Sequence analysis for social scientists

Brendan Halpin, Dept of Sociology, University of Limerick

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Outline

- What is sequence analysis?
- Why it can be worth doing, and how it complements existing approaches
- How to do it, and how to think about it
- Practical, hands-on focus, using (*inter alia*) my SADI add-on for Stata (Halpin, 2014a)

Slides available at `http://teaching.sociology.ul.ie/taiwan`

Section 1

Sequence analysis in the social sciences: some background

Sequence Analysis

- What is sequence analysis?
  - Large and active research area
  - From Andrew Abbott in mid-late 1980s, to 2015 special edition of *Sociological Methodology*
- Focuses on linear data (such as lifecourse trajectories) as *sequences*, as wholes
- Usually proceeds by defining distances between pairs of sequences, creating empirical typologies, etc

A brief history of SA in Sociology

- Andrew Abbott's long evangelism
  - Abbott (1984) - earliest, argues for focusing on sequence as well as duration
  - Abbott and Forrest (1986) - Morris dancing
  - Abbott and Hrycak (1990) - careers of Baroque musicians
- Abbott's main point: focus on sequences as wholes as an alternative to "variable-based" sociology
- However, his main practical contribution was to introduce the OM algorithm to the social sciences

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- However, his main practical contribution was to introduce the OM algorithm to the social sciences

James Coleman: 'No one's gonna pay any attention ... as long as you write about dead German musicians' (Abbott, 2001, p. 13)

Some 1st wave adopters 1/2

- Stovel et al. (1996): A sequence-oriented analysis of career data from a British bank, showing a transition between a status-based and an achievement-based system, from 1890 to 1970.
- Wuerker (1996): Treats sequences of services interactions of mental health patients in Los Angeles. A small data set, but of interest because it uses a relatively uncommon form of trajectory.
- Halpin and Chan (1998): Analyses class careers of British and Irish men to age 35 using retrospective data.

Some 1st wave adopters 2/2

- Blair-Loy (1999): Women's careers in the finance industry; identifies change across cohort in opportunity and perspective.
- Han and Moen (1999): How life and work trajectories of couples are coordinated. Dyadic, not analysis of all pairwise distances: uses OM to generate a measure of intra-couple similarity.
- Stovel (2001): Not life-course: looks at county-level histories of lynching in the Southern US, drawing strongly on arguments from Abbott and others about the necessity of taking a sequence perspective on historical explanations.

2000 debate in SMR

- Position: Abbott and Tsay (2000)
- Critiques: Levine (2000) and Wu (2000)
  - is it sociologically meaningful?
  - how do we parameterise it?
  - does it have any advantages over conventional approaches?
- Response: Abbott (2000)

Key developments since

- Widespread in many fields, especially lifecourse related:
  - transition school to work, labour market, retirement, health outcomes, time use
  - Some focus on multiple domains, dyadic approaches, cohort change in average diversity
  - Much still uses clustering to develop empirical typologies
- See Aisenbrey and Fasang (2010) and Halpin (2013) for a summary
- Rather more activity in Europe than in US
- Two important conferences:
  - LaCOSA1 2012 on Sequence Analysis: Blanchard et al. (2014) (includes historical demographers such as Michel Oris)
  - LaCOSA2 2016 on Sequence Analysis and related methods (Online proceedings: `https://lacosa.lives-nccr.ch/online-proceedings`)

Software developments

- Abbott's `optimize` program
- Our own initial work used molecular biology software borrowed from the Oxford Dept of Pathology
- Götz Rohwer's TDA included an OM module later (mid-late 1990s)
- Stata: SQ and SADI (mid-late 2000s)
- R: Traminer (mid-late 2000s)

Why do Sequence Analysis?

- Why would we want to do it
  - Holistic vs analytic?
  - Exploratory vs hypothesis testing?
  - Descriptive, visualisation
- Complexity of longitudinal processes hard to capture
- Complementary alternative to stochastic techniques which model data generation process

Sequences are messy

- Lifecourse sequences are epiphenomena of more fundamental underlying processes
- The processes are potentially complex: difficult to predict distribution of sequences
- Other techniques (hazard rate models, models of late outcome using history, models of the pattern of transition rates) give a powerful but incomplete view
- SA clearly allows us visualise complex data; possibly allows us observe features that will otherwise be missed

Potentially complex processes

- The generating processes are complex:
  - individuals bring different characteristics from the beginning
  - history matters, including via duration dependence (individuals accumulate characteristics)
  - time matters:
    - calendar time (e.g. economic cycle), state distribution may change dramatically
    - developmental time (maturation)
    - processes in other lifecourse domains
- Too many parameters to model, hard to visualise distribution of life courses, also the possibility of *emergent* features
  - Clear exploratory advantages
  - possibility of detecting things that might not be detected otherwise

Timing, sequence, quantum

- Different things can be interesting
  - Timing: when things happen
  - Sequence: in what order do things happen
  - Quantum: how much time is spent in different states (Billari et al., 2006)
- Many applications in longitudinal social science: annotated bibliography in Halpin (2013)

Non-holistic approaches

- Numerous non-holistic approaches exist
- Typically they will discard some aspect of the information in the data, and focus powerfully on another
- For instance, focus on
  - cumulated duration in states (how much but not when)
  - transition patterns between states (period-to-period but not overall)
  - time-to-event of leaving spell (spells, perhaps pooled, but lose sight of individual career).

Cumulative duration

- For instance, summarise trajectories in terms of cumulative time in each state
- Typically use as a predictor (e.g., proportion of time unemployed predicting later ill-health)
- Or as an outcome: variables measured earlier (e.g., school performance) predicting proportion of time unemployed.

