Life Course Research and Social Policies 2

Philippe Blanchard Felix Bühlmann Jacques-Antoine Gauthier *Editors*

Advances in Sequence Analysis: Theory, Method, Applications



Advances in Sequence Analysis: Theory, Method, Applications

Life Course Research and Social Policies

Volume 2

Series Editors:

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Life course research has been developing quickly these last decades for good reasons. Life course approaches focus on essential questions about individuals' trajectories, longitudinal analyses, cross-fertilization across disciplines like life-span psychology, developmental social psychology, sociology of the life course, social demography, socio-economics, social history. Life course is also at the crossroads of several fields of specialization like family and social relationships, migration, education, professional training and employment, and health. This Series invites academic scholars to present theoretical, methodological, and empirical advances in the analysis of the life course, and to elaborate on possible implications for society and social policies applications.

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Advances in Sequence Analysis: Theory, Method, Applications



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Chapter 1 Introduction: Sequence Analysis in 2014

Jacques-Antoine Gauthier, Felix Bühlmann and Philippe Blanchard

Sequences for Social Sciences

Sequence analysis (SA), the statistical study of successions of states or events, is one of the promising venues of sociological methodology. Since its introduction in the social sciences in the mid-1980s it has developed steadily and spread to many social science disciplines. It is now central to the life-course perspective where it has been used to understand trajectories of cohabitation and housing and of occupational careers or crucial transitions, such as from school to work or from employment to retirement. More recently SA has also been employed to shed light on chains of historical events, on historical evolution of political institutions and on historical life courses. The method has also been employed to investigate other temporal scales, such as sequences of daily time use or response patterns in surveys.

In a nutshell, SA models processes. It compares chronological sequences of states within a holistic conceptual model instead of observing allegedly independent observations over time. SA accounts both for individual and structural dynamics.

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Each individual displays a unique trajectory, defined as a string of states of specific nature, with specific durations and a specific order. At the same time sequences resemble each other along common subsequences showing how individuals' trajectories are contingent on social structures.

Sequence analysis has the potential to fundamentally enhance our understanding of a broad range of social processes. Partly for methodological reasons, phenomena such as family configurations, employment patterns, poverty and precariousness, political engagement or social inequalities are traditionally analysed with synchronic models. This leads to a static understanding of these phenomena that prevents researchers from understanding (a) the real temporal nature of these phenomena and (b) how these are constructed through interdependent biographical processes. This also has practical consequences: as long as a phenomenon such as poverty is analysed using synchronic data, one fails to understand intra-individual variability. Why do some people fall into poverty and others escape from it? What typical previous biographical patterns lead to such an event, and what other patterns do not? SA—along with methods such as event history analysis or structural equation models—expands our understanding of biographical trajectories and has a role to play among major, current and substantial debates in the social sciences.

This book intends to promote a broad and systematic debate that takes stock of the advances and the specific range of application of SA, that encourages a careful standardisation of the approach beyond diverging orientations, and that discovers and explores new methodological paths and combinations. The project was initiated in the aftermath of the Lausanne Conference on Sequence Analysis (LaCOSA), in June 2012, which brought together scholars from Finland, France, Germany, Italy, South Korea, the Netherlands, Switzerland, the United Kingdom, and the United States¹. The conference revealed the international spreading of the method, and the need for concertation and harmonisation beyond national clusters of sequence analysts and some inter-cluster connections. Indeed, sociologists of the life course, historians of the family, political scientists, comparativists and social statisticians had to share beyond what could be done by publishing separately in specific disciplinary journals. Distinct approaches needed to be compared, good practices needed to be established and further developments needed to be based on collectively approved directions. Finally, the conference intended to connect the sequence approach with other, more traditional approaches to longitudinal data, which is one way SA can gain greater popularity.

The book addresses several audiences: experienced SA users looking for upto-date developments by renowned, as well as innovative, younger scholars; new SA users searching for a larger view on the diverse ways of applying the method; and sociologists, historians, political scientists and specialists of other social sciences using longitudinal data and interested in new ways of dealing with them.

