 1 and the time dimension is 0.96. The mean correlation between spatial and typological distances is 0.37, and the mean correlation between temporal and typological distances is 0.54 (Figure 6.17).

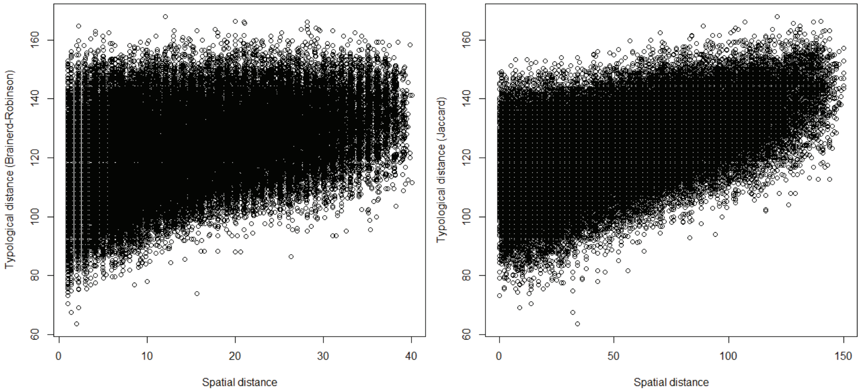


Figure 6.17. The correlation between typological (Brainerd-Robinson) distances, spatial distances (left) and temporal (right) distances (based on a randomly chosen simulation run of Experiment 6.7).

In comparison to the results of Experiment 6.2 (Table 6.2), there is little qualitative change, as the temporal dimension is dominant in explaining the typological variance, but there are quantitative differences which suggest that the decrease of the item population size (the systemic number of objects) does have an effect. The mean correlation between time and the major typological axis of variation in this experiment is high, but significantly lower than in Experiment 6.2, as their ranges barely overlap (Figure 6.16). This difference is even more pronounced when we look at the correlation between temporal and typological distances – in Experiment 6.2 the mean correlation was 0.7, and in this experiment it is 0.54, again with almost no overlap (Figure 6.18). On the other hand, the importance of the spatial dimension has increased (Figure 6.19). Therefore, the decrease of item population size has the same effect as the decrease in the mutation rate – the correlation of typological variation with time becomes lower, and the correlation with space becomes higher. In this case, the effect is not nearly as strong as in the previous experiment, but the item population size is only reduced five times in comparison to Experiment 6.2, whereas in the previous experiment (6.6), the mutation rate was reduced 50 times[37] relative to the value in Experiment 6.2.

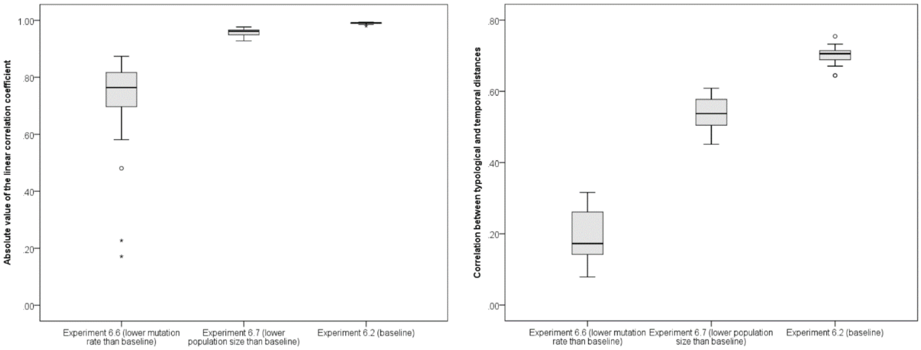


Figure 6.18. Left: Correlation between the major typological dimension (CA axis 1) and time, comparison between experiments 6.2, 6.6, and 6.7.

Right: Correlation between typological (Brainerd-Robinson) and temporal distances, comparison between experiments 6.2, 6.6, and 6.7.

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[37] Reducing the population was preferable to increasing the population size for technical reasons – computing power and memory – but the reduction could only go so far from the baseline of 100.

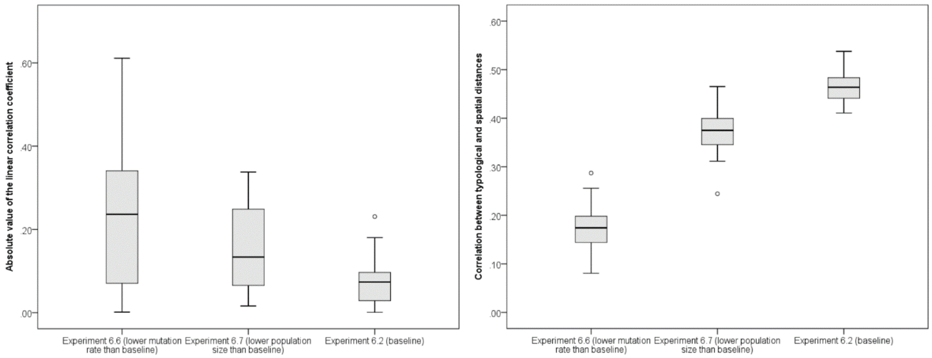

Figure 6.19. Left: Correlation between the major typological dimension (CA axis 1) and the major spatial direction, comparison between experiments 6.2, 6.6, and 6.7.

Right: Correlation between typological (Brainerd-Robinson) and spatial distances, comparison between experiments 6.2, 6.6, and 6.7.

6.2.10. The effect of the average use-life (Experiment 6.8)

In this experiment, I explore the influence of the average use-life of objects. The hypothesis is that, all other things being equal, a class of material culture with a low use-life is more likely to be temporally structured than a class with a high use-life. The low use-life means that items will be often discarded and new ones will often be made. The making of an object is an opportunity for cultural transmission and change in variant frequencies. The more there are transmission episodes per unit of time, the faster will be the cultural evolution, and the difference in variant frequencies will be greater between assemblages from different points in time. In order to test this, I ran the high interaction scenario with the setup identical to the setup for Experiment 6.2, with the difference that the use-life is set to 30 iterations. This means that this class of objects is such that its use-life is similar to the length of a human generation. This would correspond to some class of material culture that is made only once or few times during a person's lifetime. To remind the reader, in all simulations up to this point the use-life was set to 2 iterations in order to make it equivalent to the mean use-life of ceramic bowls. In Experiment 6.2, the high interaction scenario resulted in the temporally dominated pattern. We expect the increase in the use-life to decrease the importance of temporal dimension and to increase the importance of spatial dimension in accounting for the typological variation between the cell assemblages.

The mean absolute correlation between the major spatial direction and the CA axis 1 is 0.47, compared to 0.07 in Experiment 6.2, when the average use-life was 2 iterations. The mean absolute correlation between CA axis 1 and the time is only 0.05. The mean correlation between the typological and spatial distances is 0.06, and between the typological and temporal distances is 0.001 (Figure 6.20). Therefore, the increase of the average-use life of objects does indeed reduce the temporal variation and leads to an increase in the spatial variation between assemblages coming from different sites. However, we can see that the correlations are very low for both dimensions, especially when we look at the correlations between distance matrices. This is so because the assemblages actually change very little in time, as object failure is relatively rare – only 3.3% of items in each cell are discarded and new ones made, and this is when cultural transmission occurs.

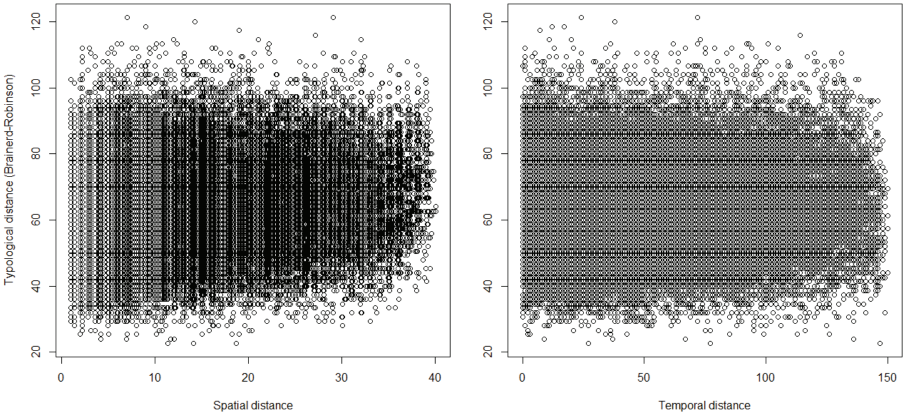

Figure 6.20. The correlation between typological (Brainerd-Robinson) distances, spatial distances (left) and temporal (right) distances (based on a randomly chosen simulation run of Experiment 6.8).

Exp. Number	Correlation (absolute values) between CA 1 and space (absolute value)	Correlation (absolute values) between CA 1 and time (absolute value)	Correlation between spatial and typological distances	Correlation between temporal and typological distances
6.1	0.96 (min =0.93, max = 0.97)	0.06 (min = 0.002, max = 0.19)	0.5 (min = 0.42, max = 0.55)	0.16 (min = 0.1, max = 0.2)
6.2	0.07 (min = 0.0002, max = 0.23)	0.99 (min = 0.98, max = 0.993)	0.46 (min = 0.41, max = 0.54)	0.7 (min = 0.64, max = 0.75)
6.3	0.09	0.96 (min = 0.94, max = 0.97)	0.29 (min = 0.2, max = 0.36)	0.44 (min = 0.36, max = 0.52)
6.4	0.97 (min = 0.91, max = 0.98)	0.13 (min = 0.002, max = 0.42)	0.62 (min = 0.54, max = 0.68)	0.43 (min = 0.36, max = 0.47)
6.5	0.3 (min = 0.003, max = 0.74)	0.83 (min = 0.52, max = 0.97)	0.33 (min = 0.18, max = 0.47)	0.47 (min = 0.29, max = 0.64)
6.6	0.23 (min = 0.001, max = 0.61)	0.71 (min = 0.17, max = 0.87)	0.17 (min = 0.08, max = 0.29)	0.2 (min = 0.08, max = 0.32)
6.7	0.15 (min = 0.02, max = 0.34)	0.96 (min = 0.93, max = 0.98)	0.37 (min = 024, max = 0.47)	0.54 (min = 0.45, max = 0.61)
6.8	0.47 (min = 0.05, max = 0.78)	0.05 (min = 0.0001, max = 0.18)	0.06 (min = 0.02, max = 0.13)	0.001 (min = -0.02, max = 0.04)

Table 6.2. Summary of the correlations between space, time, and typology for the experiments in this chapter.

6.3. DISCUSSION OF THE SIMULATION RESULTS AND THEIR ARCHAEOLOGICAL IMPLICATIONS

We can summarize the results of the simulations in several points (see also Table 6.2):

1) All other things being equal, the increase of the width of the temporal window (temporal interval from which the assemblages come from) increases the importance of temporal variation between assemblages and makes it more likely that the dominant dimension of typological variation will be time rather than space, and vice-versa, that is to say, the decrease of the

temporal window size increases the probability of temporal overlap between assemblages.

2) Other things being equal, the increase in the width of the temporal aggregation interval (the level of assemblage time-averaging) will result in the decreased temporal variation between assemblages (as the potential for overlap will increase), and therefore the spatial effects will be the main factor structuring the inter-assemblage typological variability; again, a decrease in time-averaging will lead to an opposite effect.

3) Other things being equal, changes in the spatial scale – the increase or decrease in the area of the study region – will affect the patterns in a predictable manner: when the spatial scale is reduced, the temporal variation will become more important, and vice-versa.

4) Other things being equal, the increase of the population size and/or mutation rate will increase the importance of time in structuring the formal variability of material culture. The decrease of these parameter values will decrease the importance of time and increase the importance of space.

5) Other things being equal, the lower values of the average use-life are pulling the patterns toward being time-dominated, whereas higher values increase the importance of space in the resulting patterns.

6) Other things being equal, the level of inter-community interaction (i.e. the frequency of copying variants/types from other cells) influences the patterns in such way that in conditions of low interaction, the typological variation will be structured primarily by space; whereas in the conditions of increased interaction, the typological variation will have the strongest correlation with time.

The fact that the increased interaction across space leads to time being the major structuring variable of the typological differences between assemblages may seem odd at first glance, but is actually completely logical (Loog et al. 2017). Increased frequency of interaction with the outside world gives more opportunity to people to come across and copy variants which are further away from their own settlement and microregion. The net effect of the increased transmission in space is a decrease of typological variability in space. Spatial variability will not disappear (as long as the interaction is structured by distance, regardless of the frequency), but in such circumstances the temporal variability becomes more important. Statistically, this is reflected as temporal variability explaining typological variance more than spatial variability. This result is equivalent to the results by Lipo et al. (see also Lipo et al. 2015; Lipo 2001) and their rationale for using seriation as a means to explore interactions between communities – assemblages that can be seriated chronologically are coming from communities which are integrated by interaction (Lipo et al. 1997

In theory, we could tell if the interaction was high or low between communities just by looking at whether the major typological axis of variation was correlated with space (i.e. the major spatial direction) or time[38]. In practice, this is complicated by the fact that changing the spatial and temporal scales of observation, as well as other transmission parameters, also influences whether the major structuring factor is space or time. Checking whether space or time are structuring the typological variation between assemblages is always a good starting point, but in order to infer something about the degree of interaction, we need to consult some other referential frame. One such potential frame are simulations of the kind presented in this chapter, as one can use them to predict at which spatial and temporal scales in combination with a particular interaction level a certain pattern will arise. The problem is that different combinations of observational and transmission parameters can lead to similar or identical outcomes in terms of spatio-temporal patterns. But the good news is that in some cases the problem of equifinality can be reduced, because the observational parameters are usually known (at least to some degree), and some of the transmission parameters may also be estimated (e.g. population size and use-life)[39] - or we can at least determine their lower and upper boundaries.

Another important lesson is that the patterns of typological variation are not absolute and do not depend entirely on the nature of the transmission process (e.g. whether copying from other settlements is frequent or rare), but also depend on the scale of spatial and temporal observation. Relative and absolute chronological schemes which depend on extrapolating typological sequences from key regional sites (e.g. large tells with deep stratigraphies) can work only on spatial scales where interaction is such that temporal variation affects the structure of the assemblages more than spatial variation. This is certainly not new. It was postulated a long time ago that one of the assumptions of the

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[38] This may be feasible if one studies cultural change between two major chronological phases in one region, if the phases are of similar duration (the width of the temporal window) and if time-averaging intervals are similar for most assemblages. In this case, if the pattern of correlation changes from one phase to another, then we can infer that the degree of interaction has changed, if it can be assumed that other transmission parameters are constant.

[39] In theory, we could also try to estimate the mutation rate from the archaeological data (Shennan and Wilkinson 2001), but this requires large samples, as this process may be prone to biases (Porčić 2015).

seriation method is that the assemblages to be seriated must come from a limited spatial area (Dunnell 1970; O'Brien & Lyman 1999:117-118). The limited space is only a proxy for the radius of interaction, which is actually the key variable. The cultural transmission theory allows us to explore the implications of different levels of interactions and different scales of spatio-temporal observation, in order to create a referential frame against which the empirical evidence can be projected.