Transition rate models

- Model rates of period-to-period change: e.g., monthly movement between labour market statuses
- Model origin–destination patterns: e.g., transition between class at entry to labour market, and class at age 35
- Markov models
- Very useful, good overview, can be descriptive or stochastic: tables make categorical data digestible
- Disadvantage: the focus on the t-1/t or t_0/t_T pattern means a loss of individual continuity
- Some potential to model longer Markov chains (Gabadinho, 2014)

Hazard-rate modelling

- Hazard-rate modelling is one of the dominant statistical alternative
- Either in terms of survival tables and curves (essentially descriptive)
- Or full stochastic models of the determinants of the hazard rate (Cox and/or parametric)
- Example: what characteristics speed up (or slow down) exit from unemployment?
- Very nice conceptual model of the temporal process
- Can test hypotheses
- Disadvantage: spell orientation, lack of whole-trajectory overview

Latent class analysis

- Latent class growth curve models
  - Where theory allows a developmental model of a quantitative outcome
  - Account for the structure of repeated measurement of individuals
  - Not so suitable for categorical variables
- Latent class models can be applied to careers
  - However, difficult to properly incorporate the longitudinality
  - Examples: Lovaglio and Mezzanzanica (2013); Barban and Billari (2012)

Holistic approaches

- Holistic approaches by definition treat whole trajectories as units
- Classification of sequences is a typical goal
- Usually achieved by defining inter-sequence similarity and cluster analysis
- But other aspects of similarity may be interesting
  - Variation of similarity by grouping variable (cohort, social class)
  - Dyad similarity (couples' time use, mother–daughter fertility etc)
  - Distance to pre-defined ideal types (empirical or theoretical)

Defining similarity

- Defining similarity the key challenge: must be
  - efficient
  - coherent, and
  - sociologically meaningful
- We will consider a number of methods to do this
  - Hamming distance
  - Optimal Matching distance
  - Dynamic Hamming distance
  - Time-warping measures
  - Combinatorial subsequence measures

Hamming distance and Optimal Matching

- The simplest way to compare sequences is element-wise
- Given a rule for $d(a, b)$, project it onto $D(A, B)$ as $D(A, B) = \sum_i d(A_i, B_i)$
- Requires sequence of equal length
- Hamming distance: recognises match or similarity at same time
- Simple but important case of mapping $d(a, b) \rightarrow D(A, B)$

Hamming distance example

Calculate Hamming distance

```
input s1 s2 s3 s4 s5
1 2 3 2 3
2 3 2 3 1
4 2 3 2 3
1 1 1 1 1
end

// Define the state differences
matrix scost = (0,1,2,3 \ ///
                1,0,1,2 \ ///
                2,1,0,1 \ ///
                3,2,1,0 )

hamming s1-s5, subs(scost) pwd(ham)
```

Hamming distance example

Calculate Hamming distance

```
input s1 s2 s3 s4 s5
1 2 3 2 3
2 3 2 3 1
4 2 3 2 3
1 1 1 1 1
end

// Define the state differences
matrix scost = (0,1,2,3 \ ///
                1,0,1,2 \ ///
                2,1,0,1 \ ///
                3,2,1,0 )

hamming s1-s5, subs(scost) pwd(ham)
```

Resulting distances

```
. matrix list ham

symmetric ham[4,4]
     c1   c2   c3   c4
r1    0
r2  1.2    0
r3   .6  1.4    0
r4  1.2  1.2  1.8    0
```


Optimal Matching

- Hamming recognises similarity at the same time
- If sequences have similarity that is out of alignment this will not be recognised
- OM defines similarity like Hamming, but uses insertion and deletion to allow sequences to *align*
  - I.e., it cuts bits out in order to slide other parts along to match
  - Insertion/deletion also enables comparison of sequences of different lengths
- Origins in computer science, pattern recognition, extensive use in molecular biology

OM example

OMA call

```
. oma s1-s5, subs(scost) indel(1.5) ///
             pwd(oma) length(5)
```


OM example

OMA call

```
. oma s1-s5, subs(scost) indel(1.5) ///
             pwd(oma) length(5)
```

Resulting distances

- OM distances

```
symmetric oma[4,4]
     c1   c2   c3   c4
r1    0
r2   .6    0
r3   .6   .6    0
r4  1.2  1.2  1.8    0
```

- Hamming distances

```
symmetric ham[4,4]
     c1   c2   c3   c4
r1    0
r2  1.2    0
r3   .6  1.4    0
r4  1.2  1.2  1.8    0
```


OM vs Hamming

- For most pairs the OM and Hamming distance is the same
- For the pairs (1,2) and (2,3), OM distance is less because "alignment" allows a better match
- 1 vs 2

Seq 1	1	2	3	2	3	-
Seq 2	-	2	3	2	3	1
Cost	i	0	0	0	0	i

- 2 vs 3

Seq 2	-	2	3	2	3	1
Seq 3	4	2	3	2	3	-
Cost	i	0	0	0	0	i

A more general example

To convert ABCD into CDAAB the following set of operations gives the cheapest path:

Operation	Intermediate state	Cost
Sequence 2	ABCD	= 0
		=
		=
		=
		=
		=
		=
Sequence 1	CDAAB	=

A more general example

To convert ABCD into CDAAB the following set of operations gives the cheapest path:

Operation	Intermediate state	Cost
Sequence 2	ABCD	= 0
insert C	CABCD	+1.5 = 1.5
		=
		=
		=
		=
		=
Sequence 1	CDAAB	=

A more general example

To convert ABCD into CDAAB the following set of operations gives the cheapest path:

Operation	Intermediate state	Cost
Sequence 2	ABCD	= 0
insert C	CABCD	+1.5 = 1.5
insert D	CDABCD	+1.5 = 3.0
		=
		=
		=
		=
Sequence 1	CDAAB	=

A more general example

To convert ABCD into CDAAB the following set of operations gives the cheapest path:

Operation	Intermediate state	Cost
Sequence 2	ABCD	= 0
insert C	CABCD	+1.5 = 1.5
insert D	CDABCD	+1.5 = 3.0
const A = A	CDABCD	+0.0 = 3.0
		=
		=
		=
Sequence 1	CDAAB	=

A more general example

To convert ABCD into CDAAB the following set of operations gives the cheapest path:

Operation	Intermediate state	Cost
Sequence 2	ABCD	= 0
insert C	CABCD	+1.5 = 1.5
insert D	CDABCD	+1.5 = 3.0
const A = A	CDABCD	+0.0 = 3.0
subs B→A	CDAACD	+1.0 = 4.0
		=
		=
Sequence 1	CDAAB	=

A more general example

To convert ABCD into CDAAB the following set of operations gives the cheapest path:

Operation	Intermediate state	Cost
Sequence 2	ABCD	= 0
insert C	CABCD	+1.5 = 1.5
insert D	CDABCD	+1.5 = 3.0
const A = A	CDABCD	+0.0 = 3.0
subs B→A	CDAACD	+1.0 = 4.0
subs C→B	CDAABD	+1.0 = 5.0
		=
Sequence 1	CDAAB	=