¹ The authors wish to thank the Swiss National Science Foundation (NSF), and the following units of the University of Lausanne: the Institute for Social Sciences (ISS), the Institute for Political and International Studies (IEPI), the Research Center on Political Action of the University of Lausanne (CRAPUL) and the Foundation of the 450th for their financial support to the LaCOSA conference.

Accordingly, it may be read either as a whole, by sections or by chapters. In the remainder of this introduction, we first outline some epistemological and theoretical principles that are shared by many sequence analysts. Emphasis is put on the developments of the method by specifically using concepts from social science rather than purely formal and technical terms. Second, we trace the main developments in SA over the last twenty years. We argue that due to the specific structure of the scientific field of SA, one can distinguish a relatively consensual core program and a series of innovative, emerging alternatives. Finally, the last part will present the main debates which have animated the SA communities in the last years and give the reader an overview of how these debates are reflected in the book.

What is a Sequence?

Many theories in the social sciences hypothesise historical changes and place a special emphasis on processes, orders, transitions and developments. The centrality of both institutional and biographical order and processes was particularly important in the Chicago School of sociology, which constitutes the theoretical starting point for SA in this field. Howard Becker (1963) pleaded for sequential models of social reality. In his sequential theory of deviance, he insists that explanatory factors (causes) are not simultaneously influential. A social process is divided into phases that have their own specific explanations. The final behaviour can only be explained by the chronological succession of these phases. From this perspective, the various elements of such narratives are bound not only to the immediate, but also to the remote past. Explicitly paying tribute to this school of thought, the sequence theorist Abbott (2001) claims that "social reality happens in stories", which he calls *narratives*. Considering social processes as "stories" does not mean that they are free from constraints or predetermined. They unfold in a web of constraints and opportunities.

Most narratives may be formally described with four concepts: trajectory, stage, event, and transition (Levy et al. 2005). A *trajectory* may be seen as a model of stability and long-term change (George 1993) or as a sequence of participation profiles (Levy 1991) that represents the variation over time of the different roles an individual holds in various life spheres. It is used to describe the structure of change and stability characteristics of an individual life, in one or more of its dimensions. A *stage* refers to a life period of relative structural or functional stability (family life stages, child development stages, periods of economic growth, etc.). A *transition* means a change between two stages (for example, role and structural changes during the transition into parenthood or during a political revolution). An *event* is what occurs at a given time in a given place and is something to which human beings attribute meaning. Events can be normative (e.g. birth, marriage, graduation) or non-normative (e.g. disease, war, death). Important events are often associated with a transition.

Narratives are structured patterns that have a beginning, a middle, and an end. Given the large number of possible expressions of a specific social phenomenon, looking for ideal types is a convenient solution to apprehend it as a narrative. Indeed, social processes contain typical events that unfold in a typical order. This order is influenced by factors such as personality traits, family configuration, occupation type, health status, or institutional power relationships. Narratives are therefore, in most cases, shaped both by endogenous and exogenous factors. The relative weight of these two structuring factors is variable. For instance, the current health status of an individual is very much structured by internal, (epi)genetical factors, whereas her/his current residential situation may vary according to external factors, such as the dynamics of the housing market and its links to local economical and/ or political constraints. To be relevant, however, narratives must have a unity and a coherence that is analogous to that of variables. This unity of narratives forms the basis for generalisation. This is precisely why, once generalised, a narrative may become a variable again, for example to be fed into a regression analysis (e.g., Levy et al. 2006). According to Hull (1989), narratives form coherent units because the events that build them concern a central subject (an individual, a couple, an occupation, an organisation, or a corpus of texts). He proposes another way to describe the exogenous and endogenous structure of narratives, as for him, a central subject must be seen in two ways. On the one hand there is a linkage between the events entering the narrative (internal structuring dynamic). On the other hand, one has to consider the whole relationship which links the central subject to its surroundingfor example, historical, political, organisational-narratives. In this perspective, the elements of a narrative are defined by their function in the narrative line, considered as a whole. These elements are therefore not independent from the context. A systemic perspective-taking the macro-micro link into account-is therefore central to an understanding of social narratives.