6.4. EMPIRICAL PATTERNS

6.4.1. Looking at the archaeological record

In this section, I will look at archaeological case studies where the quantitative data on type frequencies in assemblages is available. Such data sets are rarely available because they require a lot of time and great effort to generate, but they are precious, as they represent a "phenotypic" description of the archaeological record suitable for quantitative analysis. The same statistical instruments and observational procedures that were used to summarize and explore the simulated archaeological record will be used here to summarize and explore the empirical archaeological record from several case studies from different spatial, temporal and cultural contexts: the Iroquoian pottery decoration data from the 14th to 17th centuries A.D. North America (Hart et al. 2016), the prehistoric Baden culture pottery decoration data (~3600-2900 BC) from central Europe (Furholt 2009), and the data set on the pottery forms and personal ornaments from the Neolithic of Western and Central Europe (Shennan et al. 2015).

The aim of this exercise is to see whether any of the simulated patterns can be found in the real-world data. From the epistemological perspective, this should be seen as a soft version of theory testing. I refer to it as "soft" for two reasons. First, these models are not meant to be general models of cultural transmission that are assumed to be present in all times and places. The predictions are only valid for a specific kind of model with a specified parameter range. If the process of transmission unfolded according to some other model, then the predictions based on the experiments presented in this chapter are irrelevant. Second, the empirical cases do not contain all of the necessary information to perform the proper testing (representative spatial and temporal sampling of assemblages, sufficient temporal resolution). Therefore, this will be exploratory research, to see if anything similar to the patterns predicted by the simulated models can be found in the random sample of the archaeological record. The rationale is that if the neutral transmission is a good generative model, or at least a good approximation, for the stylistic variability of material culture in time and space, we should see some of the patterning predicted by the simulations in the real world as well.

6.4.2. Iroquoian pottery

Hart et al. (2016) recorded and used the pottery collar decoration data to analyze the Iroquoian interaction networks in Southern Ontario from the 14th to 17th centuries A.D. For each assemblage, they provided data on individual motif frequencies and the temporal designation into one of the 50-year periods from 1300 to 1650 A.D. The geographic distance matrix between each pair of sites is also given. Therefore, this kind of data is comparable to the simulated data in this chapter – the width of the temporal window is 300 years, the degree of time-averaging is around 50 years, and the maximal distance between two sites in the study region is 359km. I am ignorant concerning the estimates of the average use-life of the Iroquoian pots, but the cross-cultural ethnoarchaeological evidence suggests that the average use-life for pots varies between 1 and 5 years (Varien & Mills 1997). Therefore, we would expect time rather than space to be the main factor that structures the variation between assemblages.

The CA analysis was performed on the pottery collar decoration frequency data from Hart et al. (2016). The CA axes 1 and 2 account for 25.1 and 10.1% of variance, respectively. The assemblages form an arch pattern in the CA space (Figure 6.21). The temporal dimension is constructed by assigning the value of the midpoint of the appropriate temporal interval to each assemblage. The major spatial direction variable is constructed as the first axis of the metric multidimensional scaling analysis (MDS) applied to the matrix of geographic distances between the assemblages, which accounts for 64.5% variance in spatial distances.

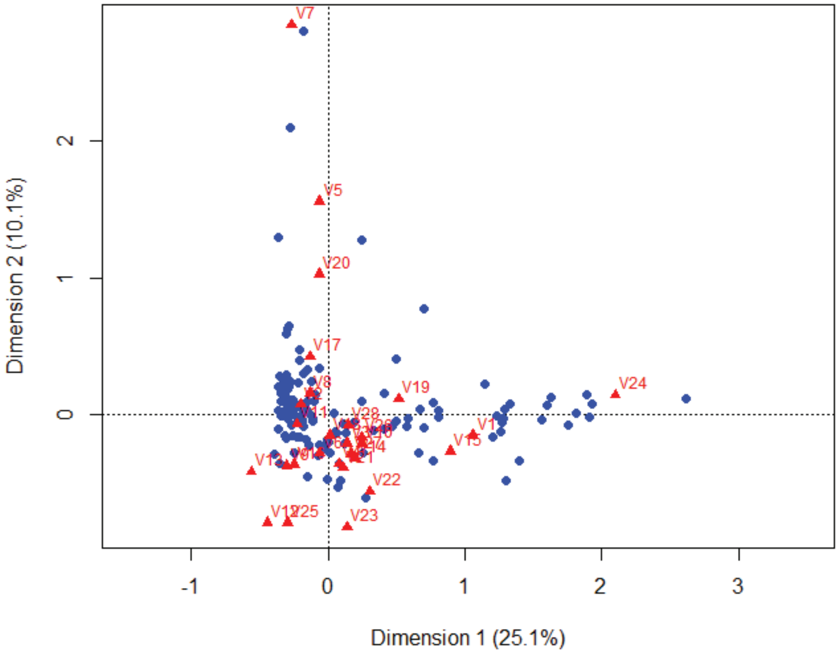

Figure 6.21. Results of the correspondence analysis performed for the Iroquoian pottery data from Hart et al. (2016): the configuration of assemblages and types in the space defined the first two CA axes.

Now we can calculate the correlation between temporal, spatial, and typological dimensions, as was done for the simulated data. The results suggest that the major typological axis (CA axis 1) is correlated with time rather than space (Table 6.3, Figure 6.22). The correlation between the CA axis 1 scores and time is -0.63. The correlation between the CA axis 1 and the major spatial direction is low (0.07) and not significant (Figure 6.23). It is the second typological dimension, reflected by the CA axis 2, which correlates moderately with space ($r = 0.56$, $p < 0.001$).

	CA axis 1	CA axis 2	Major spatial direction	Time
CA axis 1	1	-0.12	0.07	-0.63*
CA axis 2		1	0.56*	0.04
Major spatial direction			1	-0.21

Table 6.3. Pearson correlation coefficients between major typological dimensions, major spatial direction (the first MDS axis of the spatial distances matrix), and time.

*significant at the 0.001 level

This pattern is confirmed by the matrix correlation between typological, spatial and temporal distances. The correlation coefficient between the BR distances and the temporal distances is 0.24 (Mantel test $p < 0.005$), whereas the correlation of the BR distances with the geographic distances is low and not significant at the 0.05 level ($r = 0.08$, Mantel test $p = 0.076$) (Figure 6.24). The correlation between spatial distances and the BR similarity coefficients[40], on the other hand, are much higher and significant when they are calculated within each time period, and range between -0.14 and -0.52 (Hart et al. 2016: Table 2). This is exactly what we would expect – the reduction of the temporal window width increases the spatial effects.

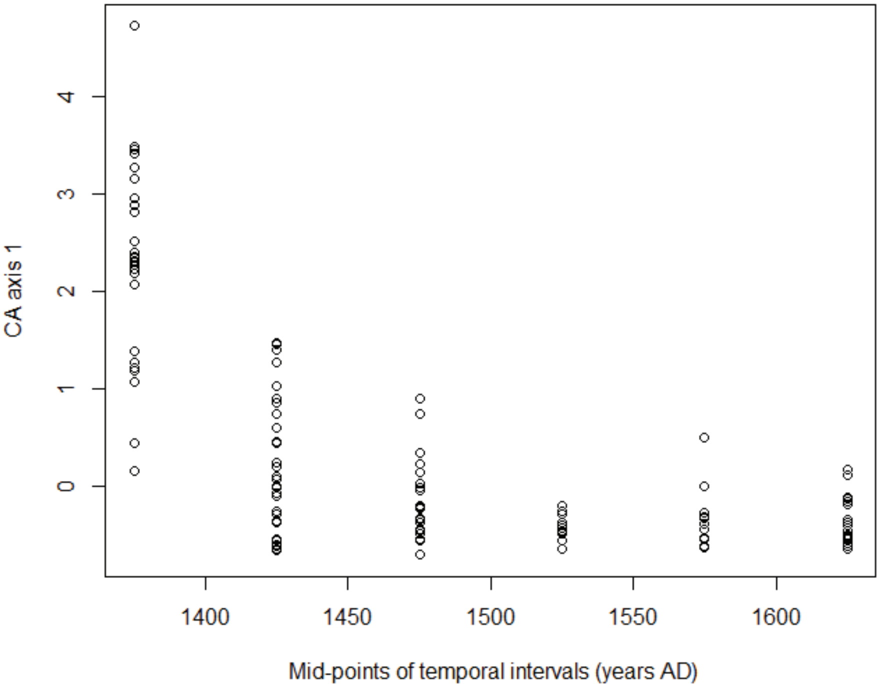

Figure 6.22. The correlation between time and the CA axis 1 for the Iroquoian pottery data from Hart et al. (2016).

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[40] Technically, Hart et al. (2016) are using BR similarity coefficients rather than BR distances, but this only influences the sign of the correlation coefficient, not its value, as BR similarity and distance are complementary measures – see Chapter 3.

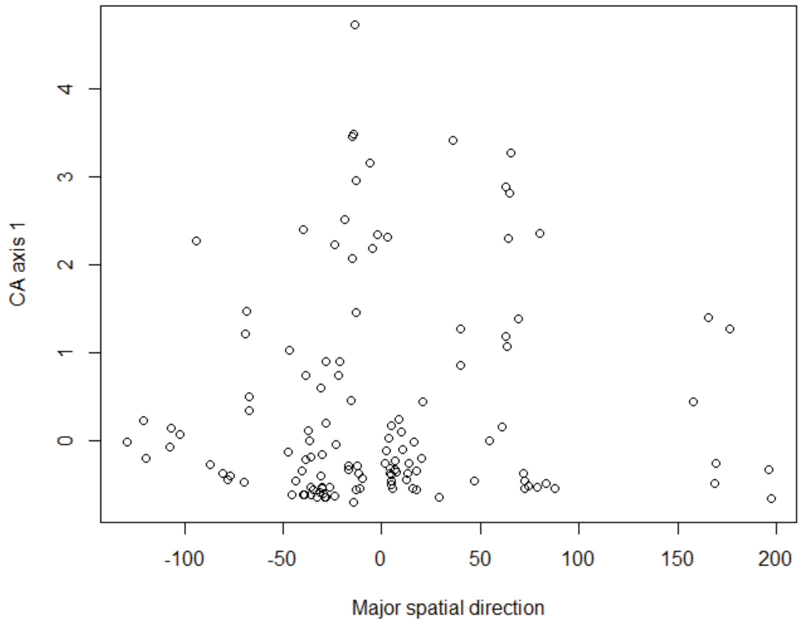

Figure 6.23. The correlation between the major spatial direction and the CA axis 1 for the Iroquoian pottery data from Hart et al. (2016).

If all other things were equal, we might have been inclined to conclude that the interaction between Iroquoian settlements was relatively high, and that therefore the temporal differences between assemblages are more pronounced than the spatial differences. This is in broad agreement with the results of Hart et al. (2016), who demonstrated that interaction networks between distant Iroquoian communities were present.

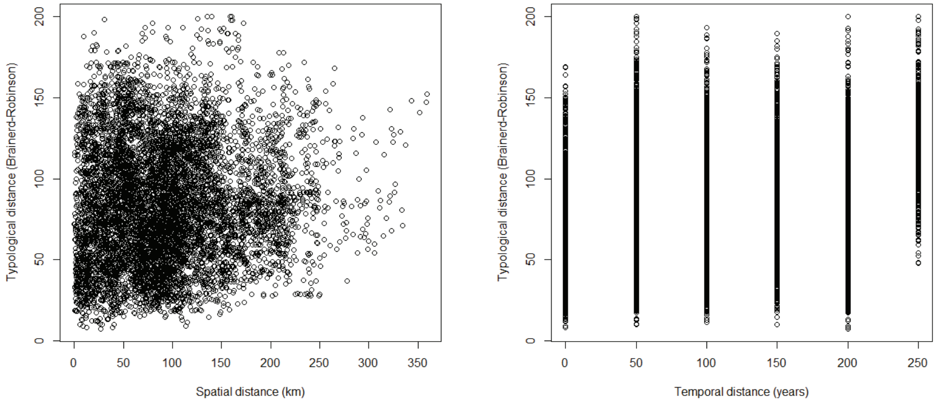

Figure 6.24. The correlation between typological (Brainerd-Robinson) distances, spatial distances (left) and temporal (right) distances (based on data from Hart et al. 2016).

6.4.3. *The variability of the Baden culture pottery*

The Baden culture is a traditionally defined archaeological culture which occupied a large area of central Europe and northern parts of southeastern Europe. In southeastern Europe it is considered a Eneolithic (Copper Age) culture (Tasić 1995), whereas in the north it is labelled as a Late Neolithic culture (Furholt 2009). The temporal span of this archaeological phenomenon was roughly between 3650 and 2800 B.C. (Horváth et al. 2008; Furholt 2009). Furholt made a detailed quantitative analysis of the Baden culture pottery by systematically recording pottery decoration motif frequencies from settlement assemblages in his core study area, which included Moravia, Upper Silesia and Lesser Poland (Furholt 2008; 2009). Furholt's (2009) data provide a rare opportunity to rigorously study the patterns of material culture variation in space and time, as the great number of assemblages were described and quantified according to a uniform recording scheme.

Correspondence analysis was applied, resulting in the horseshoe-shaped pattern (Figure 6.25) which Furholt convincingly interpreted as the temporal ordination of assemblages, by making a comparison with the available radiocarbon evidence (Furholt 2009: 65-78). Therefore, we already see that in this case it is the temporal dimension which structures the typological variability. The spatial scale of Furholt's analysis is similar to the spatial scale of the simulation space. Furholt's study area has an approximate area of 200 x 400km, with the major axis of spatial variation being the East-West axis which is around 400km long, whereas the simulated region is a rectangle with dimensions 100 x 400km, assuming that each cell is a square with 10 km-long sides. Therefore, this result is quite expected, given that the temporal window has a width of 700 years and the duration of individual Baden assemblages is unlikely to be greater than 50-100 years.

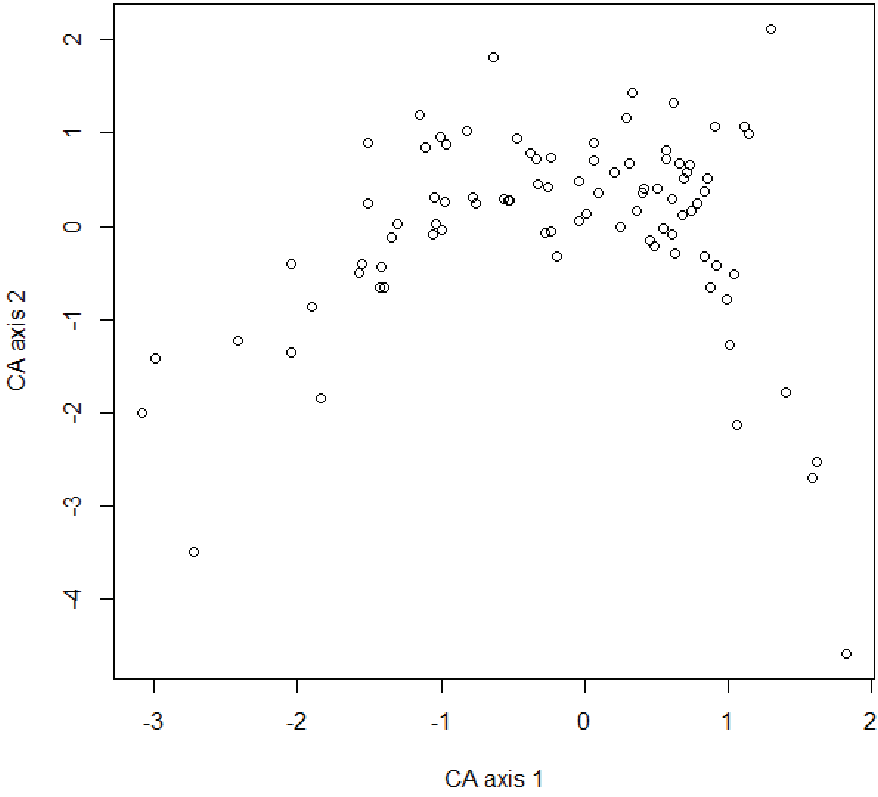

Figure 6.25. The configuration of Baden pottery assemblages in the typological space defined by the first two CA axes performed on the data from Furholt (2009).