A more general example

To convert ABCD into CDAAB the following set of operations gives the cheapest path:

Operation	Intermediate state	Cost
Sequence 2	ABCD	= 0
insert C	CABCD	+1.5 = 1.5
insert D	CDABCD	+1.5 = 3.0
const A = A	CDABCD	+0.0 = 3.0
subs B→A	CDAACD	+1.0 = 4.0
subs C→B	CDAABD	+1.0 = 5.0
delete D	CDAAB-	+1.5 = 6.5
Sequence 1	CDAAB	= 6.5

Programming OM

- OM distance is defined as the cheapest set of "elementary operations" that edit one sequence into another
- Determining the cheapest set of “elementary operations” is potentially complex – a large population of candidates
- However, it can be stated as a recursive problem and programmed very efficiently
- Understanding how it is programmed can help understand the principle of OM

OM: Recursive problem

$$\Delta_{OM}(A^p, B^q) =$$

$$min \begin{cases} \Delta_{OM}(A^{p-1}, B^q) & + indel \\ \Delta_{OM}(A^{p-1}, B^{q-1}) & + \delta(a_p, b_q) \\ \Delta_{OM}(A^p, B^{q-1}) & + indel \end{cases}$$

(Δ represents distance between sequences, and δ differences within the state space)

Implementing the recursive algorithm

Cell value: $min(c_{i-1,j-1} + \omega_{i,j},\ c_{i,j-1} + \iota,\ c_{i-1,j} + \iota)$

		s_2			
		A	B	C	D
s_1	C	2	1	0	1
	D	3	2	1	0
	A	0	1	2	3
	A	0	1	2	3
	B	1	0	1	2

	0	2	4	6	8
2					
4					
6					
8					
10					

Implementing the recursive algorithm

Cell value: $min(c_{i-1,j-1} + \omega_{i,j},\ c_{i,j-1} + \iota,\ c_{i-1,j} + \iota)$
$= min(0 + 2, 2 + 2, 2 + 2) = 2$

		s_2			
		A	B	C	D
s_1	C	2	1	0	1
	D	3	2	1	0
	A	0	1	2	3
	A	0	1	2	3
	B	1	0	1	2

	0	2	4	6	8
2					
4					
6					
8					
10					

Implementing the recursive algorithm

Cell value: $min(c_{i-1,j-1} + \omega_{i,j},\ c_{i,j-1} + \iota,\ c_{i-1,j} + \iota)$

		s_2								
		A	B	C	D		0	2	4	6	8
	C	2	1	0	1	2	2				
s_1	D	3	2	1	0	4					
	A	0	1	2	3	6					
	A	0	1	2	3	8					
	B	1	0	1	2	10					

Sequence analysis for social scientists
Session 1: Background
Programming OM (Optional)

Implementing the recursive algorithm

Cell value: $min(c_{i-1,j-1} + \omega_{i,j},\ c_{i,j-1} + \iota,\ c_{i-1,j} + \iota)$

$= min(2 + 1, 2 + 2, 4 + 2) = 3$

		s_2								
		A	B	C	D		0	2	4	6	8
	C	2	1	0	1	2	2				
s_1	D	3	2	1	0	4					
	A	0	1	2	3	6					
	A	0	1	2	3	8					
	B	1	0	1	2	10					

Sequence analysis for social scientists
Session 1: Background
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Implementing the recursive algorithm

Cell value: $min(c_{i-1,j-1} + \omega_{i,j},\ c_{i,j-1} + \iota,\ c_{i-1,j} + \iota)$

		s_2								
		A	B	C	D		0	2	4	6	8
	C	2	1	0	1	2	2	3			
s_1	D	3	2	1	0	4					
	A	0	1	2	3	6					
	A	0	1	2	3	8					
	B	1	0	1	2	10					

Sequence analysis for social scientists
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Implementing the recursive algorithm

Cell value: $min(c_{i-1,j-1} + \omega_{i,j},\ c_{i,j-1} + \iota,\ c_{i-1,j} + \iota)$

$= min(4 + 0, 3 + 2, 6 + 2) = 4$

		s_2								
		A	B	C	D		0	2	4	6	8
	C	2	1	0	1	2	2	3			
s_1	D	3	2	1	0	4					
	A	0	1	2	3	6					
	A	0	1	2	3	8					
	B	1	0	1	2	10					

Sequence analysis for social scientists
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Cell value: $min(c_{i-1,j-1} + \omega_{i,j},\ c_{i,j-1} + \iota,\ c_{i-1,j} + \iota)$

		s_2								
		A	B	C	D		0	2	4	6	8
	C	2	1	0	1	2	2	3	4		
s_1	D	3	2	1	0	4					
	A	0	1	2	3	6					
	A	0	1	2	3	8					
	B	1	0	1	2	10					

Sequence analysis for social scientists
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Implementing the recursive algorithm

Cell value: $min(c_{i-1,j-1} + \omega_{i,j},\ c_{i,j-1} + \iota,\ c_{i-1,j} + \iota)$

$= min(6 + 1, 4 + 2, 8 + 2) = 6$

		s_2								
		A	B	C	D		0	2	4	6	8
	C	2	1	0	1	2	2	3	4		
s_1	D	3	2	1	0	4					
	A	0	1	2	3	6					
	A	0	1	2	3	8					
	B	1	0	1	2	10					

Sequence analysis for social scientists
Session 1: Background
Programming OM (Optional)

Implementing the recursive algorithm

Cell value: $min(c_{i-1,j-1} + \omega_{i,j},\ c_{i,j-1} + \iota,\ c_{i-1,j} + \iota)$

		s_2								
		A	B	C	D		0	2	4	6	8
	C	2	1	0	1	2	2	3	4	6	
s_1	D	3	2	1	0	4					
	A	0	1	2	3	6					
	A	0	1	2	3	8					
	B	1	0	1	2	10					

Sequence analysis for social scientists
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Implementing the recursive algorithm

Cell value: $min(c_{i-1,j-1} + \omega_{i,j},\ c_{i,j-1} + \iota,\ c_{i-1,j} + \iota)$

		s_2								
		A	B	C	D		0	2	4	6	8
	C	2	1	0	1	2	2	3	4	6	
s_1	D	3	2	1	0	4	4	4	4	4	
	A	0	1	2	3	6					
	A	0	1	2	3	8					
	B	1	0	1	2	10					

