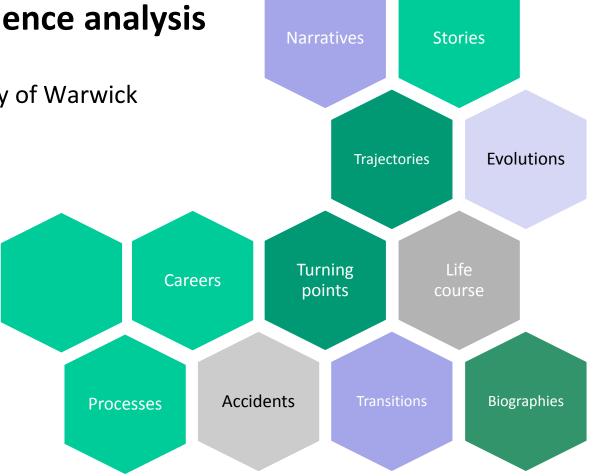


Introduction to sequence analysis

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What is a sequence?

Statistical formulation

Individual	Life domain	Alphabet of states		tl	t2	ť3	t4	t5	t6	
	A	al, a2, a3		a 2	al	a2	a 2	a2	a2	
iı	В	b1, b2	1	bl	bl	na	na	b 2	ъ2	One full
	С	cl, c2, c3, c4		cl	cl	c2	ය	c3	c3	sequence
	A	al, a2, a3		al	al	al	al	al	al	
12	В	b1, b2	1	ы	ь2	b 2	ь2	b 2	ь2	One biography
	C	cl, c2, c3, c4	1	cl	cl	e3	ತ	e3	e3	
										•

A transition between states c1 and c3

Cases

ID	Life domain	Alphabet	2000	2001	2002	2003	2004	2005	
	Work	Unemployed, at Work, Retired	W	U	W	W	W	W	One trajectory
1	Parenting	No child, One child or more	N	N	na	na	0	0	_
	Coupling	Single, in Couple, Married, Divorced/separated	S	S	C	C	M	M	One constant
	Work	Unemployed, at Work, Retired	U	U	U	U	U	U	subsequence
2	Parenting	No child, One child or more	N	0	0	0	0	0	
	Coupling	Single, in Couple, Married, Divorced/separated	S	S	M	M	D	D	

The transition happens to be a wedding

Notations

- Alphabet A° of p_a elements a_i inside life domain A: A° = $\{a_1, a_2 \dots a_{p_a}\}$
- Sequence S of length s inside life domain A:

$$S = (a_{i_1}, a_{i_2} \dots a_{i_s})$$
 with $\{a_{i_1}, a_{i_2} \dots a_{i_s}\} \subset A^{\circ}$

Subsequence S' inside sequence S:

$$S' = (a_{i_m}, a_{i_{m+1}} \dots a_{i_{m+n}})$$
 with $\{m, m+p\} \subset \{1 \dots s\}$

Non successive subsequence S" of sequence S:

$$S'' = (a_{i_q} ... a_{i_r})$$
 with $\{q ... r\} \subset \{1, 2 ... s\}$ and $q < ... < r$

• Episode S''', made of one unique state a_{s_0} :

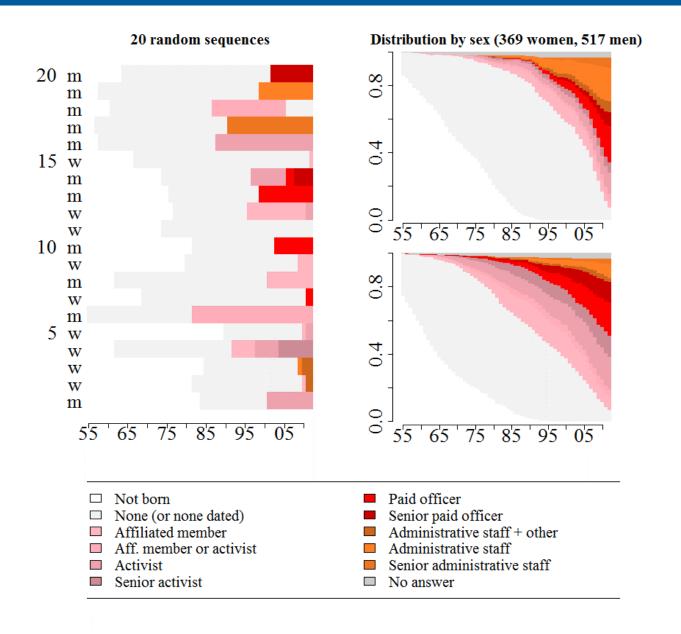
$$S''' = (a_{i_0}, a_{i_0} \dots a_{i_0})$$
 with $i_0 \in \{1, 2 \dots s\}$