We can further explore Furholt's core data set by calculating the correlation coefficients between the major spatial direction and the CA axes, as well as the Mantel correlation between geographic distances and typological distances (as measured by the Brainerd-Robinson and Jaccard coefficients). The major spatial direction is taken to be the first principal component of the transformed (from degrees to km) geographical coordinates of the assemblages, which accounts for 98.2% of variance in the assemblage positions. The correspondence analysis suggests that the CA axis 1 and CA axis 2 account for 9.2% and 6% of the total variance, respectively. CA axis 1 is moderately correlated with the major spatial direction ($r = 0.52$, $p < 0.001$; Figure 6.26). The correlation coefficient between the spatial distances on one side and the BR on the other, are very weak: 0.17 ($p = 0.001$ (Figure 6.27). In general, the Baden situation corresponds to the experiments where time is the more important structuring factor of the typological variability, but there is a moderate correlation with the major spatial direction.

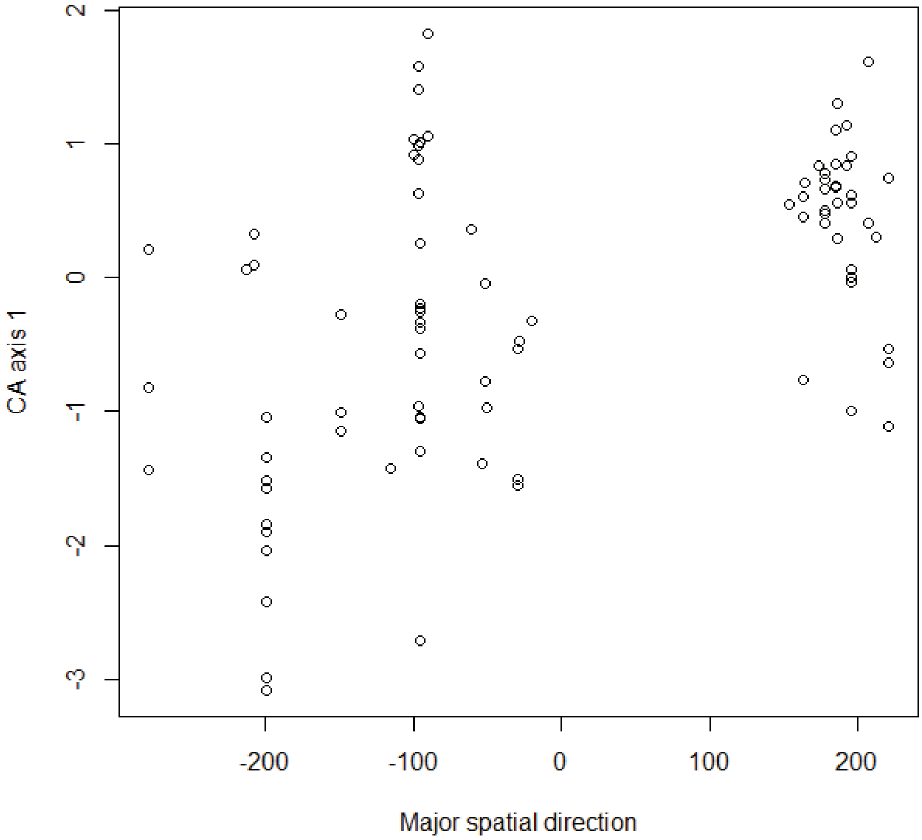

Figure 6.26. The correlation between the major spatial direction and CA axis 1 scores based on the Baden pottery data from Furholt (2009).

This may reflect the mixed effect of parameters pulling towards space- or time-dominated structures, but it may also be due to the confounding of space and time. The confounding of space and time in the typological dimension may occur when space and time are correlated. This may arise when sampling is biased and uneven, i.e. if there are more early or late assemblages in one part of the study area than in another, or if there are directional migrations or diffusion – e.g. the expansion of the Neolithic in Europe implies that there will be *a priori* correlation between time and space, as the earliest assemblages will always be clustered at the southeasternmost part of the study area. This effect is even more pronounced in the next case study.

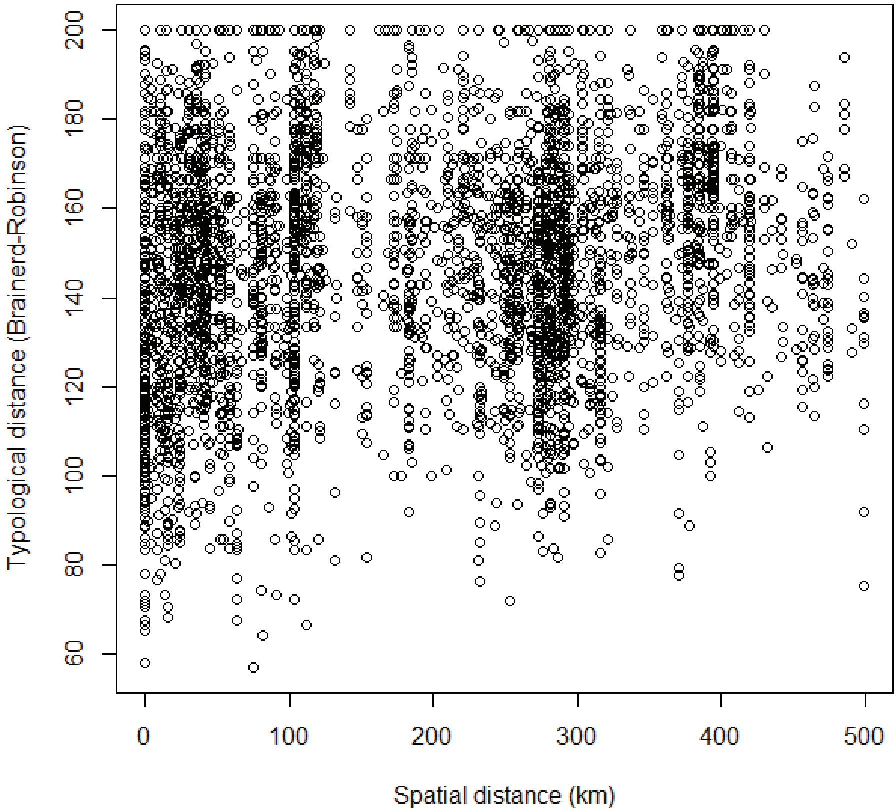

Figure 6.27. The correlation between typological (Brainerd-Robinson) distances, spatial distances (left) and temporal (right) distances (based on data from Hart et al. 2016).

6.4.4. Pottery and personal ornaments in the Western and Central European Neolithic

The quantitative data on the presence and absence of pottery decoration, pottery shapes and personal ornaments types, were recorded by Shennan et al. (2015) for almost 200 Neolithic sites in Western and Central Europe, spanning approximately 3000 years and 2500km (the major spatial direction of the spatial distribution sites is approximately from the east to the west). For each site, the authors recorded the spatial and temporal positions. The temporal window is the period between 5500 and 2450 BC, whereas the average assemblage duration is 350 years. Based on the simulations presented in this chapter, we would expect time to be the main structuring factor of the material culture variability for such wide temporal window, but in this case, the spatial window is much greater than the simulated space (the direction of the major spatial direction is 2500km, compared to only 400km in the simulations). In order to summarize the typological variation, multidimensional scaling (MDS) analysis is applied to the matrices of Jaccard distances between sites, based on pottery and ornaments data from Shennan et al. 2015 (Figure 6.28). For the pottery data, the first and the second MDS dimensions account for 9.6 and 6.1% of variance, respectively. For the ornament data, the MDS axis 1 and MDS axis 2 account for 10.4 and 6% of variance, respectively.

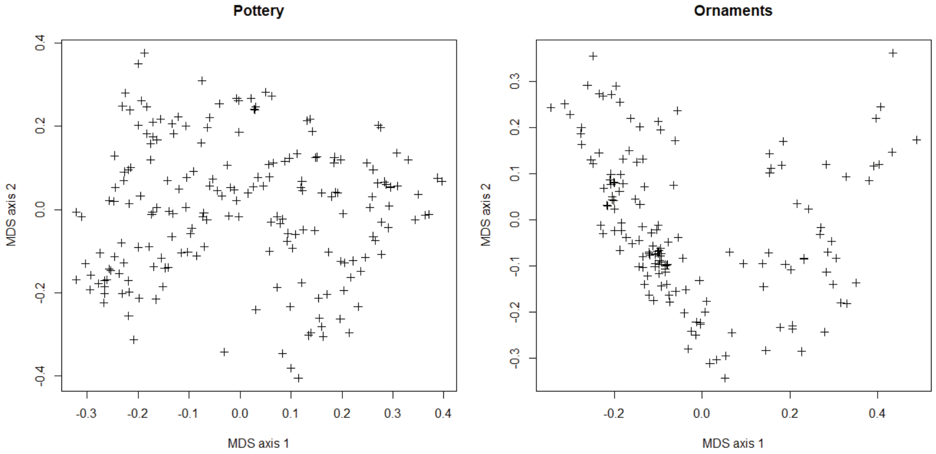

Figure 6.28. The configuration of the West and Central European Neolithic assemblages in the typological space defined by the first two axes of the multidimensional scaling analysis for pottery (left) and personal ornaments (right) (data from Shennan et al. 2015).

The pattern of correlations between the dimension of typology, space and time is complex for the pottery data. The major dimension of typological variability, the MDS axis 1, is weakly correlated with time ($r = -0,325$, $p < 0.001$) and latitude ($r = -0.232$, $p < 0.001$), with no significant correlation with longitude ($r = 0.109$, $p = 0.065$), which is the major spatial direction for the distribution of sites. The MDS axis 2, on the other hand, is moderately correlated with time ($r = -0.505$, $p < 0.001$) and latitude ($r = 0.493$, $p < 0.001$), and weakly correlated with longitude ($r = 0.245$, $p < 0.001$). In order to better understand this result, principal component analysis with orthogonal Varimax rotation was applied to the correlation matrix in Table 6.4. Three rotated components are extracted which explain 37.2%, 25.9%, and 21.1% of variance. The correlations between the original variables and rotated components are given in the loading matrix in Table 6.5. The first component is defined by the MDS axis 2, time and latitude. The second component is defined primarily by the MDS axis 1, with moderate contribution from time, whereas the third component is defined only by longitude. Therefore, the temporal dimension is the most important dimension structuring the formal variability of material culture, but it is significantly confounded by space. It should be noted that latitude and time are also weakly correlated (-0.315, $p < 0.001$), suggesting that there is a weak but significant tendency for the northern sites to be more recent than the southern ones. This is quite to be expected, given that the Neolithic arrived at different times in different parts of Europe; and in this case, it seems that this primarily reflects the difference between sites in Britain and Denmark, as there were no Neolithic sites in these regions before ~4000 BC. For this reason, the spatial direction which structures the typological variability is the N-S direction rather than the E-W direction. When we look at the correlations between the typological (Jaccard distance), spatial (Euclidean), and temporal (Euclidean) distance matrices, they are very low: 0.06 (Mantel test $p = 0.065$) for the correlation between spatial distances and typological distances, and -0.06 (Mantel test $p = 0.96$) for the correlation between temporal and typological distances (Figure 6.29).

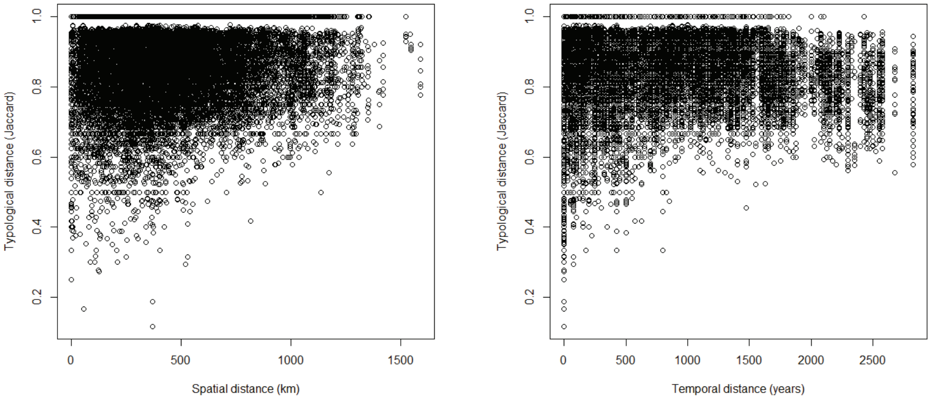

Figure 6.29. The correlation between typological (Jaccard) distances, spatial distances (left) and temporal (right) distances (based on the pottery data from Shennan et al. 2015).

The fact that there was an actual expansion of the population in space and time is what makes this situation different from the simulations which are demographically static. The major spatial direction, which is the geographic longitude i.e. the east-west direction in this case, seems not to be the major structuring factor of the material culture. This is rather strange in the light of the simulation results, given the vastness of the spatial scale – for such a large area it would seem reasonable to expect the spatial variation to dominate. This discrepancy can be explained by the fact that, unlike in the simulations, there was a population movement in Neolithic Europe which makes the static simulation models irrelevant for this empirical data. It could also be that the resolution of the assemblage composition reduced to presences and absences is masking the spatial variation which is primarily reflected in changing frequencies, whereas it makes the temporal variation more important as the mutations directly create presences.

		MDS1	MDS2	Latitude	Longitude	Time
MDS1	Pearson's r	1	0.000	-0.232*	0.109	-0.325*
	N	195	195	195	195	195
MDS2	Pearson's r	0.000	1	0.493*	0.245*	-0.505*
	N	195	195	195	195	195
Latitude	Pearson's r	-0.232*	0.493*	1	0.035	-0.315*
	N	195	195	195	195	195
Longitude	Pearson's r	0.109	0.245*	0.035	1	-0.012
	N	195	195	195	195	195
Time	Pearson's r	-0.325*	-0.505*	-0.315*	-0.012	1
	N	195	195	195	195	195

Table 6.4. Correlations between the typological, spatial and temporal dimensions for the Western and Central European Neolithic pottery data (from Shennan et al. 2015).

* Correlation significant at the 0.01 level (1-tailed).

	Rotated Component		
	1	2	3
MDS 1	-0.108	0.923	0.092
MDS 2	0.836	0.086	0.256
Latitude	0.818	-0.302	-0.043
Longitude	0.080	0.050	0.980
Time	-0.687	-0.584	0.129

Table 6.5. The rotated component loading matrix showing the correlations between the orthogonally rotated principal components and the original variables for Western and Central European Neolithic pottery data (from Shennan et al. 2015). Correlations higher than 0.5 or lower than -0.5 are in boldface.

For the personal ornament data, the patterns are completely different (Figure 6.28; Table 6.6). The major typological dimension (MDS axis 1) has a moderately strong correlation with the longitude, which is the major spatial direction in this case ($r = 0.712$, $p < 0.001$). The second important typological dimension (MDS axis 2) is moderately correlated with time ($r = 0.450$, $p < 0.001$). These results are consistent with the correlations between the distance matrices: the correlation between spatial and typological (Jaccard) distances is 0.14 (Mantel test p = 0.001), and the correlation between temporal and typological distances 0.3 (Mantel test p = 0.001) (Figure 6.30).