Implementing the recursive algorithm

Cell value: $min(c_{i-1,j-1} + \omega_{i,j},\ c_{i,j-1} + \iota,\ c_{i-1,j} + \iota)$

		s_2: A	B	C	D
s_1: C		2	1	0	1
D		3	2	1	0
A		0	1	2	3
A		0	1	2	3
B		1	0	1	2

	0	2	4	6	8
2	2	3	4	6	
4	4	4	4	4	
6	4	5	6	6	
8					
10					

Sequence analysis for social scientists
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Programming OM (Optional)

Implementing the recursive algorithm

Cell value: $min(c_{i-1,j-1} + \omega_{i,j},\ c_{i,j-1} + \iota,\ c_{i-1,j} + \iota)$

		s_2: A	B	C	D
s_1: C		2	1	0	1
D		3	2	1	0
A		0	1	2	3
A		0	1	2	3
B		1	0	1	2

	0	2	4	6	8
2	2	3	4	6	
4	4	4	4	4	
6	4	5	6	6	
8	6	5	7	8	
10					

Sequence analysis for social scientists
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Cell value: $min(c_{i-1,j-1} + \omega_{i,j},\ c_{i,j-1} + \iota,\ c_{i-1,j} + \iota)$

		s_2: A	B	C	D
s_1: C		2	1	0	1
D		3	2	1	0
A		0	1	2	3
A		0	1	2	3
B		1	0	1	2

	0	2	4	6	8
2	2	3	4	6	
4	4	4	4	4	
6	4	5	6	6	
8	6	5	7	8	
10	8	6	6	8	

Section 2: Practical Sequence Analysis

- How to carry out basic sequence analysis

Two example data sets

- We will be primarily using two data sets as examples
  - MVAD: McVicar/Anyadike-Danes data on the school-to-work transition in Northern Ireland (72 months, 6 states)
  - BSSEQ: 6 years of labour market history of women who have a birth at end of year 2 (72 months, 4 states)

Initial step: looking at life course data

- It's harder to get an overview of lifecourse that cross-sectional data
- However, a number of numeric and graphical techniques are available

Numeric summaries

We can summarise lifecourse data in terms of:

- Cumulative duration
- Number of spells
- Patterns of transition rates
  - month by month
  - start by finish
- Durations to event (time to first job, first marriage, first child)

Useful to break down these measures by covariates, and model them

Cumulative duration

```
use mvad
cumuldur state*, cd(cd) nstates(6)
reshape long cd, i(id) j(durtype)
label values durtype state
table male durtype, c(mean cd) format(%5.2f)
table grammar durtype, c(mean cd) format(%5.2f)
```

male	durtype E	F	H	S	T	U
0	29.24	12.73	10.12	7.30	5.55	7.06
1	34.96	10.75	6.81	5.00	9.12	5.36

grammar	durtype E	F	H	S	T	U
0	34.25	12.42	6.07	4.44	8.09	6.74
1	23.02	8.47	18.93	13.62	4.32	3.64

Number of spells

```
. nspells state*, gen(nsp)
. tab nsp grammar, col nofreq
```

nsp	grammar 0	1	Total
1	6.17	4.65	5.90
2	20.24	24.81	21.07
3	30.70	33.33	31.18
4	19.21	19.38	19.24
5	12.52	6.98	11.52
6	4.12	6.20	4.49
7	3.95	1.55	3.51
8	1.37	2.33	1.54
9	1.03	0.78	0.98
10	0.34	0.00	0.28
11	0.34	0.00	0.28
Total	100.00	100.00	100.00

Transition rates

```
use mvad

reshape long state, i(id) j(t)

by id: gen last = state[_n-1] if _n>1

label values last state

tab last state, row nofreq
```


Transition rates

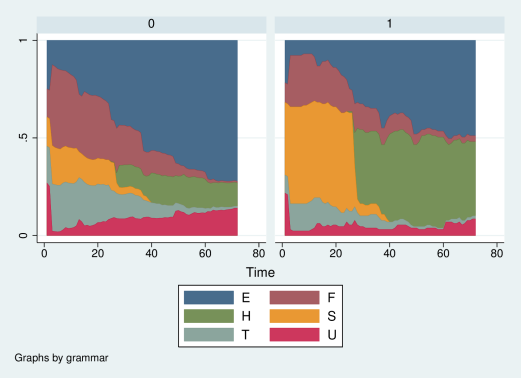
last	state E	F	H	S	T	U	Total
E	22,039	115	56	39	58	146	22,453
	98.16	0.51	0.25	0.17	0.26	0.65	100.00
F	227	7,927	54	8	33	73	8,322
	2.73	95.25	0.65	0.10	0.40	0.88	100.00
H	60	1	5,787	0	3	11	5,862
	1.02	0.02	98.72	0.00	0.05	0.19	100.00
S	59	50	74	4,120	19	23	4,345
	1.36	1.15	1.70	94.82	0.44	0.53	100.00
T	197	21	0	4	4,973	69	5,264
	3.74	0.40	0.00	0.08	94.47	1.31	100.00
U	182	120	9	39	64	3,892	4,306
	4.23	2.79	0.21	0.91	1.49	90.39	100.00
Total	22,764	8,234	5,980	4,210	5,150	4,214	50,552
	45.03	16.29	11.83	8.33	10.19	8.34	100.00

Graphs

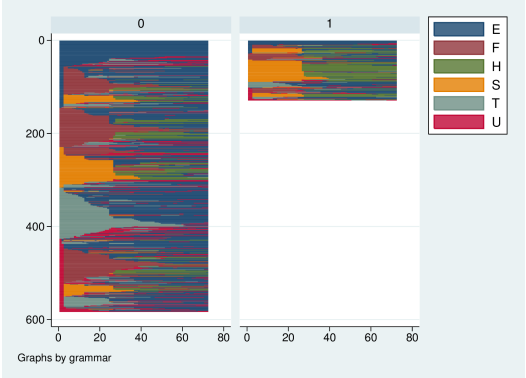
Graphs give us an even better overview. Consider