Biography B made of sequences

$$S_A, S_B \dots S_M$$
 composed from alphabets $A^{\circ}, B^{\circ} \dots M^{\circ}$:

$$\begin{array}{lll} B &=& (S_A, S_B \dots S_M) \\ B &=& \left[(a_{i_1}, a_{i_2} \dots a_{i_s}), (b_{j_1}, b_{j_2} \dots b_{j_s}) & \dots & (m_{k_1}, m_{k_2} \dots m_{k_s}) \right] \\ with && \left\{ a_{i_1}, a_{i_2} \dots a_{i_s} \right\} \subset \mathbf{A}^{\circ}, && \left\{ b_{j_1}, b_{j_2} \dots b_{j_s} \right\} \subset \mathbf{B}^{\circ} & \dots & \left\{ m_{k_1}, m_{k_2} \dots m_{k_s} \right\} \subset \mathbf{M}^{\circ} \end{array}$$

What is a sequence?



What does sequence analysis do?

- Describes and represents sequences with statistics and plots
- Compares and classifies sequences
- Mines sequences
- Extracts/creates prototypical/discriminating sequences
- Links sequence profiles with external variables
- And more connections with other, non sequential methods.

Applications

- Sociology of work
 - Historical evolution of female trajectories of finance executives? (Blair-Loy 1999)
- Life course analysis
 - How do work, relationship and housing trajectories relate to quality of life? (Wiggins et a.. 2007)
- History
 - Do multi-positionning along time follow some universal cursus honorum? (Lemercier 2005)
- Ethnography
 - Can evolutions in English folk dance steps be derived from a unique historical pattern? (Abbot & Forrest 1986)
- Geography
 - How do patterns of travelling behaviours relate to sociodemographics? (Schlich 2003)
- Linguistics
 - Can a writing style be recognized through the analysis of typical phrases? (Barzilay & Lee 2002)

Other applications (implemented or potential)

- ▶ Work, relationship and housing trajectories related to quality of life (Wiggins et al. 2007)
- Multi-positioned careers in XIXth century economic committees (Lemercier 2005)
- Shopping decisions inside a market or along an online session (Joh et al. 2003)
- Worldly dynamic of diffusion of social legislation between countries? (Abbott & Deviney 1992)
- Engaging and disengaging processes in social movements (Fillieule and Blanchard 2013)
- Places visited in a trip (Saarlos et al. 2010)
- Historical evolution of the structure of scientific articles (Abbott and Barman 1997)
- ► Topics, arguments or keywords in a face-to-face or online conversation
- Stages of development of a story (novel, speech, fairy tale...)
- Mobilising events along a protest cycle
- Sounds, gestures or skills acquired along a child's development
- Etc.

Shortages of usual statistical methods

What methods?

- Basics
 - Summary statistics on individuals and groups
 - Handmade mining and counting of sequences
 - Excel sequence graphs
- Multivariate
 - Clustering
 - Correspondence analysis
 - Synchronic regression models
- Longitudinal
 - Time series
 - Event history
 - Regression models with time included

Their limits

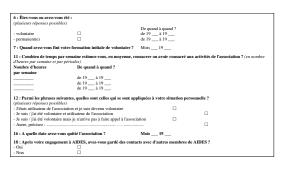
- Focus on continuous variables
- Focus on 1 or 2 events to explain
- Ignore length of subsequences
- Ignore order of states
- Strict dependence on one given time axis
- Censorship
- No global view on sequences
- Graphs not adpated and hard to make

What is new with sequence analysis?

- 1. Holistic approach
- 2. Strong descriptive ambition
- 3. Accounts for the nature of states or events (categorical data)
- 4. ... for the length of each episode
- 5. ... and for their order
- 6. Does not make any hypothesis about the shape of distribution of states or about the underlying cause of sequences
- 7. Various individuals, various Ns, various lengths.

A standard treatment sequence

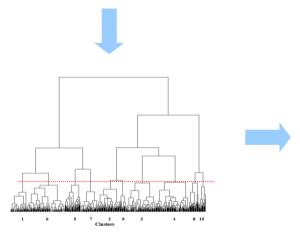
- 1. Collecting data: questionnaire, archives, web-dataset...
- 2. Conceptualizing trajectories to be studied: nature of stages, time limits, time unit...
- 3. Building a sequential dataset: alphabet, data cleaning and formatting.
- 4. Exploring: summary measures, plots, mining.
- 5. Pair comparison of sequences: choice of a metric, calculation of NxN distance matrix ("DM")
- 6. Exploring/synthesizing DM: cross-tabs, clustering, ANOVA...
- 7. Describing and interpring the outputs (tables, clusters, tests, regressions...)
- 8. Exploring and mining again sequences according to the results.