Abbott (2001, Chap. 4) differentiates three levels of complexity for sequential models with respect to the recurring or non-recurring nature of events and according to the number of dimensions taken into account:

"Stage theories" or "natural histories" describe biographical or historical stages through which most of the units of observation seem to pass. They obey an internal process logic, relatively independent from contextual influences (for example, child developmental stages, compulsory education in highly standardised countries, legislative or public agenda processes).

"Careers" show more variability than natural histories. They are dependent on the context, more contingent, and also include recurrent events and states. They typically include trajectories of education, occupational careers, residential trajectories, or activist careers.

At the more complex level of "Interactional fields", a whole network of interdependent sequences belongs to various relevant dimensions that form a system (family, occupation, residence, health, welfare regime, political stability, etc.).

The Core Program of Sequence Analysis

The research trend in sequence analysis was structured in the 1990s and 2000s around a core program with a limited number of methodological options. This core program studies life trajectories of individuals living in a contemporary period. It mostly refers to sequences of equal length, with age as a time axis and year as a time unit. Sequence samples comprise hundreds to thousands of individuals. The data processing runs from coding to sequence formatting, to sequence comparison usually by means of optimal matching analysis (OMA), followed by clustering to build typologies of sequences. Typical representatives of the core program are Blair-Loy (1999), about US female executive careers in finance; Halpin and Chan (1998), about professional mobility in Ireland and the United Kingdom; Pollock (2007), about joint employment, housing and family careers in British households; Bühlmann (2008) about the careers of engineers and managers; Robette (2010), about pathways to adulthood in France; or Stovel et al. (1996), about the long-term transformation of banking careers. The next section summarises the main steps of sequence comparison as developed in the above-cited studies.

Sequence Comparison in a Nutshell²

Sequence analysis can be applied to any type of time-related phenomenon. As these phenomena are often multidimensional, the considered processes must first be decomposed in distinct dimensions or fields. The various positions that characterise a given dimension must be reduced to a finite, non-ambiguous number of states called an alphabet. An individual sequence in this perspective is the succession of the observed states for one unit of observation over a given time period. There are several ways to compare sequences. In the following we will describe the one usually employed in the core program: the optimal matching analysis (Kruskal 1983). Let us consider one possible way to model individual occupational status(es) in a sequential perspective. We first need to define a finite set of such statuses, as for instance $O = \{G = education, P = part time employed, F = full time employed, H = at home\}$. We need longitudinal data in order to attribute a specific status to each time unit (e.g., years) for a given time frame, e.g. between the ages of 16 and 35 (Table 1.1).

Having done this, we need to know how (dis-)similar these sequences of statuses are. This is done by estimating the number of elementary operations of substitution, insertion or deletion (generically called *indel*), which are necessary to transform one sequence (source) into another one (target). Each elementary operation is associated with a given cost, that can be unitary, theory driven or data based (Gauthier et al 2009). The number of elementary operations that are necessary to perform the

² All computations presented in this example are made using the R statistical environment (R Development Core Team 2011) and the associated TraMineR package for the sequence comparison (Gabadinho et al. 2011).