- Chronograms
- Survival plots
- Index plots
- Transition rate time-series

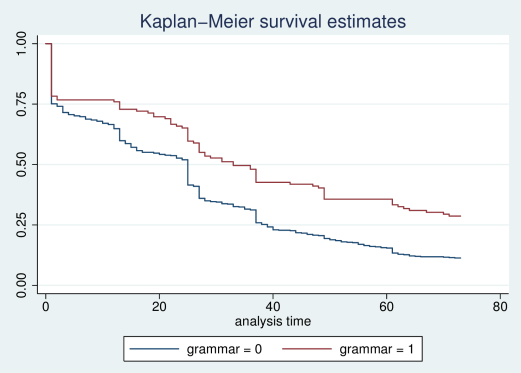
Chronograms



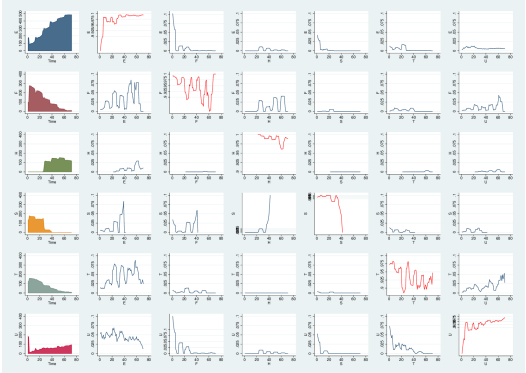
Index plots



Survival plots: time to first job



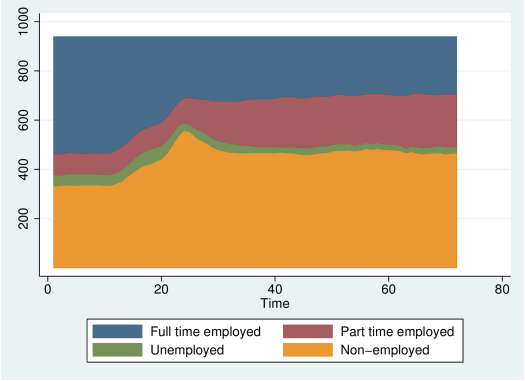
Transition rate time-series



Sequence analysis of real data

Now let's do some sequence analysis of real lifecourse data

Chronogram, mothers' labour market history (BS)



OM on BS data

```
use bsseq
matrix scost = (0,1,2,3 \ ///
                1,0,1,2 \ ///
                2,1,0,1 \ ///
                3,2,1,0 )
oma state*, subs(scost) indel(1.5) pwd(oma) len(72)
matlist oma[1..5,1..5]
```

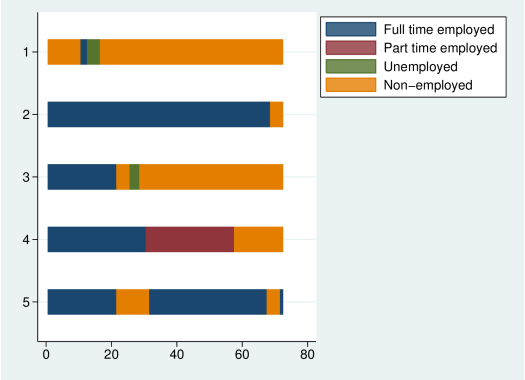

OM output

```
. oma state*, subs(scost) indel(1.5) pwd(oma) len(72)
Normalising distances with respect to length
(0 observations deleted)
417 unique observations
nrefs:     0

. matlist oma[1..5,1..5]

             |        c1         c2         c3         c4         c5
-------------+--------------------------------------------------------
          r1 |         0
          r2 |  2.694444          0
          r3 |  .7777778   1.916667          0
          r4 |  1.861111   .8333333   1.083333          0
          r5 |  2.277778   .4583333   1.541667   .8333333          0
```


Hamming for comparison

```
. hamming state*, subs(scost) pwd(ham)

. corrsqm ham oma
VECH correlation between ham and oma: 0.9946


. matlist ham[1..5,1..5]

             |        c1         c2         c3         c4         c5
-------------+--------------------------------------------------------
          r1 |         0
          r2 |  2.694444          0
          r3 |  .7777778   1.916667          0
          r4 |  1.861111   .8333333   1.083333          0
          r5 |  2.277778         .5   1.583333   1.222222          0
```


First five sequences



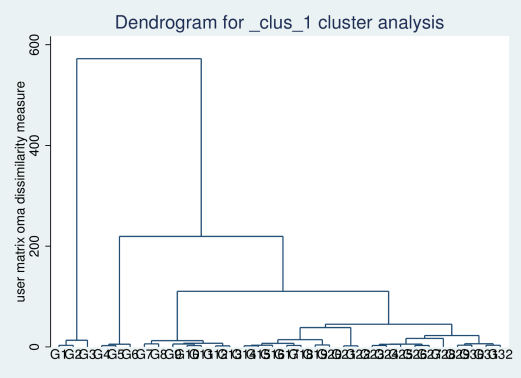
What to do with distances?

- Pairwise distance matrices are an intermediate point
- One useful thing: create a data-driven classification
- Use cluster analysis, typically using Ward's linkage
- Number of clusters is a matter for thought, 8 is convenient for exposition (but see also Halpin (2016))

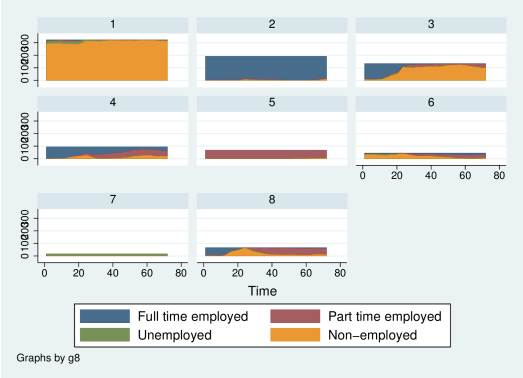
Clustering OM

```
clustermat wards oma, add
cluster generate g8=groups(8)
cluster dendrogram, cutnumber(32)
chronogram state*, by(g8)
chronogram state*, by(g8) proportional
```