In the case of personal ornaments, the spatial variation is more important than the temporal variation in structuring the variance of the assemblages, when we look at the MDS axes. Whether this is an effect of the vast amount of space or the lower level of intercommunity copying rates is difficult to say without further analysis.

		MDS1	MDS2	Latitude	Longitude	Time
MDS1	Pearson's r	1	0.000	-0.157*	0.712*	0.020
	N	166	166	166	166	166
MDS2	Pearson's r	0.000	1	0.060	0.013	0.450*
	N	166	166	166	166	166
Latitude	Pearson's r	-0.157*	0.060	1	-0.003	0.487*
	N	166	166	166	166	166
Longitude	Pearson's r	0.712*	0.013	-0.003	1	0.082
	N	166	166	166	166	166
Time	Pearson's r	0.020	0.450*	0.487*	0.082	1
	N	166	166	166	166	166

Table 6.6. Correlations between the typological, spatial and temporal dimensions for Western and Central European Neolithic pottery data (from Shennan et al. 2015).

* Correlation significant at the 0.05 level (1-tailed).

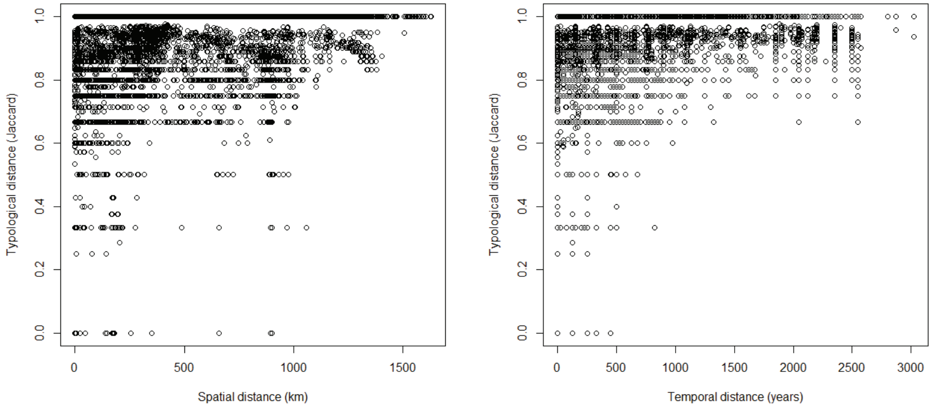

Figure 6.30. The correlation between typological (Jaccard) distances, spatial distances (left) and temporal (right) distances (based on data from Shennan et al. 2015).

What is interesting is that the two classes of material culture, pottery and personal ornaments, seem to have had different underlying transmission dynamics. This was clearly shown by Shennan et al. (2015), and is also apparent in the results of the current analysis. Given that the spatio-temporal window and the assemblage durations are similar for these two classes of material culture, the results of the simulations from this chapter would suggest several non-exclusive hypotheses for the observed patterns:

1) The intercommunity copying rate (the interaction) is not the same for pottery and personal ornaments, i.e. the probability of copying from a different community was higher for pottery than for personal ornaments. Given the potential importance of personal ornaments for group identity, the lower degree of transmission or lower distance of transmission would make sense.

2) The average use-lives for pottery were shorter than for the personal ornaments. While the use-life estimates for pottery can be reliably made from the ethnoarchaeological and ethnographic data, and are usually between ~1 and ~5 years for all classes except for storage pottery (Varien and Mills 1997), I am not aware of the use-life estimates for personal ornaments. Again, given their importance for personal (or group?) identity, I would speculate that they have much longer use-lives than pottery e.g. in the range of decades rather than years. If this is true, it would make the temporal dimension less important in the case of personal ornaments.

3) The systemic number of pottery vessels was higher than the number of personal ornaments, therefore the pottery population size was effectively larger than the ornament population size. There are usually more pottery vessels in a household than people, whereas the number of personal ornaments in use is more likely to be closer to the actual number of people. Given that the systemic number of objects that I referred to as the population size is positively correlated to temporal domination in structuring assemblages, the implication would be that we would expect time to have more structuring influence in the case of pottery than in the case of personal ornaments. If the mutation rate is equal for pottery and for personal ornaments, we could make the additional empirical prediction that we should have more types/variants for pottery than for personal ornaments. In theory, we could check this prediction by counting and comparing the number of pottery types to personal ornament types. However, this is not possible in this particular case, as personal ornaments are described as presences and absences of types corresponding to discrete objects, whereas pottery assemblages are described as presences and/or absences of shape

types and vessel decorations, so the potential number of paradigmatically defined types (based on the intersections of morphological types and decoration variants) is much larger than the number of shapes or decorations alone, as they can be combined. This is further complicated by the fact that the definition of types (i.e how the material is classified into types, that is to say, how the boundaries between types are defined) can influence the results. This problem has wider importance in archaeology, far beyond this particular hypothesis, and it will be discussed in detail in the next chapter.

4) The mutation rate was greater for the pottery than for the personal ornaments. As elaborated in Chapters 2 and 3, the mutation rate has two components – in other words, the introduction of a new type/variant may occur for one of two reasons. The first reason is the copying error and the second reason could be the intentional action proceeding from the conscious decision to innovate. I am ignorant as to whether there are any differences between these two classes of material culture in terms of the copying error. As for the intention to innovate, it is unknown whether it makes sense to assume that some classes of material culture are more likely to have a higher baseline probability of being innovated then some others. In theory, we could try to estimate the copying error experimentally for the two classes of material culture, and we could try to estimate the mutation rate from archaeological data, but both of these options are extremely difficult to conduct in practice. Therefore, this hypothesis is very difficult to test.

5) The attributes of pottery vessels and personal ornaments were transmitted in accord with different transmission models. I explored the neutral model and its consequences in this chapter for the sake of convenience and because it is the baseline model, but there is nothing to guarantee that this is the right model for any of them, or that both classes of material culture were transmitted in the same way. This hypothesis would require further theoretical research and further empirical research.

6.5. SUMMARY OF THE EMPIRICAL CASE STUDIES

To be clear, I cannot give a definite answer to the question of why Neolithic pottery and personal ornaments show different patterns of spatiotemporal variation, or what exactly is the reason for the patterns observed in Iroquoian or Baden pottery, as I cannot test any of the hypotheses proposed above owing to a lack of data. But this was not the purpose of this exercise. The idea was to demonstrate that the similar patterns as predicted by the models of cultural transmission implemented via computer simulation can be identified in the archaeological record. Even more important is that the knowledge gained through the theoretical work in this chapter allows us to formulate hypotheses which are testable both in principle and in practice, with further efforts directed at data collection. Moreover, the simulations provide us with means of trying out different parameter values so we can use the parameter values that can be estimated empirically as input for the simulations and conduct a parameter search for those that cannot be easily estimated from the archaeological data (e.g. in an Approximate Bayesian Computation framework research such as Crema et al. (2014a; 2016) and Kovacevic et al. (2015)).

7

CONCLUDING THOUGHTS

Chapter 7

CONCLUDING THOUGHTS

7.1. THE CONTRIBUTION

My main intention with this book has been to use the theoretical framework of cultural transmission theory in order to explore some of the classic problems of archaeological inquiry. The reader may ask why this particular theory is better than some other theory, and what is new here? Obviously, most of the problems discussed in this book are as old as archaeology itself. The computer simulations and most of the statistical tools are also not new, and have all been used many times before in order to study the formal variability of material culture in space and time. Even the idea of cultural transmission i.e. diffusion of culture, is an old anthropological concept implicitly present in anthropology and archaeology from an early stage (Eerkens & Lipo 2007). However, the prospect of modeling some aspects of culture as population phenomena, where descent with modification occurs, opens up many theoretical and methodological possibilities for archaeologists. The structure of cultural transmission theory, especially its reliance on quantitative models, makes it possible to model dynamically the generative processes of the formal variability of material culture, and explore the many possible (pre)histories and track their fingerprints in the archaeological record. I hope that the simulations in this book clearly illustrate this point.

As the research for this book progressed, I began to wonder if the findings I have presented were trivial, in the sense that everyone would know what to expect from a model without simulations. For example, anyone familiar with isolation by distance in biology could have predicted that we would have spatial gradients of variants across space. It seems to me that this impression of triviality is only partly true. Someone with a background in population genetics or quantitative modeling in general would probably be able to predict what the equilibrium pattern would be like, but on the other hand, it would be very difficult to specify how much time would it take for a system to reach equilibrium, or what parameter combinations would lead to one outcome rather than another. The fact that the simulations have been parametrized in such way as to emulate a generic preindustrial or prehistoric situation is what makes the results useful for archaeological middle-range theory-building (in both senses of the term “middle-range”). Finally, the match between the patterns generated by the simulations of the neutral transmission in space, the empirical patterns, e.g. the clines in the frequencies of cultural variants revealed by Shennan (1978) in the seminal study of the Bell Beaker archaeological culture, completes the circle which connects the theory and data in our understanding of the problem of archaeological cultures. Just as Neiman’s (1995) simulations demonstrate how the patterns in time arise from this simple model of transmission, we can see how the patterns in space can also be generated by the same model. This does not mean that the neutral model is responsible for generating the patterns that we identify as archaeological cultures in all times and all places, but it stands as a possible indication that we do not necessarily need anything more complicated than this model to explain the patterns that we see. This clearly shows how we can go beyond archaeological cultures, to study spatial variation in the analytical and systemic way proposed and anticipated by David Clarke a long time ago (Clarke 1978). However, the fact that simple models which do not assume anything about group identity, such as the neutral model, can produce spatial structuring of material culture, does not mean that in principle there can be no groups which also produce distinct material culture. The reality of archaeological cultures as discrete phenomena needs be established on a case by case basis (Shennan et al. 2015).

The usefulness of a theory is, among other things, measured by its ability to generate testable hypotheses. This feature of cultural transmission theory has been demonstrated in all three key chapters of this book. Perhaps the most illustrative examples come from the previous chapter. I first used cultural transmission theory to model the past dynamics, and then I theoretically explored the effects of transmission and observational variables on the resulting patterns. This was an exercise in theory-building, and the end result of this purely theoretical investigation was information about how the relevant parameters individually and through interactions structure the patterns of variation of material culture in time and space. When patterns similar to the ones encountered in the simulations were identified in the archaeological record, I was able to formulate hypotheses based on the background theoretical knowledge.

Another example is the relation between time-averaging and unimodality.The phenomenon of unimodality has been explored in Chapter 5. The results confirm what other researchers, such as Madsen (2020), have suggested. Unimodality is not a defining criterion of the seriation sequence. The semblance of unimodality, or in rare cases the perfect unimodality of types, that we observe in the archaeological record is the consequence of the transmission process in combination with time-averaging. The imperfect unimodality of sequences is not a result of a sampling error, but a feature of the transmission process itself, and of the fact that the equilibrium is dynamic rather than static, as stochastic noise is always present. Surprisingly, unimodality and seriation accuracy are only weakly correlated, but this conclusion is limited to the correspondence analysis as a seriation technique.

The results of the research presented in Chapter 5 can also be viewed as yet another empirical corroboration of cultural transmission theory, as the predictions of the theory regarding the increase of unimodality as a function of increasing degree of time-averaging were borne out by the empirical evidence when archaeological assemblages were time-averaged by merging the assemblages from the adjacent stratigraphic units. The theory also predicts the patterns of temporal intensity of archaeological cultures.

7.2. THE LIMITATIONS, AND PROSPECTS FOR FURTHER RESEARCH

7.2.1. General comments

The research presented in this book is limited in many ways, and I will try to cover explicitly all the major weaknesses and limitations that I am aware of. The identification of limitations is important for the critical evaluation of results and for defining the prospects for further research to overcome the limitations. Many of these crosscut the most fundamental issues in archaeology regarding the systematics and the construction of typologies, so ideas about how to solve this problem from the perspective of the cultural transmission theory should be seen as an indirect contribution of the theoretical exercises in this book.

The limitation which seems most apparent is that the number of models and the range of parameters explored are small. Therefore, the simulation experiments undertaken in this book are neither comprehensive nor systematic. There are many models which were not explored (e.g. prestige bias, guided variation, cultural selection…).

7.2.2. *Demographic aspects*

Perhaps the greatest conceptual limitation of the simulations presented in the previous chapters is the lack of demographic dynamics. All of the models and scenarios presented assume that the population size is stationary – it neither grows nor declines in size, as there are no changes in fertility, mortality, or migration rates. Therefore, such models are relevant only for situations where population fluctuations are relatively small. It may be argued that at the millennial scale, and with the exception of major demographic processes such as the Neolithic demographic transition (Bocquet-Appel 2011), this was true for most of prehistory. However, there were certainly fluctuations at smaller temporal scales, and the theory suggests that changes in the population size, and especially booms and busts, must have had significant implications for the formal variability of the material culture in time and space (Rorabaugh 2014; Shennan 2000; 2013; Shennan & Bentley 2008). The inclusion of the demographic dynamics would not only make the models more realistic but would add a significant theoretical dimension. Among other things, it would be useful to see how population growth and decline influence the temporal patterns, and how this may affect seriation.

7.2.3. *Equilibrium assumption*

Another major limitation of this study is the equilibrium assumption, which is not realistic in most cases. So the simulations presented here are also static in this sense. I am assuming in the simulations that a single transmission model is valid for hundreds and thousands of years, and I am mostly looking at the patterns when the system is in the equilibrium. The lack of demographic variability precludes any temporary deviations from equilibrium. The models with the equilibrium assumption may be useful for theoretical considerations, but for practical purposes, non-equilibrium models are more suitable and effective (Kandler & Shennan 2013; Crema et al. 2016).

7.2.4. *The range of spatial interaction*

The interaction between communities has at least two aspects which can be modelled: frequency and range of interaction. In this book, I have kept the range constant by always using the inverse of the squared distance as a kind of generic and default value for preindustrial communities. Only in Chapter 4 do I brief discuss the effects of the spatial range of interaction on pattern in space; in general, this topic remains underexplored in this book (for example, I did not vary this parameter in any of the experiments in Chapter 6). The spatial range of interaction can depend on the technology of transport (e.g. horse) or on the political geography, so it is nor unreasonable to suggest that this parameter of interaction varied in the past (in other words, that in one phase the interaction was more local, whereas in another the range was wider), which should be reflected in the spatial patterns of stylistic variability of material culture. This remains to be explored in the future, and the simulations presented in this book can be used to do so.

7.2.5. The scale of transmission and the number of attributes

Another set of limitations is to be found in the way the traits are modeled. I simulated the transmission process of a single meme without specifying the scale. For example, the simulated variants and types may be thought of as states of a single attribute, such as anthropomorphic figurine eye types or vessel decoration motifs, or as morphological types (e.g. bowl shapes). This kind of modeling follows an established tradition in cultural transmission research, but it does not allow for exploring the complexities that may arise when different attributes are transmitted in accord with different models, especially in combination with the practice of archaeological systematics – the construction of types from attributes. For example, how do the frequencies of paradigmatically defined types behave in space and time when the attributes used to define the types are transmitted in different ways? This would require a multilevel modeling – multiple attributes would be copied and the types would be constructed based on the attribute states.