ID	Age	Э																			
	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	
1	G	G	G	G	G	G	F	F	F	F	F	F	Р	Р	Н	Н	Н	Н	Н	Н	
2	G	G	F	F	F	F	F	F	F	F	F	F	F	F	F	Р	F	F	F	Р	
3	G	G	G	G	G	G	G	G	F	F	F	F	F	F	F	Р	Р	Р	Р	Р	
4	G	G	G	G	F	F	F	F	F	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	

 Table 1.1
 A set of four sequences of length 20, built with four symbols (F, G, H and P)

Table 1.2	The substitution
costs matr	ix

	G->	F->	H->	P->
G->	0	2	2	2
F->	2	0	2	3
H->	2	2	0	2
P->	2	3	2	0

Indel cost=1

transformation is called the distance between the two sequences; the greater the distance, the more dissimilar the sequences. As there are many different transformation strategies to make this transformation, the recursive dynamic programming algorithm (Levenshtein 1966) enables one to find the optimal matching between two sequences—that is, the particular combination of elementary operations needed to transform one into the other at a minimal cost. For sequences of equal lengths, when substitution costs are unitary and indel cost values are set to half of that of a substitution, the resulting distance is equivalent if one uses a substitution or an insertion followed by a deletion. If sequences are of different lengths, *indels* fill the gaps and distance normalisation strategies may be considered. In the following example we compute a user-defined substitution cost matrix in which all costs are set to 2, except the one between symbols F and P, which is set to 3. This means that in certain cases, insertion-deletion is less costly than substitution (Table 1.2).

The resulting alignment (Table 1.3) needed four substitutions and twelve indels to transform the sequence 1 into the sequence 2, hence the (optimal distance between them is $(4*2+12*1)=20.^3$

We then compute all the pairwise distances between sequences and gather them in a distance matrix (Table 1.4).

The next step is to group the sequences at hand (e.g. by means of a cluster analysis) in order to build typologies of sequences by reducing the complexity of the data. A convenient way to represent the grouping process is to display a dendrogram (Fig. 1.1) of Ward's hierarchical ascending clustering procedure (Ward 1963).

The dendrogram shows the greater proximity of sequences 1 and 4 compared to 2 and 3. In this simple example, by cutting the tree above the first branching and below the second one, we can create two groups of structurally homogeneous sequences.

³ Note that the use of indel costs changes the length of the alignment (that is, the temporality) while keeping its structure, whereas using substitutions only keeps the temporality, but changes the structure of the sequences.

Table 1.	ы Т	he op	timal	alignr	nent																					
		2	3	4	5	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
Seq 1	5	G	Ţ	I	Ι	G	G	G	G	F	F	F	F	F	F	Ρ.				L d	H	H	Н	Н	Η	Н
Trans.	ш	Щ	Γ	Ι	I	S	S	S	S	Щ	Щ	Щ	Щ	Щ	ш	щ	I	_	_	Ш	D	D	D	D	D	D
Costs (C	0	-		-	7	7	7	7	0	0	0	0	0	0	0	1	1	-	0	1	1	1	1	1	1
Seq 2	5	G	F	F	Ы	F	F	F	F	F	F	F	F	F	Ц	P.	Ц	ĽL.	ĽL.	d			I	I	I	1
Trans. =	tran	sform	lation,	, wher	e E =	equive	alent, 2	S = suł	ostituti	ion, I :	= inser	tion, I	D = de	letion												



This reduction of complexity allows us to create a categorical variable that assigns each sample unit to a specific, typical group of sequences (Table 1.5). Eventually, in order to contextualise the individual sequences, this variable may be used in further statistical analyses, as for instance logistic regression or multiple correspondence analyses.

The Core Program: How did we End Up Here?

One may wonder how the standard options of the core program emerged. They result from a process of convergence and selection between research programs led by scholars from different disciplines and different countries. This process was not managed or coordinated by some central individual or team. The one who evidently could have played such a role, Abbott, left the field at the end of the 1990s without formally proposing a specific guideline to follow. His book *Time Matters* (Abbott

2001), in the shape of a testimony of his work on sequences, deals with the limits of standard methods used to treat longitudinal data in the social sciences and what objectives social sciences should seek to attain in order to formalise social life as a narrative or sequence. His expectation was that from his own empirical experiments on sequences, diverse techniques and tools would burgeon, compete with each other, and eventually contribute to improving our understanding of this new object (Demazière et al. 2011). For the time being, the collective aggregation and convergence of efforts around a standard line in social sciences resulted from a series of factors (Blanchard Forthcoming 2014):