Dendrogram

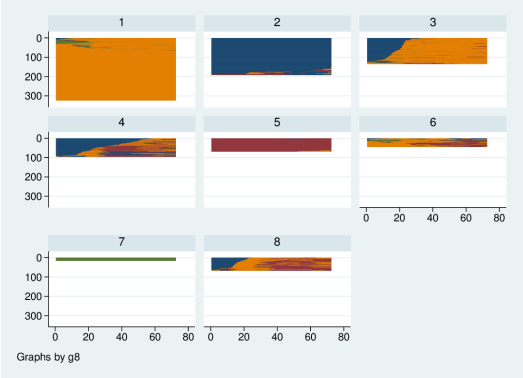


Chronogram by cluster

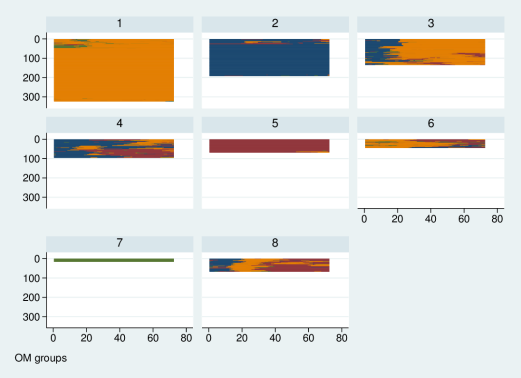


Chronogram, proportional

Indexplot



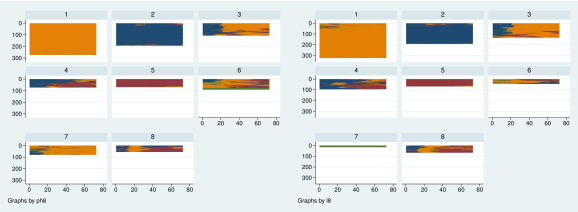
Indexplot in dendrogram order



Details: how it was done

```
clustermat wards oma, add
cluster generate g8 = groups(8)
cluster generate g999 = groups(800), ties(fewer)

chronogram state*, by(g8)
chronogram state*, by(g8) prop

reshape long state, i(pid) j(t)
sqset state pid t
sqindexplot, by(g8, legend(off))
sqindexplot, by(g8, legend(off)) order(g999)
```


Compare Hamming (L) and OM (R) solutions



ARI and permtab

	Hamming							
OM	1	2	3	4	5	6	7	8
1	273	0	1	0	0	1	48	0
2	0	192	0	0	0	0	0	0
3	0	0	85	0	1	16	32	0
4	0	0	10	69	0	0	0	16
5	0	0	0	0	68	0	0	0
6	0	1	0	0	0	44	0	0
7	0	0	0	0	0	16	0	0
8	0	0	10	4	0	14	0	39

- Kappa-max: 0.7791
- Adjusted Rand Index: 0.7818

Hamming and OM

- Often with lifecourse data, Hamming and OM generate quite similar results
- However, where they differ it is with more complex sequences

Complexity of sequences

- Complexity of sequences is relevant: more complex means less likely to be similar (and perhaps, similarity is more interesting)
- How to measure? Number of spells is part of it
- Also distribution of time
- A single long spell is the simplest sequence
- Many spells in many different states is very complex

Shannon Entropy

- Information theory relates complexity to "entropy"
- More complex objects are harder to describe, cannot be compressed
- Shannon Entropy: $\epsilon = -\sum p_i \log_2 p_i$ where p_i is the proportion of months in state i
- Takes account of diversity of state but ABABAB counts as no more complex than AAABBB

Example: entropy

```
entropy state*, gen(ent) cd(pcd) nstates(4)
nspells state*, gen(nsp)
gen ent2 = ent*nsp/72
table g8, c(mean ent mean ent2 mean nsp) format(%6.3f)
```

```
------------------------------------------------
       g8 |  mean(ent)  mean(ent2)   mean(nsp)
----------+-------------------------------------
        1 |       0.150       0.008       1.536
        2 |       0.100       0.004       1.359
        3 |       1.143       0.061       3.560
        4 |       1.053       0.057       3.684
        5 |       0.074       0.003       1.235
        6 |       1.252       0.091       4.844
        7 |       0.000       0.000       1.000
        8 |       1.489       0.097       4.597
------------------------------------------------
```


Elzinga's turbulence

- In Elzinga (2010) a measure of complexity is proposed that is more appropriate for spell data
- It is based on duration weighted spells, and on subsequence counting
- It combines a measure based on the number of distince subsequences, with a measure of the variance of their durations
- It is (only) available in TraMineR
- However, in practice the simpler Shannon entropy correlates highly with it

Regular expressions

- If sequences are represented as text, text-processing tools such as "regular expressions" can be used to sort between them
- Refer to lab notes for more details

```
stripe state*, gen(seqst)
list seqst in 1/5,clean
count if regexm(seqst,"^A+$")
count if regexm(seqst,"^AAAAAA+.*DDDDDD.*AAAAAA.*$")
count if regexm(seqst,"AB.*AB")
```

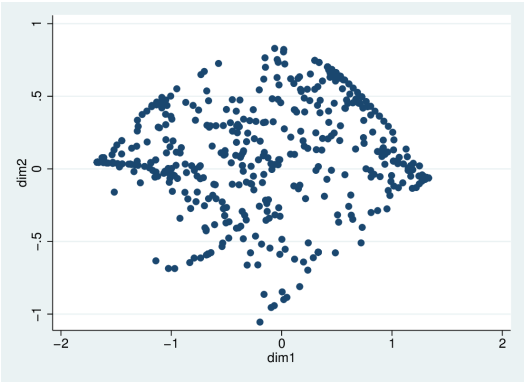

Multi-dimensional scaling (optional)

- The other "obvious" thing to do with pairwise distances is multi-dimensional scaling
- The network of distances implies a coherent space: can we re-construct it?
- Preferably with dimensions much less than number of sequences!
- Standard MDS uses principal component analysis