7.2.6. Modeling the mutation event

I treated the meme variants or types as discrete entities in the simulations. The apparent limitation is that the mutations are simulated rather mechanically. What was not simulated is the fact that perfect copying fidelity is not possible for material culture (at least in not in preindustrial times). As noted in Chapter 3, the mutations are modeled as a cultural equivalent of an infinite allele model in population genetics (Ewens 2004: 111–119). When a mutation occurs, a new variant is simply added to the pool of existing variants without distinguishing whether the mutation arose as a result of the copying error or as a deliberate innovation, i.e. there is no information as to how similar it is to the previous variants. This makes it hard to make a correspondence between the number of variants observed in the archaeological record and the number of variants in the simulated assemblages. As noted, the determination of the number of variants or types is a complex issue in archaeology (Dunnell 1971; Lyman 2021a). In the empirical examples presented in the chapters of this book, we do not see as nearly as many variants in the archaeological record compared to the number of mutations that we get in the simulations, even with very low mutation rates. Part of this difference can be explained by the fact that archaeological assemblages are usually very small fractions of the population of produced and accumulated items. But the central issue seems to be the definition of types.

It should also be noted that mutations are modeled in such a way that each mutation always produces a completely new variant – it is assumed that the potential number of variants is infinite (for an infinite allele model, see Ewens 2004: 111-119). This rules out the possibility of rediscovering some variants which have been lost in previous time steps. This is obviously not realistic, as it might happen that some long-lost variant will be rediscovered at some point by coincidence. The impact of this possibility should be explored in the future, especially for those attributes which do not have an ample space to vary. Again, this is related to the issue of what really counts as a new variant.

7.2.7. The modeling of types – problems with the reality and discreteness of meme variants

For the broad brush strokes of the theoretical explorations undertaken here, this rough and unsophisticated way of modeling is sufficient. However, the issue of systematics is critical for modeling the generating processes for the purposes of empirical research. How we define types and how we measure mutation rates must be comparable between the models and the observations that we make on the artifacts. Whether a particular instance will be classified as mutation or assigned to an existing type will depend on the resolution of the classification. Let us look at the eye types of the anthropomorphic figurines from the Central Balkan Late Neolithic that were used to illustrate the effects of time-averaging on unimodality in Chapter 5. Should the similar specimens be considered as manifestations of a single type, or should they all be classified as different types because they are not completely identical? This is the old "lumper" vs. "splitter" dilemma of the typologist. Paradigmatic classification cannot resolve this problem, even when the attributes are continuous dimensions – if we want discrete classes for occurrence or frequency seriations, the degree of lumping/splitting will depend on the width of the intervals by which we choose to divide the continuous variation into discrete classes. If the types are defined by lumping too much variability into the same class - I will call this typological averaging -, then the spatio-temporal patterns may be obscured and the mutation rate will be low. The same effect will occur if the mutation does not exclusively involve the invention of an absolutely (never before invented) novel variant, e.g. if a lost type/variant is reinvented by accident (or by intention). Therefore we have a rather unsatisfactory situation that the number of types, i.e. our observational units, partially determines the patterns that we may observe.

Are the types real? Are the types discrete? These are two conceptually different but practically related questions. The question of the reality of types brings us back to the Ford-Spaulding debate (Ford 1954a; b; Spaulding 1953). The debate was summarized by O'Brien and Lyman (2000: 207-213) and expressed in terms relevant for cultural transmission theory, so I present their account of the debate here. In this debate, Spaulding's position was that there were real socially relevant and recognized (emic) types in the past which could be reconstructed by statistically exploring the associations of attributes. Ford, on the other hand, was not concerned with the discovery and reconstruction of real types (e.g. cultural or emic classifications of material culture). His position was that types should be constructed by the analyst for a purpose – in his case, the purpose of constructed types was to measure time. In Ford's view, analytical types were arbitrary constructions produced by the archaeologist in such a way as to be maximally chronologically sensitive. So, from one perspective, types are certainly real, in the sense that there must have been *concepta* (*sensu* Clarke 1978) in people's minds of some culturally recognized types. On the other hand, we know that there are no two identical objects – variation is the only real thing. Even when potters aim to reproduce exactly the same object there are always intra-individual and inter-individual variations in the shapes of the finished products (Gandon et al. 2018; Gandon et al. 2020; Gandon et al. 2021). This is so because copying error is always present (Eerkens 2000; Eerkens & Lipo 2005; Premo 2020; Hamilton & Buchanan 2009; Kempe et al. 2012). Cultural transmission theory resolves the ontological dilemma between essentialism and materialism which stands behind the Ford-Spaulding debate. The view that types are real is essentialist, whereas the idea that only variation is real and that types are analytical constructs is a materialist position (O'Brien & Lyman 2000). Cultural transmission theory implies that they are both. The person who copies an object or an attribute of an object is copying (or reconstructing in her/his mind - -see Scott-Phillips 2017) a certain meme, a cultural variant. But this process inevitably introduces error and variation, which at some point may become part of the meme variant itself.

The difficulty with types may be illustrated by an example. Let us consider a single continuous attribute of an object or, even better, a continuous dimension which summarizes the shape of an object (e.g. the first principal component of the morphometric analysis). Imagine that this variable is distributed as in the graph in Figure 7.1 – the distribution is trimodal, which means that individual measurements cluster around three particular values. How do we interpret this? One possible interpretation would be that there are three types and people are trying to copy one of the three types. Due to copying errors, people cannot exactly reproduce the shape of an artifact, so there is a variation around the mean for each type. The types are discrete in people's heads, but the copying process creates a continuum of values. This is Read's rationale for the identification of types from empirical data (Read 2007). However, another interpretation is also possible. We can say that there are an infinite number of types (for each possible value of the dimension in the graph), whereas the distribution in Figure 7.1 is telling us about the frequency of copying for each type (plus error).

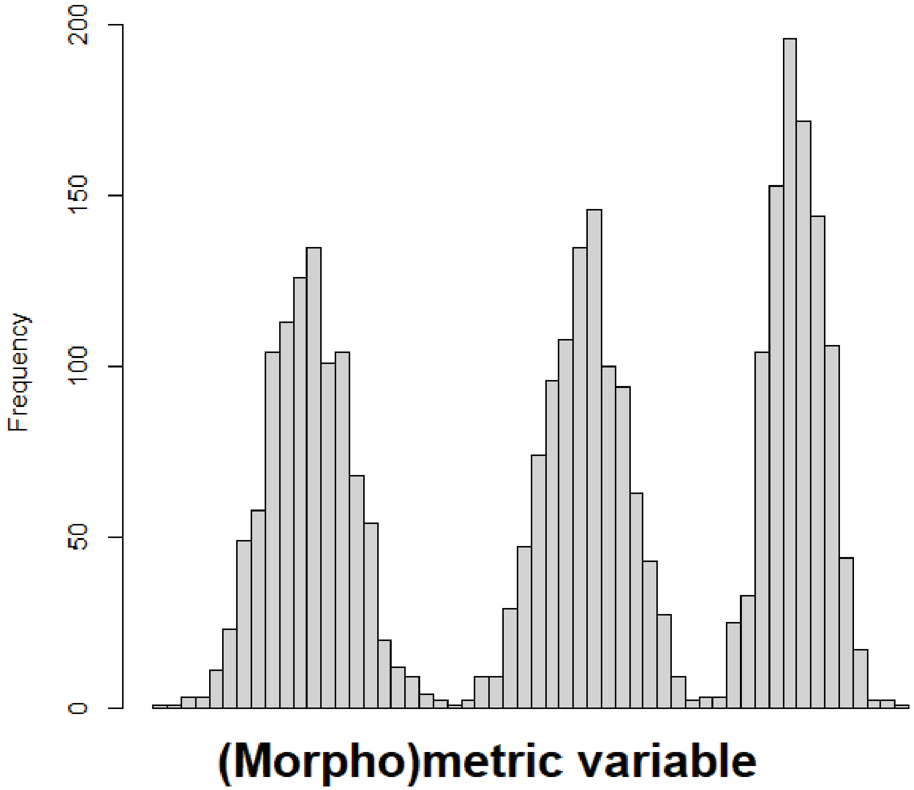

Figure 7.1. The histogram of a hypothetical metric variable or a morphometric summary dimension (e.g. principal component scores based on a number of correlated metric attributes).

This digression finally leads us to the following question. Is it useful that our theory and models be formulated in terms of discrete variants, or would it be better to develop the transmission models which are expressed in terms of continuous variables? Should we strive for the total phenotypic description of material culture (e.g. as in the geometrical morphometric approach), rather than define broad types? Perhaps we do not need to perform discretization, at least for the classification of shape, as was necessary before, but can work directly at the very high resolution provided by the direct numerical description of the shape. Thus it would make sense to explore the implications of cultural transmission on the probability density distributions of continuous attributes in a similar way as was done for the frequency structure of discrete variants and types (e.g. Rorabaugh 2014). The issue of systematics has generally been underrated and neglected in archaeology (Lyman 2021b; a), and the research in this book suffers from the same problem, as I have simulated the types/variants as ready-made without delving into how they are constructed. But cultural transmission theory offers a perfect framework to investigate the interplay of attribute transmission and the construction of typologies and classifications, and this is something that needs to be pursued in the future.

7.3. THE FEASIBILITY OF A CULTURAL TRANSMISSION RESEARCH PROGRAM IN ARCHAEOLOGY

The simple models presented in this book make predictions in terms of patterns of type frequencies in space and time. Culture-historical archaeology has been the dominant paradigm for decades almost everywhere in the world. Thousands of site reports have been published where the focus was on the description, both verbal and visual, of the typological variation. One would expect that this would make empirical investigation more expedient and feasible than some kind of analysis which would require a class of data which has only recently become available through expensive and time-consuming laboratory work. But this is not the case. It is actually very difficult to generate archaeological data comparable to the simulation output presented here, or compatible with the predictions of cultural transmission theory in general. There are two related major problems concerning the application of cultural transmission theory in archaeology – the insufficient quantity/quality of the data, and the lack of a uniform way of recording the formal variability of material culture. Even though one can think of endless publications with tables showing excavated pottery, flints or figurines, the actual assemblage sizes are very low, and in most cases the best one can do is record the data on the level of presences and absences, rather than frequencies. More ambitious researchers may go on and record data from museum collections, but this is an extremely time- and labour-consuming process, and therefore the number of recorded assemblages cannot be high. But even if one succeeds in producing a frequency structure description of the greater number of assemblages (e.g. Furholt 2009), the second major problem claims the stage – the incomparability of recording methods between different researchers. Unlike zooarchaeology, where the assemblages are always comparable, as one counts the number of identified specimens of universally agreed-upon categories such as species, in the traditional archaeological description of the material culture there is no such standard, as there is no such thing as a natural type of a pot or stone projectile. For this reason, every large-scale study of the formal variation of material culture usually starts from zero, which slows down the accumulation of knowledge and progress of science immensely. There is no ideal solution for this problem, but the new technology of recording data (3D scanning and digital photography) combined with the methods of geometric morphometrics (see Demján et al. 2022) and AI algorithms, may bring us closer to building the big data sets that could provide the detailed "phenotypic" description of the archaeological record which is necessary for the implementation of the evolutionary approach in archaeology.

Cultural transmission theory provides the theoretical and methodological bridges that connect the traditional archaeological topics with modern research methods and ideas, without falling into the old traps of cultural and typological essentialism. It also provides a way to utilize and extract new information from the legacy of archaeological material and data. Hopefully, this book provides yet another illustration of how we can use these exciting new intellectual and analytical tools to provide a fresh perspective on the old problems, and to show how "boring" and "tedious" elements such as types, attributes, classifications (Lyman 2021b) can contribute to and become a part of what Kristiansen (2014) labelled the third science revolution in archaeology.

GLOSSARY

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Anti-conformist transmission – A form of cultural transmission where there is a bias towards rare variants. There are different versions of the anti-conformist model – the bias can be strictly limited to the rarest variants, which are usually cultural mutations (completely new variants), or it can refer to a subset of the least frequent cultural variants, with some predefined frequency threshold.

Archaeological culture – A group of sites, bounded in space and time, with a similar material culture.

Attribute – Any characteristic of an artifact, measured on any of the scales (nominal, ordinal, interval, or ratio). In the context of statistical analysis, attribute is a variable which can take certain values (the number and kind of values depending on the scale of measurement). For example, *color* and *height* are attributes of a ceramic vessel. Synonyms for the term attribute are dimension and character.

Attribute state – The value which a given attribute can take. In the context of statistical analysis, an attribute state is a concrete value taken by a variable. For example, an attribute state for an attribute *color of a pot* can be *red*, or an attribute state for an attribute *height* can be 20cm.

Assemblage – A set of artifacts which are treated as one archaeological unit, deposited over a certain period of time. Assemblages are defined at different spatial and temporal scales, depending on the research agenda and practical limitations. For example, assemblages may refer to groups of objects found in pits on a site, or to groups of objects from sites in a region.

Axelrod model – A model of cultural transmission, named after Robert Axelrod, who formulated the model (Axelrod 1997). In this model, the probability of cultural transmission between entities (e.g. individuals or groups) is proportional to the current level of similarity between them. This kind of preference is usually labelled as homophily. In simple terms, this model states that people are more likely to interact with (and copy cultural elements from) people who are similar to themselves.

Brainerd - Robinson similarity/distance – A quantitative measure of similarity between two assemblages based on the relative frequencies of types in assemblages, introduced by George Brainerd (1951) and William Robinson (1951). The similarity between pairs of assemblages can take values between 0 (no similarity at all) to 200 (all types have equal frequencies). The Brainerd-Robinson similarity measure can be transformed into distance by subtracting from 200. Distance values near 0 correspond to the highest similarity (identical composition of assemblages) between a pair of assemblages, whereas distance values close to 200 indicate low similarity.

Conformist transmission – A form of cultural transmission where there is a bias towards the most frequent variants. There are different versions of the conformist model – the bias can be strictly limited to the most frequent variant, or it can be more loosely defined to refer to a subset of the most frequent cultural variants, with some predefined frequency threshold.

Content biases – Biases which depend on the content of the cultural variant, i.e. their idiosyncratic properties. For example, short stories are easier to remember and transmit than long stories; more efficient arrow design is more likely to be replicated than a less efficient one.

Context biases – Biases which depend on the context of transmission. In this case, the cultural variant is more likely to be transmitted not because of its intrinsic properties, but because of its specific context – it could be the propensity to copy the most or the least frequent variants (see conformist or anti-conformist transmission), or the bias may stem from the bearer of the cultural variant (prestige or perceived similarity to oneself).

Correspondence analysis – A multivariate statistical technique used to explore the relations between categorical variables and entities described on these variables, based on the frequencies of categories within each entity. In archaeology, it is often used as a seriation technique, or more generally, to explore the relations between assemblages and categories of units comprising assemblages (e.g. species composition in zooarchaeological assemblages coming from different sites or contexts within a site). The main results of a correspondence analysis is a scatterplot graph which simultaneously represents the entities and categories – entities and categories which are close to each other on this graph have similar relative frequencies of entities belonging to different categories. For example, two site assemblages which are close in the space defined by the first two correspondence analysis axes have similar proportions of types.

Cultural attractors – Cultural variants or meme variants which are for cognitive reasons (e.g. easier to remember) or ecological reasons (e.g. easier to perform, sing or pronounce) more probable outcomes of the transformation within the cultural transmission process than others. The cultural attractor is an important concept in cultural attraction theory (also known as cultural epidemiology theory).

Cultural attraction theory – An evolutionary theory of culture which views the process of cultural transmission as a process of transformation of cultural information, rather than as simple replication. This theory suggests that within each cultural transmission episode there is a shift from the original meme variant towards meme variants which are cultural attractors – cultural variant(s) which are a more probable outcome of transformation than others. Unlike the “standard” cultural transmission theory formulated by Boyd and Richerson (1985), the difference between a model and a copy is not only due to random error or intention, but is a product of transformations which, for cognitive or ecological reasons, have an inbuilt bias towards particular cultural variants (meme variants or attribute states).