- 1. The dominance of Abbott's legacy from his methodological and empirical papers—still one of the most cited papers in the field;
- 2. A theoretical need for statistical sequential approaches that had to be fulfilled empirically;
- 3. The strength of applications in the sociology of work and employment and their specific expectations in terms of sequences;
- 4. The availability of good-quality sequential datasets based on surveys, whether retrospective questionnaires or panels;
- 5. The modest number of software implementations, which gave a decisive advantage to those applications first to be developed for the social sciences, namely *Optimize* (Abbott and Prellwitz 1997) and *tda* (Rohwer and Poetter 2007), then the *TraMineR* package in *R* (Gabadinho et al. 2011);
- 6. The limited number of sequence analysts who are facing a much larger population of sociologists who are using traditional methods, which compelled the former to stick to basics and promote a minimum core program so as to meet the journals' reviewers' requirements—chosen mainly among the latter.

All these factors reinforce each other and explain the present state of SA in social sciences: cumulativity, yet limited to some kinds of data, research questions, research designs, and treatment strategies. At this stage no exhaustive recipe book is available, but the (implicit) consensus around a set of core options can be found in several venues. The beginner may refer to Abbott and his colleagues' introductory articles (Abbott 1995; Abbott and Tsay 2000; Macindoe and Abbott 2004), to two rather short textbooks (Aisenbrey 2000; Robette 2011), and to a few papers partly following some pedagogic purpose (Lesnard 2006; Blanchard 2011; Gauthier 2013). The most comprehensive overview on the methodological advances of SA in the last decade can be found in Aisenbrey and Fasang (2010). Social and political science courses within academic method schools are also proposed in Germany (Berlin, 2007), the United Kingdom (Essex, 2007; Manchester, 2009), France (Lille, 2009, 2010, 2011), Switzerland (Geneva, 2009, 2012), Austria (ECPR-Vienna, 2012), the United States (Columbia, 2011) and Canada (Ontario 2012). The core program is progressively establishing itself, although at the present stage of development, the (uncoordinated) priority is put on the development of new lines and variants.

Variants to the Core Program

The provocative question "What Have You Done for Us Lately?" addressed by Joel Levine to Abbott in 2000 can be enlarged: What have we done in the last 14 years? What alternatives have been proposed to the core program? Which ones have also been tested empirically? The following is a short review of sequence data, methods for the calculation of dissimilarity between sequences and methods used to process and interpret dissimilarities.

First, data may diverge from the standard frame. They may relate to non-contemporary individuals, as did Oris and Ritschard's transposing life course interrogations to Nineteenth-Century East Belgium (see Chap. 8. They may not deal with human individual data, such as Stovel's (2001) analysing sequences of local lynching events in the Deep South (1882-1930) as marks of micro-level narratives of political violence. Data may use time units other than years or months; for example 10-minute slots in time-budgets may be used (Lesnard 2008). They may not relate directly to standard clock time, as with Buton et al. (see Chap. 10), who consider sequences of votes from ballots with irregular timing over 25 years. Data may also encompass small-N populations, which is the case with Abbott and DeViney's (1992) study of welfare development in 18 industrialised countries. Sequence lengths may also be unequal, such as life-long AIDS activists' careers with varied ages in Fillieule and Blanchard's study (2012). Some of these alternative data bring new challenges to the standard approach, regarding data formatting and treatment, as well as the interpretation of results. For example non-standard time measurement creates specific event sequences that require specific tools; small-N populations change the way the results are generalised to a larger population (as long as the sample is not the full population, as in Abbott and DeViney 1992); and sequences of uneven lengths affect the interpretation of elementary operations applied by OM, especially in terms of balance between indel costs and substitution costs.