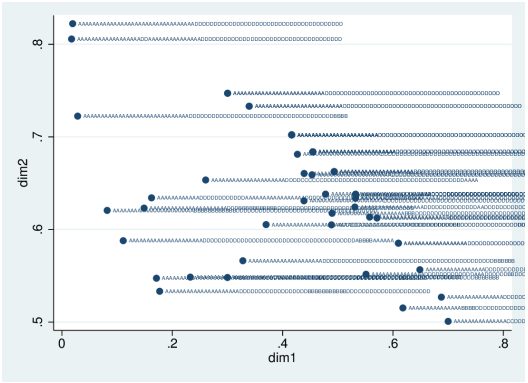
Example

```
. mdsmat oma, dim(3)
(row names of (dis)similarity matrix differ from column names; row names used)

Classical metric multidimensional scaling
    dissimilarity matrix: oma

                                                Number of obs        =       940
    Eigenvalues > 0      =       188            Mardia fit measure 1 =    0.7556
    Retained dimensions  =         3            Mardia fit measure 2 =    0.9932

    ----------------------------------------------------------------------------
              |                  abs(eigenvalue)          (eigenvalue)^2
      Dimension |  Eigenvalue     Percent    Cumul.      Percent    Cumul.
    ------------+---------------------------------------------------------------
              1 |   1205.3971       67.73     67.73        98.57     98.57
              2 |   95.282325        5.35     73.08         0.62     99.19
              3 |   44.082404        2.48     75.56         0.13     99.32
    ------------+---------------------------------------------------------------
              4 |   28.932307        1.63     77.19         0.06     99.38
              5 |   23.350698        1.31     78.50         0.04     99.41
              6 |   12.040492        0.68     79.17         0.01     99.42
              7 |   10.398137        0.58     79.76         0.01     99.43
              8 |   8.8446418        0.50     80.26         0.01     99.44
              9 |   6.3672493        0.36     80.61         0.00     99.44
             10 |   6.1013343        0.34     80.96         0.00     99.44
    ----------------------------------------------------------------------------
```

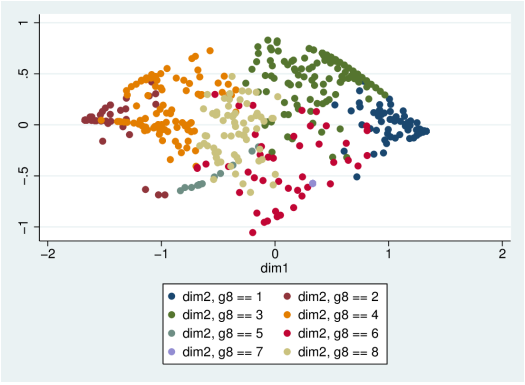
Scatterplot



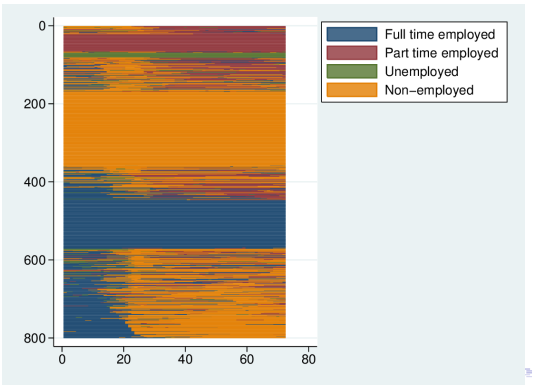
Scatterplot



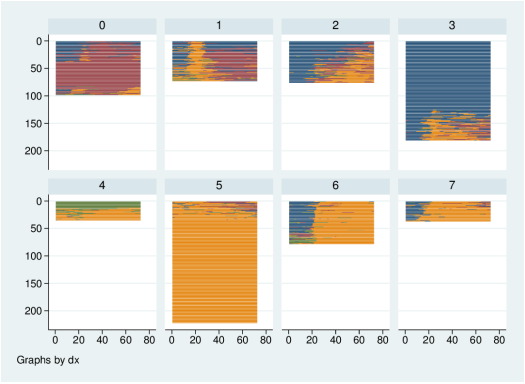
Scatterplot by cluster solution



Avoid clustering: Indexplot ordered by 1st MDS dimension



Partitioning by MDS



Are substitution costs a problem?

- Repeated claims in the literature:
  - that sociologists don't know how to set substitution costs,
  - that we can't match the effectiveness of molecular biology
- Yes, our analytical goals are often much less well defined than those of the biologists
- No, substitution costs are not an intractable problem

Mapping states to sequences

- The essence of SA is mapping a view of a state space onto a view of a trajectory space: $d(s) \rightarrow D(S)$
- We start with *knowledge* or a *view* of how states relate to each other (what states are like each other, what states are dissimilar)
- With a suitable algorithm we map this perspective onto trajectories through the state space: what trajectories are more or less similar
- The nature of the algorithm determines
  - Whether the mapping makes sense
  - Exactly how the structure of the state space affects the structure of the trajectory space

OMA coherent?

- Can we expect OMA to provide a coherent $d(s) \rightarrow D(S)$ mapping?
- Elementary operations are intuitively appealing:
  1. $D(\mathtt{ABC}, \mathtt{ADC}) = f(d(\mathtt{B}, \mathtt{D}))$
  2. $D(\mathtt{ABCD}, \mathtt{ABD}) = f(\mathit{indel})$
  3. minimising concatenation of these two operations to link any pair of trajectories
- If 3 is reasonable, 1 and 2 determine how state space affects trajectory space

Thinking about state spaces and distances

- Costs can be thought of as distances between states
- If state space is $\mathbb{R}^n$, distance is intuitive
- If state space is categorical, how define distance?
  - State space as efficient summary of clustered distribution in $\mathbb{R}^n$: distances are between cluster centroids
  - State space can be mapped onto specific set of quantitative dimensions; each state located at the vector of its mean values; Euclidean or other distances between vectors
  - States can be located relative to each other on theoretical grounds

Transitions and substitutions

- Transition rates frequently proposed as basis for substitution costs
- Critics of OMA complain of substitution operations implying impossible transitions (e.g., Wu)
- Even proponents of OMA are sometimes concerned about "impossible" transitions (e.g., Pollock, 2007)
- But substitutions are not transitions, not even a little bit!
  - substitutions happen across sequences, $D(\texttt{ABC},\texttt{ADC}) = f(d(\texttt{B},\texttt{D}))$ (similarity of states)
  - transitions happen within sequences (movement between states)

Informative transition rates

- No logical connection between substitutions and transition rates
- but under certain circumstances transition rates can inform us about state distances
- If state space is a partitioning of an unknown $\mathbb{R}^n$, movement is random (unstructured), and the probability of a move is inversely related to its length, then
- Distance between states will vary inversely with the transition rates
- However, these conditions usually not met