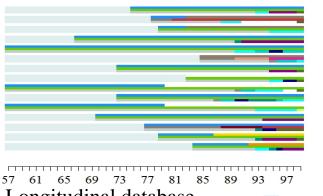
Questionnaire

id	i1	i2	i3	i4	i5	i6	i7	i8	i9	i10
1	0	13	2	6	22	16	6	3	17	6
2	13	0	15	17	29	26	17	16	25	17
3	2	15	0	6	20	15	6	3	16	6
4	6	17	6	0	22	15	0	3	14	0
5	22	29	20	22	0	17	22	21	18	22
	16	26	15	15	17	0	15	14	10	15
7	6	17	6	0	22	15	0	3	14	0
8	3	16	3	3	21	14	3	0	15	3
9	17	25	16	14	18	10	14	15	0	14

NxN distance matrix

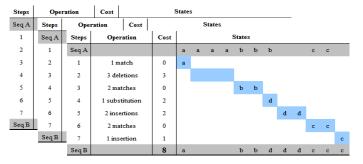


Clustering

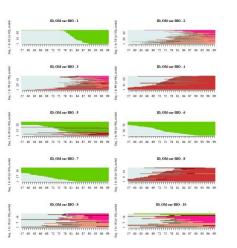


Longitudinal database

3 cost matrices



3D optimal matching



(cross

Description of clusters (cross-tabs, regressions)

Plots (hist. / biogr. / biol. times)

Subsequence mining

Typology of biographies

Methods for sequence comparison (1)

- "Common chunks" of sequences (Elzinga 1986; CHESA 2007)
 - Relative proportion of common states (Elzinga 1986)
 - LCP: Longest common prefix/suffix (Elzinga 1986; Gabadhino et al. 2011)
 - LCS: Longest common subsequence (Elzinga 1986; Gabadhino et al. 2011)
 - LCS with discarded duration (Dijkstra & Taris 1995)
 - Number of distinct common subsequences (Elzinga 1986)
 - Number of matching subsequences (Elzinga 1986)

Advantages

- Intuitive procedures
- Provides intuitive measures of (dis)similarity
- Potentially very powerful

Disadvantages

- High calculation cost
- Not all implemented in current packages
- Little collective empirical feedback so far.

Methods for sequence comparison (2)

- **"Optimal matching"** (Sankoff and Kruskal 1983; Abbott and Forrest 1986; Elzinga 2003)
 - 1. Define elementary operations
 - Substitution, Insertion, Deletion, Match
 - 2. Attribute "cost" to each elementary operation
 - Substitution costs: anti-identity, objective and transition costs, empirically trained, mixed
 - Insertion and deletion: usually fixed, close to half of average scost
 - Match: usually 0
 - 3. Compare sequences by pairs, incrementally from first to last spell
 - 4. Select cheapest sequence of operations (Needleman & Wunsch 1970)

Optimal matching: the straight way

Steps	Operation	Cost	States										
Seq A			a	a	a	a	b	b	b	c	c		
1	1 match	0	a										
2	2 substitutions	4		b	b								
3	1 substitution	2				d							
4	2 substitutions	4					d	d					
5	1 substitution	2							c				
6	2 matches	0								c	c		
Seq B		12	a	b	b	d	d	d	c	c	c		

- a Not involved in Aides yet
- b Involved
- c Not involved anymore

Optimal matching: Optimising

Steps	Operation	Cost	States											
Seq A			a	a	a	a	b	b	b			c	c	
1	1 match	0	a											
2	3 deletions	3												
3	2 matches	0					b	b						
4	1 substitution	2							d					
5	2 insertions	2								d	d			
6	2 matches	0										c	c	
7	1 insertion	1												c
Seq B		8	a				b	b	d	d	d	c	c	c

- a Not involved in Aides yet
- b Involved
- c Not involved anymore

Optimal matching: Optimising

Sequences:

s=CAMBRIDGE g=CAMPING

Distance Sequence alignment:

- 1) substitute $s_4(B:P)$, $s_5(R:I)$, $s_6(I:N)$, $s_7(D:G)$ delete $s_8(G)$, $s_9(E)$ => d=10
- 2) substitute $s_4(B:P)$, delete $s_5(R)$, substitute $s_6(D:N)$, delete $s_8(E)$ => d=6

Source: Schlich (2001)