A second field of variants comes with the way sequences are processed. It may take quite different directions from the one privileged today in the majority of studies. Much has been written about the possible variations regarding costs, including empirically machine-trained substitution costs (Gauthier et al. 2009), indel costs varying with states, substitution costs varying with data-based time (Lesnard 2010), or indel costs varying with the state's neighbourhood in the sequence (Hollister 2009), although no consensual doctrine has yet emerged on costs. Less attention has been paid to other variations. For example, instead of incremental, state-by-state comparison, as in OM, sequence comparison may use holistic criteria based on the search for chunks of common subsequences. One may use the longest common subsequence (actually a variation of OMA with lower indel costs), or the longest common prefix (Elzinga 2006). One may also compare without aligning, either by introducing alternative sets of elementary operations, such as swaps, by comparing

pairs of ordered elements, or by applying a correspondence analysis to the matrix of time spent by period in each state (e.g., Deville and Saporta 1980). These different approaches rely on diverging conceptions of sequences and give privilege to different mathematical tools. As a result, they put the accent on distinct aspects of social time, as Robette and Bry (2012) do in their synthetic comparison of sequence metrics with simulated and real datasets. The strategy of comparison itself may not rely on complete pairwise OM but on a comparison with ex ante ideal-typical sequences (Wiggins et al. 2007). The lengths of sequences may be standardised (Abbott and Hrycak 1990, and the dissimilarity matrix normalised (Han and Moen 1999), in both cases with noticeable consequences on how the results are interpreted. One may even imagine an optimal path inside the OM pairwise comparison array that would be different from simply the cheapest one resulting from the Needleman and Wunsch (1970) algorithm. This would lead again to a different pairwise dissimilarity structure.

Third, the choice of methods associated with the dissimilarity calculation also varies notably, as well as the way they are combined. These complementary methods may take diverse roles relative to the SA core program, as described above. They may be more or less autonomous from SA, previously developed in other fields, or reversely specific to SA; they may be used at various stages of the treatment process, either before or after the calculation of pairwise dissimilarities (in case any dissimilarity is calculated). For example, measures of sequences' complexity are imported from the theory of entropy, then applied to algorithmic information theory and molecules comparison, and later adapted to social sequences (Elzinga 2010). They can be used at the exploration stage or after some OM-based clusters have been distinguished. Similarly, multidimensional scaling, not specific to sequences either, is useful to sort out both sequence populations and clusters (Piccarreta and Lior 2010). Validity and sensitivity analyses (e.g., Hollister 2009; Aisenbrey and Fasang 2010) as well as simulation experiments (Bison 2009; Robette and Bry 2012), at the end of the treatment process, can tremendously improve the robustness of OMA and SA.

As Aisenbrey and Fasang show (2010), waves of innovation have run through the sequence community (if we may call it so) over the last 15 years. Yet, looking back, it appears that many of the alternative data and methods had been explored or at least suggested by the works of Abbott and his colleagues, on empirical (Abbott and Barman 1997; Abbott and DeViney 1992; Abbott and Forrest 1986; Abbott and Hrycak 1990) as well as methodological aspects (Abbott 1995; Abbott and Tsay 2000). Sequence analysts have been right to give more concrete and systematic insights into what was often left at the stage of intuitions by the pioneer. What global picture emerges from these variants? What federating concepts can bring unity back to the picture? This is what this book intends to bring answers to. Let us sketch some of them in the last part of this introduction.

Some Currently Debated Issues—the Chapters of this Book

The contributions of this book address central current debates in the field of SA. A particular emphasis was put on contributions' using new and unusual data, applying the method to phenomena beyond the mainstream life course research and on an extension of the disciplinary scope of SA. A few chapters rely on previously published fieldwork, but they either extend the empirical field further, or propose new methodological options that change the results. The book is organised in four sections: (a) How to Compare Sequences, (b) Life Course Sequences, (c) Historical and Political Sequences, (d) Visualisation of Sequences and their Use for Survey Research.