Cultural diffusion – The transmission of cultural information between individuals and groups in space and time.

Cultural drift – Changes in frequencies of cultural variants caused by the effects of sampling from a finite population. When cultural variants are copied without bias (i.e. with probability proportional only to their current frequencies), and when the population size is finite, some variants will by chance be copied more than others, which will increase their frequency and probability of being copied in the next generation.

Cultural mutation – An appearance of a new cultural variant as a consequence of copying error in the transmission process or as a consequence of a deliberate act of innovation (e.g. as a consequence of individual learning or decision).

Cultural selection – An increase in the frequency of variants in the process of cultural transmission, where some of the variants have a higher probability of being transmitted due to their intrinsic or contextual properties. For example, an arrowhead design with superior performance is more likely to be transmitted.

Dual inheritance theory – Otherwise known as *gene-culture coevolution theory*, this theory holds that humans have two separate, but interacting channels of inheritance: biological and cultural. In this theory, both of these inheritance systems are conceptualized as Darwinian evolutionary systems.

Extensional definition of types – Definition of types based on the idiosyncratic properties of the objects being classified (Dunnell 1971; O'Brien & Lyman 2000). An analyst groups the objects into types based on their similarity, without having an *a priori* established set of dimensions or attributes and their potential values. Definitions of classes in such a classification are derived from the properties of the objects themselves, as the conditions for membership are based on an enumeration of the members of a class (Dunnell 1971; O'Brien & Lyman 2000).

Guided variation – A model of cultural transmission where the mutations are not random, but are biased towards existing cultural preferences. Such directional mutations are then further transmitted in an unbiased manner.

Homophily – In general, this refers to the preference for interaction with people who are similar to each other. In cultural transmission research, it refers to the preference for copying cultural traits from models culturally most similar to oneself.

Horizontal transmission – The social learning of cultural information from members of the same generation.

Infinite allele model – A model in population genetics where the number of potential alleles introduced by mutations is large, so that each new allele is different from the existing ones.

Isochrestic variation – The term proposed by James Sackett (1982) to define the concept of style in anthropology and archaeology. It refers to the choice between functionally equivalent alternatives when making an object, and the variation which results from such decisions.

Isolation by distance – Isolation by distance refers to the probability of interaction between individuals and communities depending on their spatial distance. There is an inverse correlation between interaction and distance – communities/individuals which are less distant will have a higher probability of interaction than those which are far away. When it comes to cultural transmission, the main effect of isolation by distance is the spatial structuring of culture in the form of cultural clines and the fall-off of cultural similarity in space.

Jaccard similarity/distance – A quantitative measure of similarity between two entities (artifacts or assemblages) based on the presence and absence of attribute states, but not taking into account shared absence. It was introduced by Paul Jaccard (1912). It can take values from 0 to 1, with 0 denoting no similarity at all, and 1 denoting that two entities share all attribute states, i.e. they are identical on the attributes which are analyzed. Jaccard distance is derived by subtracting the value of the Jaccard similarity from 1. Distance values close to 1 indicate low levels of similarity, whereas distance values close to 0 indicate high levels of similarity.

Mantel test – The technique of calculating the statistical significance of the correlation between two distance matrices based on random permutations of the original data, formulated by Nathan Mantel (1967). In the context of matrix correlation, the permutation test is used instead of the standard significance test, since the assumption of independence of observations does not hold when the units of observations are distances between pairs of observations. This is so because the same entity (e.g. same assemblage) will be present in more than one pair.

Matrix correlation – Pearson’s or Spearman’s correlation coefficient between two sets of distances (e.g. typological and spatial), where the units of observation are pairs of entities (usually assemblages) being compared and the variables are the two distance values associated with each pair. For example, if we are looking for a correlation between spatial and typological distances, each pair of assemblages has two coordinates, the spatial distance and the typological distance between them. The statistical significance of these associations is usually tested with the Mantel test (see Mantel test).

Meme – A “unit” of cultural inheritance, introduced by Richard Dawkins (1976), loosely analogous to gene in biological inheritance. Unlike for a gene, there is no consensus on the physical manifestation and interpretation of a meme, or specification of its scale (e.g. a meme can be a motif in a story or an entire story; a position of a single note in a tune or an entire melody). Some scholars conceptualize meme as a physical unit – a specifically activated neural structure in the brain – whereas others use it only as a metaphor.

Meme variant – A specific realisation of a meme, analogous to allele in biology. For example, a meme could be an eye type of an anthropomorphic figurine, whereas triangular and circular eyes would then represent particular meme variants.

Natural selection – The increase of frequency of genes or cultural variants which confer adaptive advantage to individuals – those which increase the probability of survival and reproduction.

Neutral evolution – A differential reproduction/replication of variants (biological or cultural) caused by the sampling effects (chance) in finite populations. The frequencies of successful variants do not increase because they confer some adaptive advantage, as in the case of natural selection, but owing to chance.

Neutral (unbiased) transmission – A cultural transmission process where there is no bias or preference for any of the variants, which means that the probability of their transmission is proportional to their current frequencies.

Oblique transmission – Social learning of cultural information from members of the parental generation other than one's parents.

Paradigmatic classification – In systematics, a method of creating classes by intersection of all of the attributes (dimensions) by which an artifact is described (Dunnell 1971; O'Brien & Lyman 2000). For example, if anthropomorphic figurines are described by two attributes such as eye shape (with attribute states circular (C) and triangular (T)) and color (with attribute states red (R) and black (B)), then the potential classes (types) are CR, CB, TR, and TB, where the first letter marks the attribute state of the eye shape, and the second one marks the attribute state of the color.

Phylogenetics – A study of evolutionary relationships between entities with an aim to reveal the structure of ancestor-descendant relations. Cultural phylogenetics is concerned with a reconstruction of the evolutionary history of cultural elements based on their attributes, where the main aims are to identify the presence of the phylogenetic signal and to establish the historical-evolutionary tree, which shows how the cultural elements are related to each other in terms of sharing common ancestors or being in ancestor-descendant relations to each other.

Prestige bias – Bias towards cultural variants held by individuals of high status (prestige).

Seriation – A method of relative dating in archaeology based on the principle that the units (artifacts or assemblages of artifacts) should be arranged in a sequence, such that the most similar units are next to each other.

Time-averaging – The process which affects the properties of archaeological assemblages as objects deposited at different times within a wider temporal interval are aggregated into a larger temporal unit, as archaeologists are unable to resolve their chronology at finer temporal scales. For example, a pottery assemblage from a cultural layer on a site which was accumulated over 50 years without clear stratigraphic breaks will be treated as one unit. This assemblage is time-averaged, as the frequencies of pot types do not reflect the structure of a set of objects deposited in a single moment in time or some narrow temporal interval like a year, but represent a mixture of several deposition episodes over the duration of an archaeological unit.

Type – In this book, the term type is understood as a paradigmatic class – which means a specific combination of attributes states. It is synonymous with cultural variant or meme variant in this context. The types are sometimes conceptualized as abstractions, or idealisations, and operationalised through statistical summaries, but this is not the view taken here.

Unimodality – Refers to the distribution of relative frequencies of types within assemblages arranged in a sequence. Unimodal sequences are such that relative frequencies of each type in a sequence exhibit one of three patterns: 1) increase, peak, decrease 2) increase, peak 3) peak, decrease. The peak is the maximum relative frequency of a type found in one or several assemblages which are being seriated, when ordered into a sequence.

Universal Darwinism – A generalization of the basic principles of Darwinian evolution applied to any system, regardless of its physical medium, where three conditions are met: 1) presence of transmission of information between entities in a population (descent) 2) potential for the generation of new information (modification) 3) potential for the differential preservation of information (evolutionary process).

Vertical transmission – Refers to the process whereby children learn cultural information from their parents.

APPENDIX

APPENDIX 1

R CODE FOR THE SIMULATION OF CULTURAL TRANSMISSION IN SPACE AND TIME FOR THE NEUTRAL, CONFORMIST, AND ANTI-CONFORMIST MODELS

Generating the spatial grid

```
l = 20 #number of cells on the x axis

w = 20 #number of cells on the y axis

Dataset <- matrix(0, l*w, 2)

Dataset[,2] <- rep(c(1:w),l)

x <- c()

for(i in 1:l){

x <- c(x, rep(i,w))

}

Dataset[,1] <- x

plot(Dataset[,1], Dataset[,2]) #plots the grid

The simulation
```

```
#######Function for sampling (unknown source)

resamp <- function(x,...){if(length(x)==1) x else sample(x,...)}

########

###Function for counting modes

Mode <- function(x) {

mastervariants <- as.numeric(levels(factor(x)))

varcount <- c(rep(0,length(mastervariants)))

for(m in 1:length(mastervariants))

       {

       index <- which(x==mastervariants[m])

       varcount[m] <- length(index)

       }

indexvar <- which(varcount==(max(varcount)))

result <- mastervariants[indexvar]

result <- resamp(result, 1)

return(result)

}

#########Loading the spatial grid and calculating the probability of interaction based on the inverse squared distance

distraw <- dist(Dataset[,1:2], method=”euclidean”, upper = TRUE, diag =TRUE, p = 2)

distraw <- as.matrix(distraw)
```

```
simraw <- 1/(distraw^2)

######Basic simulation setup

Nz = 100   #Living (systemic) assemblage size

Nlok = length(Dataset[,1]) #Number of cells

NU = 0.005 # the mutation rate

M = 0.1#probability of intercommunity interaction

conf = 0 #probability of conformist behavior

conserv = 0 #probability of keeping the same variant – the
retention bias (not used in any of the simulations in the book)

novel = 0 # probability of anti-conformist behavior



######Generating probabilities of interaction based on the
distances between sites

for(i in 1:Nlok) {

       for(j in 1:Nlok) {

if(i==j) {simraw[i,j]=100};

}

}

for(i in 1:Nlok) {

indexne1 <- as.vector(which(simraw[i,]!=100))

simraw[i,indexne1] <- simraw[i, indexne1]*(M/
sum(simraw[i,indexne1]))
```

```
index1 <- as.vector(which(simraw[i,]==100))

simraw[i,index1] = 1-M

}

sum(simraw[1,2:Nlok])

moddist <- simraw

#################################### Simulation

Iter = 1000 #Number of iterations (duration of the simulation
run)

L = 2 #average item use-life

z = 1/L

pocetni <- round(runif(Nz, 1,10),0)

lokmatr <- cbind(pocetni, matrix(0, Nz, Iter-1))

Nzarh = round(Nz*z,0)

lokmatrarh <- matrix(0, Nzarh, Iter-1)

ANTR <- list(lokmatr)

for(k in 1:Nlok) {

ANTR[[k]] <- lokmatr

}

ARH <- list(lokmatrarh)

for(k in 1:Nlok) {

ARH[[k]] <- lokmatrarh
```

```
}

inov = max(pocetni)+1

tempinov <- c()

INOV <- list()

for(k in 1:Nlok){

INOV[[k]] <- c(NA)

}



for(m in 2:Iter){

cat(m,'\n')

      for(q in 1:Nlok) {

            arhindeks <- sample(1:Nz, Nzarh, replace=FALSE)

                  ARH[[q]][,(m-1)] <- ANTR[[q]]
[arhindeks,(m-1)]

            ANTR[[q]][-arhindeks,m] <- ANTR[[q]]
[-arhindeks,(m-1)]

for(i in 1:length(arhindeks)) {

stoh1 <- sample(c(1,2,3,4,5), 1, prob=c(conf, (1-NU-conf-novel-
conserv), NU, novel, conserv))

if(stoh1 == 1) {ANTR[[q]][arhindeks[i],m] <- Mode(ANTR[[q]][,m-
1])} else {wer = 1}

if(stoh1 == 3) {ANTR[[q]][arhindeks[i],m] <- inov; tempinov <-
c(tempinov, inov); inov = inov + 1;} else {wer = 2}
```

```
if(stoh1 == 2) {lok<- sample(c(1:Nlok),1, prob=moddist[q,]); h
<- sample.int(Nz,1); ANTR[[q]][arhindeks[i],m] <- ANTR[[lok]]
[h,(m-1)];} else {wer=3}

if(stoh1 == 4) {if(is.na(INOV[[q]][1])== FALSE) {ANTR[[q]]
[arhindeks[i],m] <- resamp(INOV[[q]],1);} else {lok<-
sample(c(1:Nlok),1, prob=moddist[q,]); h <- sample.int(Nz,1);
ANTR[[q]][arhindeks[i],m] <- ANTR[[lok]][h,(m-1)];};} else
{wer=4}

if(stoh1 == 5) {ANTR[[q]][arhindeks[i],m] <- ANTR[[q]]
[arhindeks[i],m-1];} else {wer=5}

}

if(length(tempinov)==0) {INOV[[q]] <- c(NA)} else {INOV[[q]] <-
tempinov}

tempinov <- c()

                                 }

}
```

Collecting output data (for synchronous assemblages, as in Chapter 5)

```
#####Time -averaging

startpoint= 100# set the start limit of the aggregation interval

endpoint= 149  # set the end limit of the aggregation interval

dataraw <- matrix(0, Nlok, Nzarh*(endpoint-startpoint+1))

for(q in 1:Nlok) {

dataraw[q,] <- as.vector(ARH[[q]][,startpoint:endpoint])
```

```
}

#Generating the data matrix

mastervariants <- as.numeric(levels(factor(dataraw)))

varcount <- matrix(0, Nlok, length(mastervariants))

for (g in 1:(Nlok)) {

cat(g,'\n')

for (m in 1:length(mastervariants)) {

index <- which(dataraw[g,]==mastervariants[m])

varcount[g,m] <- length(index)

};

}

varcount ####The output data matrix with cell assemblages in
rows and types in columns. Each cell of the matrix gives the
frequency of the ith type in the jth assemblage.
```

Collecting output data (for asynchronous assemblages, as in Chapter 6)

```
ss = 600 #lower boundary of the temporal window (in iterations)

se = 750  #upper boundary for the midpoint of the temporal
window (e.g. if

#the desired width of the temporal window is 200 iterations, the
length of #the time-averaging interval is 50 iterations, and the
lower boundary is #600, then this upper boundary should be set
to 750).
```

```
interval=50 #the length of time-averaging interval (in
iterations)

dataraw <- matrix(0, Nlok, Nzarh*interval)

timepoint <- c(1:Nlok) #midpoints of aggregation intervals

for(q in 1:Nlok) {

startpoint= sample(c(ss:se),1)

endpoint= startpoint+interval-1

timepoint[q] <- (startpoint+endpoint)/2

dataraw[q,] <- as.vector(ARH[[q]][,startpoint:endpoint])

}


#Generating the data matrix

mastervariants <- as.numeric(levels(factor(dataraw)))

varcount <- matrix(0, Nlok, length(mastervariants))

for (g in 1:(Nlok)) {

cat(g,'\n')

for (m in 1:length(mastervariants)) {

index <- which(dataraw[g,]==mastervariants[m])

varcount[g,m] <- length(index)

};

}
```

```
varcount ####The output data matrix with cell assemblages in
rows and types in columns. Each cell of the matrix gives the
frequency of the ith type in the jth assemblage.
```