How to Compare Sequences

Sequence comparison is core business for SA. It also connects with the way sequences are generated and with their structural characteristics. What do sequences mean and how should they be treated from a social science perspective? The first part includes reflections about the genesis and the explanation of sequences, about the definition of what a meaningful sequence is and about the mathematical premises of comparison. The chapters of the first part examine sequence comparison from three different angles: Shin-Kap Han (see Chap. 2) in his chapter "Motif of Sequence, Motif in Sequence" tries to identify motifs as dominant and salient elements of sequences. He asks how and why we might be able to identify a part of a sequence that can effectively represent the sequence as a whole. Borrowing from music theory, social network analysis and molecular biology, he explores possible futures of the method and shows how Abbott's work can be carried on. Laurent Lesnard (see Chap. 3) proposes a deepening of the theoretical anchoring of SA. Challenging some of the technical solutions of cost setting that have been developed in the last years, he urges SA to return to sociological theories of time and to set costs according to the sociological meaning of time, as developed by Durkheim, Elias and Bourdieu. Complementary to this theoretical reinforcing of sequence comparison, Cees Elzinga's chapter (see Chap. 4) clarifies the mathematical foundations of sequence comparison. He discusses the axiomatic of sequence distances, both OMbased and subsequence-based, before articulating distance and similarity and showing that the two concepts are not exactly symmetrical and may lead to diverging partitions for instance. Brendan Halpin (see Chap. 5) investigates different narratives and measures of similarity and dissimilarity between sequences, comparing the OM algorithm, a duration-weighted combinatorial subsequence algorithm, with a newly developed time-wrapping algorithm. It appears that the time-wrapping algorithm can be parameterised in a way that provides a bridge between algorithms such as OM (for which time is a flexible scale) and combinatorial subsequence algorithms (for which time is a scale-less order). The time-wrapping algorithm therefore has good chances for an empirical link between different "narratives" of similarity, which to date have been too distant from each other within the SA universe.

Sequence Analysis and the Life Course

The second section is located within the life course paradigm, the most fruitful paradigm for SA for the last fifteen years. As the large number of applications of SA on biographical process has shown, life course trajectories—occupational careers, residential trajectories or family trajectories-often feature structures of timing and order that are particularly suited to be understood by SA. Nevertheless, this line of work is not exhausted, as demonstrated by these three chapters. Anette Fasang (see Chap. 6) attempts to more seriously take into account the initial theoretical promises of SA on the non-linearity of processes. She identifies three important domains where SA could make a major contribution: multidimensional lives, linked lives and destandardisation. She shows for instance how Elder's (1985) idea of linked lives can be enriched by a cross-fertilisation with recent trends in network analysis and an emphasis on dyadic relationships among siblings, parents and partners. In summary, she argues—both with and against Abbott—for a more theoretically informed and deductive use of SA and refuses to pigeonhole it as an exclusively explorative method. In their chapter Julia Dietrich, Håkan Andersson and Katariina Salmela-Aro (Chap. 7) explore how SA can be used in a discipline that to date has not been very receptive towards sequence analytical approaches: psychology. This neglect is far from self-evident. To the contrary, developmental psychology and life-span psychology are considered to be important elements of an interdisciplinary approach to life course research. Hence, Dietrich et al. explicitly use concepts from a developmental psychological approach to study educational trajectories and to investigate how these trajectories are related to psychological resources and career goals. They show that the links between trajectories and mental dispositions-such as beliefs, attitudes, personality attributes and so on-are still seldom examined. We can learn from their chapter that psychology (in particular developmental psychology) is a promising disciplinary area of further application of SA in the future. Finally, Michel Oris and Gilbert Ritschard (see Chap. 8) employ SA to enhance our historical knowledge about family formation. They are able to show that in the first half of the 19th century, among peasants and daily labourers from Ardennes and the Pays de Herve, despite a general high age at the moment of marriage, one can observe an impressive variety of trajectories. In particular, they find evidence for a group with very late motherhood-a discovery which questions and nuances the mainstream explanations to history of family formation in Europe.