APPENDIX 2

R CODE FOR THE SIMULATION OF THE AXELROD MODEL

Generating the spatial grid

```
l = 20 #number of cells on the x axis

w = 20 #number of cells on the y axis

Dataset <- matrix(0, l*w, 2)

Dataset[,2] <- rep(c(1:w),l)

x <- c()

for(i in 1:l){

x <- c(x, rep(i,w))

}

Dataset[,1] <- x

plot(Dataset[,1], Dataset[,2]) #plots the grid
```

The simulation

```
#######Function for sampling (unknown source)
```

```
resamp <- function(x,...){if(length(x)==1) x else sample(x,...)}

########

###Function for counting modes

Mode <- function(x) {

mastervariants <- as.numeric(levels(factor(x)))

varcount <- c(rep(0,length(mastervariants)))

for(m in 1:length(mastervariants))

        {

        index <- which(x==mastervariants[m])

        varcount[m] <- length(index)

        }

indexvar <- which(varcount==(max(varcount)))

result <- mastervariants[indexvar]

result <- resamp(result, 1)

return(result)

}

#########Loading the spatial grid and calculating the probability
of interaction based on the inverse squared distance

distraw <- dist(Dataset[,1:2], method=”euclidean”, upper = TRUE,
diag =TRUE, p = 2)

distraw <- as.matrix(distraw)

simraw <- 1/(distraw^2)
```

```
##############Function for calculating the Brainerd-Robinson
distances/similarities (Alberti 2021b)

library(vegan)

############B-R similarity coefficent function###

BRsim <- function(x, correction, rescale) {

  if(require(corrplot)){

    print("corrplot package already installed. Good!")

  } else {

    print("trying to install corrplot package...")

    install.packages("corrplot", dependencies=TRUE)

    suppressPackageStartupMessages(require(corrplot))

  }

  rd <- dim(x)[1]

  results <- matrix(0,rd,rd)

  if (correction == T){

    for (s1 in 1:rd) {

      for (s2 in 1:rd) {

        zero.categ.a <-length(which(x[s1,]==0))

        zero.categ.b <-length(which(x[s2,]==0))

        joint.absence <-sum(colSums(rbind(x[s1,], x[s2,])) == 0)

        if(zero.categ.a==zero.categ.b) {
```

```
          divisor.final <- 1
        } else {
          divisor.final <- max(zero.categ.a, zero.categ.b)-joint.
absence+0.5
        }
        results[s1,s2] <- round((1 - (sum(abs(x[s1, ] /
sum(x[s1,]) - x[s2, ] / sum(x[s2,]))))/2)/divisor.final, digits=3)
      }
    }
  } else {
    for (s1 in 1:rd) {
      for (s2 in 1:rd) {
        results[s1,s2] <- round(1 - (sum(abs(x[s1, ] /
sum(x[s1,]) - x[s2, ] / sum(x[s2,]))))/2, digits=3)
      }
    }
  }
  rownames(results) <- rownames(x)
  colnames(results) <- rownames(x)
  col1 <- colorRampPalette(c(“#7F0000”, “red”, “#FF7F00”,
“yellow”, “white”, “cyan”, “#007FFF”, “blue”, “#00007F”))
  if (rescale == F) {
    upper <- 200
```

```
    results <- results * 200

  } else {

    upper <- 1.0

  }

  return(results)

}



######Basic simulation setup

Nz = 100   #Living (systemic) assemblage size

Nlok = length(Dataset[,1]) #Number of cells

NU = 0.005 # the mutation rate

M = 0.1#probability of intercommunity interaction

conf = 0 #probability of conformist behavior

conserv = 0 #the probability of keeping the same variant – the
retention bias (not used in any of the simulations in the book)

novel = 0 # the probability of anti-conformist behavior (not
used in any of the simulations in the book)



######Generating probabilities of interaction based on the
distances between sites

for(i in 1:Nlok) {

       for(j in 1:Nlok) {
```

```
if(i==j) {simraw[i,j]=100};

}

}

for(i in 1:Nlok) {

indexne1 <- as.vector(which(simraw[i,]!=100))

simraw[i,indexne1] <- simraw[i, indexne1]*(M/
sum(simraw[i,indexne1]))

index1 <- as.vector(which(simraw[i,]==100))

simraw[i,index1] = 1-M

}

sum(simraw[1,2:Nlok])

moddist <- simraw

################################## Simulation

Iter = 1000 #Number of iterations

L = 2 #average item use-life

z = 1/L

pocetni <- round(runif(Nz, 1,10),0)

lokmatr <- cbind(pocetni, matrix(0, Nz, Iter-1))

Nzarh = round(Nz*z,0)

lokmatrarh <- matrix(0, Nzarh, Iter-1)

ANTR <- list(lokmatr)
```

```
for(k in 1:Nlok) {

ANTR[[k]] <- lokmatr

}

ARH <- list(lokmatrarh)

for(k in 1:Nlok) {

ARH[[k]] <- lokmatrarh

}

inov = max(pocetni)+1

tempinov <- c()

INOV <- list()

for(k in 1:Nlok){

INOV[[k]] <- c(NA)

}



for(m in 2:Iter){

cat(m,'\n')

#####Generating the matrix of current typological similarity
between pairs of cells###

dataraw <- matrix(0, Nlok, Nz)

for(p in 1:Nlok) {

dataraw[p,] <- as.vector(ANTR[[p]][,(m-1)])
```

```
}

mastervariants <- as.numeric(levels(factor(dataraw)))

varcount <- matrix(0, Nlok, length(mastervariants))



for (g in 1:(Nlok)) {

for (n in 1:length(mastervariants)) {

index <- which(dataraw[g,]==mastervariants[n])

varcount[g,n] <- length(index)

};

}



tipsim <- BRsim(varcount, correction=F, rescale=T)

tipsim <- as.matrix(tipsim)

index <- which(tipsim < 0.5) # the value in the brackets is the
similarity threshold for the interaction (it is a rescaled BR
similarity coefficient which can take values from 0 to 1)

tipsim[index] = 0

moddist1 = moddist

for(p in 1:Nlok) {

if(sum(tipsim[p,which(tipsim[p,]!=1)])==0)
{tipsim[p,]=tipsim[p,]; moddist1[p,p]=1}
else {tipsim[p,which(tipsim[p,]!=1)]
<- tipsim[p,which(tipsim[p,]!=1)]/
sum(tipsim[p,which(tipsim[p,]!=1)])}
```

```
}

probsim = moddist1*tipsim

for(u in 1:Nlok) {

korig <- probsim[u,][which(probsim[u,]!=(1-M))]

if(sum(korig)==0) {probsim[u,u]=1} else {korig <- (M*korig)/
sum(korig); probsim[u,][which(probsim[u,]!=(1-M))] = korig}

}

       for(q in 1:Nlok) {

             arhindeks <- sample(1:Nz, Nzarh, replace=FALSE)

                    ARH[[q]][,(m-1)] <- ANTR[[q]]
[arhindeks,(m-1)]

             ANTR[[q]][-arhindeks,m] <- ANTR[[q]]
[-arhindeks,(m-1)]

for(i in 1:length(arhindeks)) {

stoh1 <- sample(c(1,2,3,4,5), 1, prob=c(conf, (1-NU-conf-novel-
conserv), NU, novel, conserv))

if(stoh1 == 1) {ANTR[[q]][arhindeks[i],m] <- Mode(ANTR[[q]][,m-
1])} else {wer = 1}

if(stoh1 == 3) {ANTR[[q]][arhindeks[i],m] <- inov; tempinov <-
c(tempinov, inov); inov = inov + 1;} else {wer = 2}

if(stoh1 == 2) {lok<- sample(c(1:Nlok),1, prob=probsim[q,]); h
<- sample.int(Nz,1); ANTR[[q]][arhindeks[i],m] <- ANTR[[lok]]
[h,(m-1)];} else {wer=3}

if(stoh1 == 4) {if(is.na(INOV[[q]])== FALSE) {ANTR[[q]]
[arhindeks[i],m] <- resamp(INOV[[q]],1);} else {lok<-
sample(c(1:Nlok),1, prob=probsim[q,]); h <- sample.int(Nz,1);
```

```
ANTR[[q]][arhindeks[i],m] <- ANTR[[lok]][h,(m-1)];};} else
{wer=4}

if(stoh1 == 5) {ANTR[[q]][arhindeks[i],m] <- ANTR[[q]]
[arhindeks[i],m-1];} else {wer=5}

if((((stoh1==2)|(stoh1==4))&(q != lok))==TRUE) {tempinov <-
c(tempinov, ANTR[[q]][arhindeks[i],m]);} else {wer=344}

}

if(length(tempinov)==0) {INOV[[q]] <- c(NA)} else {INOV[[q]] <-
tempinov}

tempinov <- c()

                           }

}
```

Collecting output data

```
#####Time -averaging

startpoint= 100# set the start limit of the aggregation interval

endpoint= 149  # set the end limit of the aggregation interval

dataraw <- matrix(0, Nlok, Nzarh*(endpoint-startpoint+1))

for(q in 1:Nlok) {

dataraw[q,] <- as.vector(ARH[[q]][,startpoint:endpoint])

}

#Generating the data matrix

mastervariants <- as.numeric(levels(factor(dataraw)))
```

```
varcount <- matrix(0, Nlok, length(mastervariants))

for (g in 1:(Nlok)) {

cat(g,'\n')

for (m in 1:length(mastervariants)) {

index <- which(dataraw[g,]==mastervariants[m])

varcount[g,m] <- length(index)

};

}

varcount ####The output data matrix with assemblages in rows and
types in columns. Each cell of the matrix gives the frequency of
the ith type in the jth assemblage.
```

APPENDIX 3

R CODE FOR THE SIMULATION OF THE NEUTRAL, CONFORMIST AND ANTI-CONFORMIST MODEL OF CULTURAL TRANSMISSION FOR THE SINGLE COMMUNITY CASE

```
#######Function for sampling (unknown source)

resamp <- function(x,...){if(length(x)==1) x else sample(x,...)}

########

###Function for counting modes

Mode <- function(x) {

mastervariants <- as.numeric(levels(factor(x)))

varcount <- c(rep(0,length(mastervariants)))

for(m in 1:length(mastervariants))

       {

       index <- which(x==mastervariants[m])

       varcount[m] <- length(index)

       }
```

```
indexvar <- which(varcount==(max(varcount)))

result <- mastervariants[indexvar]

result <- resamp(result, 1)

return(result)

}

####Basic simulation setup

t = 1000 # Number of iterations (duration of the simulation run)

Pt = 100 #Item population size

L = 2 #average item use-life

z = 1/L

mu = 0.005 #mutation rate

conf = 0 #s probability of conformist behavior

novel = 0# probability of anti-conformist behavior (not used in
any of the simulations in the book)

conserv = 0 # probability of keeping the same variant – the
retention bias (not used in any of the simulations in the book)

arh <- list()

P <- rep(Pt,t) #Population size

S = P #systemic number of items

antr <- sample(c(1:10), S[1], replace=TRUE)

inov = max(antr) + 1
```

```
for(i in 1:t) {


Nzarh = round(z*length(antr),0)

arhindeks <- sample(1:length(antr), Nzarh, replace=FALSE)

arh[[i]] <- antr[arhindeks]

antrold <- antr



stoh <- runif(length(arhindeks), 0,1)

mutindeks <- which(stoh <= mu)

retindeks <- which((stoh>mu)&(stoh<=(mu+conserv)))

confindeks <- which((stoh>(mu+conserv))&(stoh<=(mu+conserv+conf)))

novelindeks <-
which((stoh>(mu+conserv+conf))&(stoh<=(mu+conserv+conf+novel)))

neindeks <- c(mutindeks, retindeks, confindeks, novelindeks)

inovektor <- c(inov:(inov+length(mutindeks)-1))

if(length(mutindeks)>0) {antr[arhindeks][mutindeks] <- inovektor;
inov =  inov+length(mutindeks)-1+1;} else {wer=1}

if(length(retindeks)>0) {antr[arhindeks][retindeks] <-
antr[arhindeks][retindeks]} else {wer=1}

if(length(confindeks)>0) {antr[arhindeks][confindeks] <-
rep(Mode(antrold), length(confindeks))} else {wer=1}

if((i>1)&(length(novelindeks)>0)) {antr[arhindeks][novelindeks]
<- resamp(inovektorold, length(novelindeks),replace=TRUE)} else
{wer=1}
```

```
inovektorold <- inovektor

if(length(neindeks)>0) {antr[arhindeks][-neindeks] <-
resamp(antrold, length(arhindeks[-neindeks]), replace=TRUE)}
else {antr[arhindeks] <- resamp(antrold, length(arhindeks),
replace=TRUE)}

}
```

Collecting output data

```
accuminterval = 100  #length of the aggregation interval in
number of iterations

brojkoraka = t/accuminterval

mastervariants <- as.numeric(levels(factor(unlist(arh))))

varcount <- matrix(0, brojkoraka, length(mastervariants))

g = 1

for(i in seq(1, t, accuminterval)) {

for (m in 1:length(mastervariants)) {

index <- which(unlist(arh[i:(i+accuminterval-
1)])==mastervariants[m])

varcount[g,m] <- length(index)

};

g = g+1

}
```

varcount # The output data matrix with assemblages (in the true temporal sequence) in rows and types in columns. Each cell of the matrix gives the frequency of the ith type in the jth assemblage.

APPENDIX 4

MODIFICATION OF THE SERIATION COEFFICIENT AND THE ASSOCIATED R CODE

A4.1. THE PROBLEM WITH THE SERIATION COEFFICIENT

The first issue has to do with the seriation or unimodality coefficient from Porčić (2013a). If we look at this coefficient (Equation 5.1) as a function of O (observed number of modes), for fixed Max (maximum number of modes) and E (expected number of modes), it is apparent that it is a linear function of O, the observed number of modes:

$$-\frac{1}{Max-E} \qquad \text{(Eq. A4.1)}$$

The slope of this function is equal to $-\frac{1}{Max-E}$. As both Max and E are positive integers, this means that the slope will always be less than one, and its magnitude will be highly influenced by the potential maximum number of modes (Max) – the larger the maximum for a given number of types, the smaller the slope. If we look at how the seriation coefficient of a data matrix with 40 assemblages and 20 types changes as a function of the observed number of modes (ranging from 20 to the maximum of 400 modes), expressed as both the total number of modes and the number of modes per type, we will notice that S decreases very slowly (Figure A4.1).

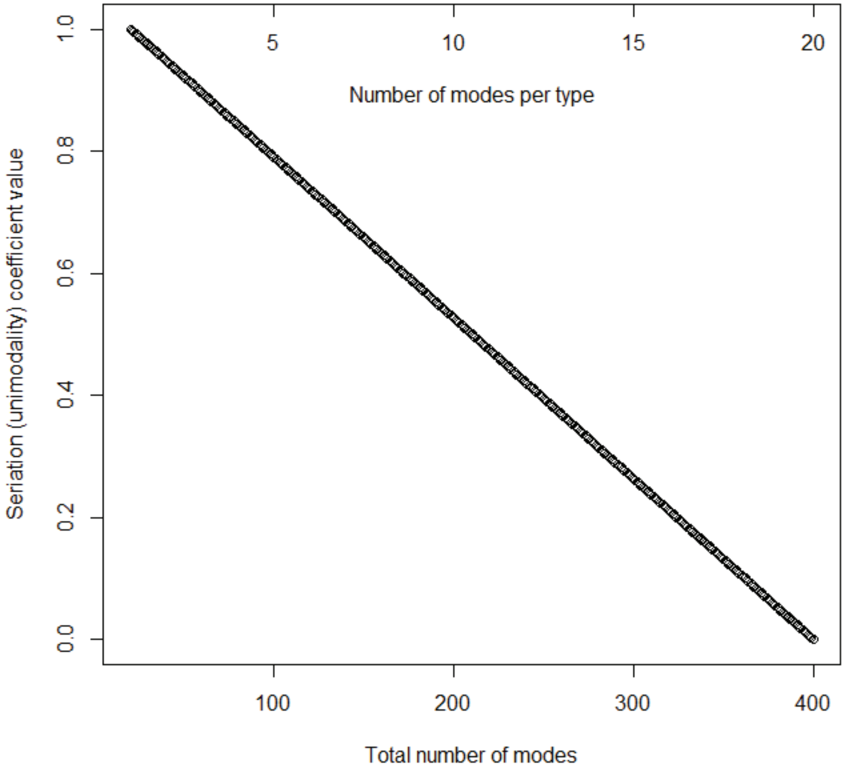

Figure A4.1. The seriation coefficient for the hypothetical data set containing 40 assemblages and 20 types changes linearly, as a function of the total number and the number of modes per type.