Political Sequence

The third section opens up the empirical perspectives beyond contemporary life course to historical and political phenomena. On the one hand, it becomes a part of the prosopographical approaches in history. When studying historical periods by means of collective biographies of specific birth cohorts or particular social groups, historians have begun to employ SA in order to understand types of careers and trajectories. On the other hand, the sequential chains of historical events themselves are being studied. Following the pioneering study of Katherine Stovel on sequences of lynching in the US south (2001), scholars are trying to understand institutional change through SA.

In this part of the book, we present two contributions from the first type and one from the second type: Pierre Merklé and Claire Zalc (see Chap. 9), in an uncommon contribution to Holocaust research, investigate trajectories of persecution of a group of Jewish inhabitants of the French town of Lens. Their micro-historical approach of the Holocaust sheds new light on the trajectories and patterns of persecution, and they also raise a series of important methodological and ethical issues-related to the very particular factors which gave form to these trajectories. François Buton, Claire Lemercier and Nicolas Mariot (see Chap. 10) present another innovative application of SA: they investigate electoral participation on the basis of a signature list of a single French polling station-during more than 25 years and over 44 ballots. This yields in a dynamic account of electoral participation, allows the researchers to understand electorate households and thus poses intriguing questions to traditional, static measures of voting behaviour. Matthew Wilson (see Chap. 11) shows how superficially political scientists usually treat sequence phenomena. Regarding order and timing, existing theories were more speculative than empirical. SA can contribute a lot to explain the much debated democratisation processes. Wilson takes a macroscopic perspective, both geographically and historically, following Abbott and DeViney (1992) on welfare state regimes. Taking into account the order of the steps of democratisation, SA improves the classification of political regimes.

Visualisation of Sequences and Their Use for Survey Research

Visualisation issues have a long tradition and are still debated. Synoptic capacity of visualisation has an enormous impact on the diffusion of research findings, especially if these findings are based on innovative analytical approaches (Tufte 1997). However, as stated above, SA procedures still lack a consensus on how to best represent sequences. The fact that an increasing number of large longitudinal data sets are now available to researchers in social sciences may boost the use of SA and therefore the need for adequate and effective ways to think graphically about sequences and communicate the results. Thus, there is a need to evaluate the possible mapping strategies that may apply to results stemming from SA, their respective strengths and weaknesses, and their specific range of application.

Chapters in the fourth section discuss visualisation from different angles. In an innovative contribution, Ivano Bison (see Chap. 12) proposes a morphologic approach to individual careers by converting sets of individual sequences into network graphs. Based on the occupational careers of women and men, this formal exploration aims at uncovering to-date hidden configurational patterns by a complete change of data visualisation perspective. This analytical shift provides a new structural basis for interpreting individual and collective life course dynamics. In their contribution, Denis Colombi and Simon Paye (see Chap. 13) emphasise the

importance of considering alternative time references and therefore focus on the links existing between events and trajectories. To this aim, individual sequences are synchronised not according to age, but to some important common event, which can be endogenous or exogenous to the considered sequences. In a study of academic careers, they show how such an event-based synchronisation of trajectories can create visually powerful new insights into trajectories. Christian Brzinsky-Fay (see Chap. 14) presents and discusses the advantages and limitations of the main, as well as the less conventional, visualisation options associated with the specific sequential data typically used in the field of social science. His chapter brings together the need for researchers to capture specific features of (or types of) sequences and the formal visualisation strategies derived from Cleveland's rules of perception.

Alexandre Pollien and Dominique Joye (see Chap. 15) apply SA to survey metadata. They analyse contact attempts as social interactions between interviewer and interviewee, each with specific socio-demographic characteristics, a process which leads to diverse degrees of accessibility and cooperation. Using information about the sampled population and a non-response survey, they map prototypical sequences on key variables, thereby showing how SA can enhance sample correction and open new pathways towards data quality improvement.

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