A4.2. FIXING THE SERIATION COEFFICIENT

As noted earlier, it is the maximum number of modes that exerts the great influence on the slope. For a fixed number of types and observed number of modes, increasing the maximum number of modes has a strong non-linear effect on the seriation coefficient (Figure A4.2), causing the seriation coefficient to increase very quickly. The maximal number of modes as it was defined in Porčić (2013a) was dependent on only two parameters: the number of assemblages and the number of types. It was also dependent on an unstated assumption that the data were such that by permuting the assemblages it was possible to find a sequence with the number of modes equal to the calculated maximum. But for many real data sets this is not the case.

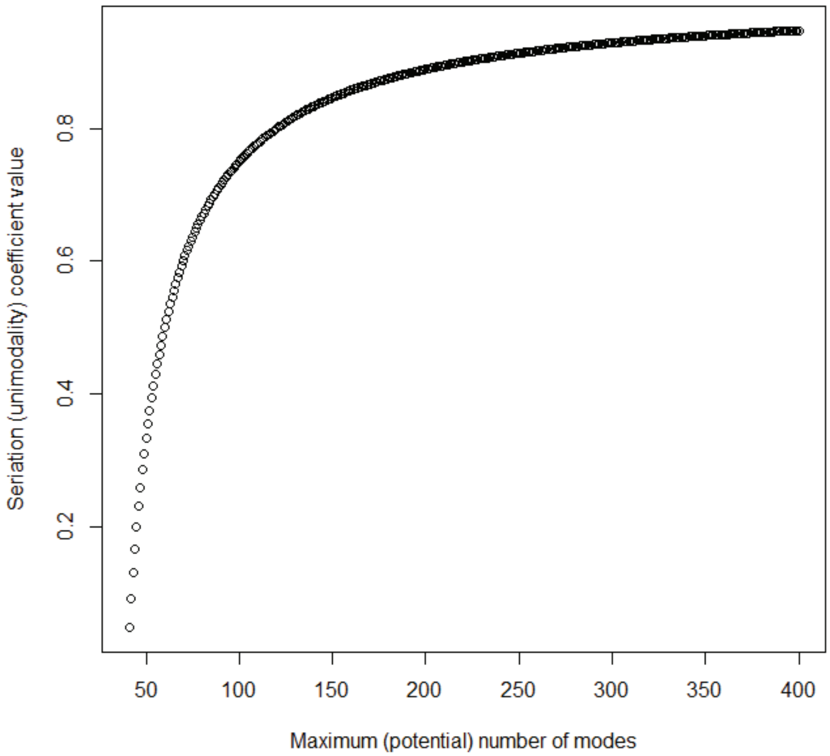

Figure A4.2. The values of the seriation coefficient for the fixed number of modes increases very quickly with the increase of the maximal number of modes.

The procedure for calculating the maximal number of modes needed for the calculation of the seriation coefficient may sometimes grossly overestimate the true maximum and thus inflate the value of the coefficient, as it assumes that all assemblages have different proportions of types. This overestimation will occur if there is a great number of tied values (different assemblages having the same proportion of a type). Whereas this is very unlikely for the non-zero values of proportions, cases where many assemblages have zero counts for some types are relatively common in archaeology. For this reason, it is necessary to find a way to make a more realistic estimation of the potential maximum number of modes in order not to inflate the seriation coefficient.

There are two solutions of this problem. The first is to use the results of the permutation test for significance testing in order to estimate numerically the maximum number of nodes that can occur by permuting the frequencies of the original data set (Porčić 2013a). The permutation procedure counts the total number of modes for each permutation. The maximum number of modes observed across all generated permutations would be a realistic numerical estimate of the potential number of modes of the random data. However, this may be an underestimate, as randomization of the data is not the same thing as finding a sequence that has the maximum number of nodes.

The second solution is analytically to arrive at a way to calculate the potential maximum number of modes based on the actual data. This second solution is followed in this book. All calculations of the seriation coefficient S1 are based on this solution.

A4.3. THE WAY OF ESTIMATING THE POTENTIAL MAXIMAL NUMBER OF MODES FOR A PARTICULAR DATA TABLE

In order to calculate a realistic estimate of the maximum number of modes based on the actual data, the following steps are performed for each type. First, the assemblages are sorted in ascending order, based on the proportion of the particular type that is being considered. This sequence is then split by the median into two ranked subsets that I shall call the high and the low value sets. If the number of assemblages (*n*) is even, then the number of elements in the subsets will be equal; if not, then the high value set should include the median, whereas a zero should be added to the end (to be the last value) of the low subset. The next step is to subtract the corresponding values (i.e. those having the same position or index) of the high and low subsets. This could also be expressed in vector notation. The high value subset is **h**, the low value subset is **l**, and the difference vector **d**, where i denotes the index (always an integer) of each assemblage.

For the case with an even number of assemblages, the equations are:

$$\begin{aligned}
\mathbf{l} &= (x_1, x_2, \ldots, x_{\frac{n}{2}}) \\
\mathbf{h} &= (x_{\frac{n}{2}+1}, x_{\frac{n}{2}+2}, \ldots, x_n) \qquad \text{(Eq. A4.2)} \\
\mathbf{d} = \mathbf{h} - \mathbf{l} &= (\, x_{\frac{n}{2}+1} - x_1), (x_{\frac{n}{2}+2} - x_2), \ldots, (x_n - x_{\frac{n}{2}})
\end{aligned}$$

For the case with an uneven number of assemblages, the equations are:

$$\begin{aligned}
\mathbf{l} &= (x_1, x_2, \ldots, x_{i_{median}-1}, 0) \\
\mathbf{h} &= (x_{i_{median}}, x_{i_{median}+1}, \ldots, x_n) \qquad \text{(Eq. A4.3)} \\
\mathbf{d} = \mathbf{h} - \mathbf{l} &= (\, x_{i_{median}} - x_1), (x_{i_{median}+1} - x_2), \ldots, (x_n - 0)
\end{aligned}$$

The potential maximum number of modes for a given type is equal to the number of non-zero entries of the difference vector **d**, whereas the potential maximum of the number of modes for an entire dataset (including all types) is the sum of calculated maximum values for each type. To see why this is so, we should look at the figure where this procedure is represented graphically. If we align the high and the low value subsets as presented in Figure A4.3, with the high value subset on the left side, and use these high-low value subset pairs to create a sequence starting from the top, the result will be a sequence with the maximum possible number of modes, as the value on the left will always be higher or equal to the value on the right, because one comes from the subset that is lower and the other that is higher than the median. In this way we are maximizing the alternation between higher and lower values, thus producing the sequence with the maximum number of modes possible for a given set of type proportions.

The zero in a case of uneven number of assemblages is added only as a computational convenience i.e. to make the number of elements in both subsets equal, so that the vector notation and programming are applicable. The highest value of the high value subset will always be higher than the highest value of the low value subset, unless they are all equal to the median.

It should be noted that this method might also overestimate the potential maximum number of modes, as the types are considered independently (which is not possible in reality, because reordering assemblages for one type also means reordering them for all other types). In any case, this method will be used to estimate the potential maximum number of modes for all the analyses that follow.

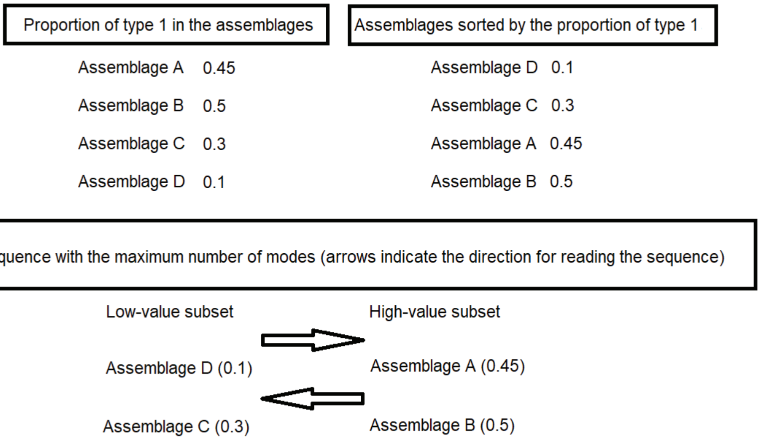

Figure A4.3. Schematic representation for establishing the sequence with the maximum number of modes for a given type.

A4.5. R CODE

A4.5.1. The code for the estimation of the potential maximal number of modes from the empirical data

```
MAXmod <- function(x) {

d <- length(x)

x <- sort(x)

medindex <- median(c(1:d))

if(d %% 2 == 0) {xhigh <- x[(0.5*d+1):d]; xlow <- x[1:(d*0.5)]}
else {xhigh <- x[medindex:d]; xlow <- x[1:(medindex-1)]}

if(d %% 2 != 0) {xlow <- c(xlow,0)} else {xlow=xlow}

difference <- xhigh - xlow

MAXmod <- length(difference[which(difference>0)])

if(var(x)==0) {MAXmod = 1} else {MAXmod = MAXmod}

MAXmod

}
```

The input for this function is the matrix where entries are the proportions of types (columns) in assemblages (rows).

A4.5.2. The new function for calculating the total number of modes of a sequence

When I published the original paper on the construction of the seriation coefficient I also included the R code as supplementary electronic material (Porčić 2013a). The function for counting the number of modes from a relative frequency data table was taken from one of the *R* internet forum posts (I am guilty of not citing the source, as I thought that it was a generic piece of code) which came up in a Google search. In the meantime, I noticed that this function can in very rare circumstances (when the equal proportions are in a sequence) produce erroneous counts. For this reason, I wrote my own code for counting the number of modes:

```
#Defining function for counting modes

Nmod <- function(x) {

diff <- c()

for(i in 1:(length(x)-1)) {

diff[i] <- x[i] - x[i+1]

}

sign <- sign(diff)

signotherthanzero <- sign[which(sign != 0)]

n = 1

if(length(signotherthanzero)<2) {Nsingle=1} else {

for(i in 1:(length(signotherthanzero)-1)) {

diff2 <- signotherthanzero[i]-signotherthanzero[i+1]

if(abs(diff2)!=2) {n = n} else {n = n + 1}

}

}

rof = signotherthanzero[1]

nchanges <- n

if(length(signotherthanzero)<2) {Nmod=Nsingle} else {if(nchanges
%% 2==0) {if(rof==1) {Nmod= nchanges*0.5+1} else {Nmod =
nchanges*0.5}} else {Nmod=(nchanges+1)/2}}
```

```
Nmod

}
```

A4.5.3. *The new code for the seriation permutation test*

Given the changes I made in the function for estimating the potential maximal number of modes and the function for counting the number of modes, I present a revised version of the full code for the seriation permutation test based on Porčić (2013a):

R CODE FOR PERFORMING THE PERMUTATION SIGNIFICANCE TEST

```
library(ca)   #library ca has to be installed

library(plyr) #library plyr has to be installed

Perm <- 1000  # Perm sets the number of permutations for the
randomization test. The default is 1000 but it can be changed by
the user.

PERM <- c(1:Perm)

#Defining function for counting modes

Nmod <- function(x) {

diff <- c()

for(i in 1:(length(x)-1)) {

diff[i] <- x[i] - x[i+1]

}

sign <- sign(diff)

signotherthanzero <- sign[which(sign != 0)]

n = 1
```

```
if(length(signotherthanzero)<2) {Nsingle=1} else {

for(i in 1:(length(signotherthanzero)-1)) {

diff2 <- signotherthanzero[i]-signotherthanzero[i+1]

if(abs(diff2)!=2) {n = n} else {n = n + 1}

}

}

rof = signotherthanzero[1]

nchanges <- n

if(length(signotherthanzero)<2) {Nmod=Nsingle} else {if(nchanges
%% 2==0) {if(rof==1) {Nmod= nchanges*0.5+1} else {Nmod =
nchanges*0.5}} else {Nmod=(nchanges+1)/2}}

Nmod

}

#Defining function for calculating the potential maximum number
of modes

MAXmod <- function(x) {

d <- length(x)

x <- sort(x)

medindex <- median(c(1:d))

if(d %% 2 == 0) {xhigh <- x[(0.5*d+1):d]; xlow <- x[1:(d*0.5)]}
else {xhigh <- x[medindex:d]; xlow <- x[1:(medindex-1)]}

if(d %% 2 != 0) {xlow <- c(xlow,0)} else {xlow=xlow}

difference <- xhigh - xlow
```

```
MAXmod <- length(difference[which(difference>0)])
if(var(x)==0) {MAXmod = 1} else {MAXmod = MAXmod}
MAXmod
}
#Reading data#
# Select and Copy a complete data table (without the assemblage and type labels i.e. without header) from a spreadsheet
data <- read.table(“clipboard”) #after copying the data from the spreadsheet, run this line
#Performing correspondence analysis (CA) on the data and calculating the number of modes for the CA solution
M <- length(data[1,])
a <- c(1:M)
b <- c(1:M)
data2 <- as.matrix(data)
ord <- ca(data)$rowcoord[,1]
data <- as.matrix(data)
data1 <- cbind(ord, data)
data1 <- as.data.frame(data1)
G <- arrange(data1, desc(ord))
matr <- G[,2:(M+1)]/(apply(G[,2:(M+1)],1, sum))
```

```
for(j in 1:M) {

a[j] <- Nmod(matr[,j])

}

sum(a) #gives the observed total of modes

####################Calculating the seriation (S) unimodality
coefficient for the empirical data#####################

maxcol <- c()

for(j in 1:M) {

maxcol[j] <- MAXmod(matr[,j])

}

MAXanalit = sum(maxcol)

S = (MAXanalit - sum(a))/(MAXanalit-M) ### Seriation coefficient
(S)

# Generating the distribution of total number of modes with
randomized data

for(i in 1:Perm) {

for(j in 1:M) {

data2[,j] <- sample(data[,j], replace = FALSE)

}

ord <- ca(data2[which(rowSums(data2)>0),])$rowcoord[,1]

data2 <- as.matrix(data2)

data3 <- cbind(ord, data2[which(rowSums(data2)>0),])
```

```
data3 <- as.data.frame(data3)

G <- arrange(data3, desc(ord))

matr <- G[,2:(M+1)]/(apply(G[,2:(M+1)],1, sum))

for(j in 1:M) {

b[j] <- Nmod(matr[,j])}

PERM[i] <- sum(b)}

hist(PERM)          # Draws a histogram of randomized total
number of modes

quantile(PERM, 0.05) # Gives the value of the 5th percentile of
the randomized distribution of total number of modes
```

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