Deceptive transiton rates

- Example: using voting intentions as a way of defining inter party distances
- UK: relatively high Con–LibDem two-way flows; ditto Lab–LibDem
- But Con–Lab transitions much lower: implies a potentially incoherent space (non-metric, more below)
  - $d(\text{Con},\text{Lab}) > d(\text{Con},\text{LibDem}) + d(\text{LibDem},\text{Lab})$
- Procedure confuses party state space and voter characteristics
- Voter polarisation/loyalty is trajectory information, not state information
- Another type of problem: irrelevant distinctions can cause similar states to have low transition rates

Take "space" seriously

- Very useful to think in spatial terms
  1. State space as efficient summary of clustered distribution in $\mathbb{R}^n$
  2. State space mapped onto specific set of quantitative dimensions
  3. State space defined on theoretical grounds
- For 1 and 2, explicitly multidimensional, in case 2 dimensions are explicit
- For 1 and 3, we can attempt to recover the implicit dimensions

Looking at state spaces

- Two very simple state spaces:
  - Single dimension, equally spaced:

0	1	2	3
1	0	1	2
2	1	0	1
3	2	1	0

- All states equidistant – $n-1$ dimensions

0	1	1	1
1	0	1	1
1	1	0	1
1	1	1	0

Structure passes through

- State space structure passes through to trajectory space structure
  - Distances between states clearly affect distances between trajectories containing high proportions of those states
    - If $d(\texttt{"A"},\texttt{"B"}) << d(\texttt{"A"},\texttt{"C"})$ then $D(\texttt{"..AAAA.."},\texttt{"..BBB.."})$ will tend to be less than $D(\texttt{"..AAAA.."},\texttt{"..CCC.."})$
  - Differential distances promote alignment: AADDAAA and AAADDAA are more likely to be aligned to match the DD if $d(\texttt{"A"},\texttt{"D"})$ is large
  - If the state distances are non-metric, the trajectory distances may also be non-metric (at least between trajectories consisting of near 100% one state)
  - Unidimensional states spaces will tend to be reflected strongly in 1st principle component of trajectory space

Designing state spaces

- Be explicit about state spaces and what distances mean
- Think spatially
  - Choose high or low dimensions, but have your reasons
- Simplify state space as far as possible
  - Drop irrelevant distinctions
  - Drop longitudinal information: let the sequence encode the temporal information, make state space cross-sectional

Dropping temporal information

- e.g., Simplify marital status:

	Living alone	Living with partner
Legally married	Separated	Married
Not legally married	Single, never married, post-cohabitation, divorced	Cohabiting

- The sequence will distinguish adequately between the various "single" states
- Parity sequences: Women's annual fertility history
  - in parity terms: 000112333344444
  - in birth event terms: 000101100010000

Costing OM: a tractable problem

- Substitution costs make a big difference
  - but largely understandable in operation
  - and an asset – more meaningful state space, more meaningful trajectory space
- Think spatially! Use data and geometric models
- Simplify
- Let the sequence do the temporal work

Alternatives to OM and Hamming

- OMA is the dominant but not the only approach
- It receives justified and unjustified criticism in terms of its fit to lifecourse data
- One axis of critique relates to costs: Dynamic Hamming sidesteps this
- Another relates to whether token strings are:
  - a good way to represent life-course processes (continuous time, discrete state space, infrequent transitions)
  - and whether operations on token-strings match sociological difference

Alternatives

- Hollister's LOM and my OMv attempt to fix OM by paying attention to the local context of operations (but fail: non-metric)
- TWED "warps time" and has more sensitivity to spell order
- Lesnard's Dynamic Hamming estimates substitution costs from the data and does no alignment
- Elzinga's duration-weighted combinatorial measures pay strict attention to spell order and duration
- See Halpin (2014b) for a discussion
- See Studer and Ritschard (2014) for a comprehensive review of distance measures

An aside: Metric spaces

- To treat a dissimilarity as a distance, it must be compatible with a "metric space"
- Everyday 3D Euclidean space is metric, but we can relax many of the characteristics of Euclidean space and still think in spatial terms, using e.g., cluster analysis and MDS
- Four conditions are required
  - $d(x,x) = 0$; identity
  - $d(x,y) \geq 0$; non-negativity
  - $d(x,y) = d(y,x)$; symmetry
  - $d(x,y) \leq d(x,z) + d(z,y)$; the "triangle inequality"
- LOM and OMv do not satisfy the triangle inequality

Dynamic Hamming

- Dynamic Hamming takes a completely different slant: no alignment
- Similarity at the same time only, where similarity is defined by time-dependent transition patterns
  - While changes are common differences matter less
  - While change is rare, differences are more marked
- Naturally appropriate for "clock" time, e.g., daily, weekly, annual patterns
- Less obviously appropriate for "developmental" time, where a common feature is people taking the same route at different speeds
- Lesnard (2006); Lesnard and de Saint Pol (2009); Lesnard (2010), implemented by him (seqcomp), in Traminer and SADI

Combinatorial approaches

- Combinatorial methods are a completely different approach to sequence comparison
- Proposed by Elzinga (2003, 2005)
- Compare sequences in terms of common "subsequences" rather than string-edits

Counting sequences

- The sequence ABC has as subsequences:
  - the null (empty) string
  - A, B and C
  - AB, AC and BC
  - and ABC itself
- A sequence of length l has 2^l subsequences
- If elements are repeated not all subsequences are distinct

Combinatorial measures

- Elzinga has proposed a number of measures that count subsequences
  - Longest common subsequence
  - Number of common subsequences
  - Number of matching subsequences
- A completely different logic, combinatorial rather than string-editing: "the same states in the same order"
- One particularly attractive approach: number of matching spell-subsequences weighted by duration (I refer to it as "X/t")

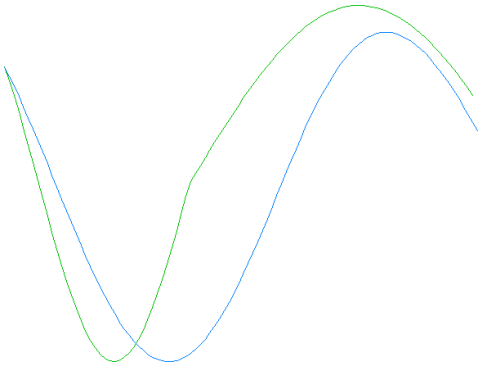
Warping time

- What of time-warping?
- Abbott and Hrycak (1990) use the term to suggest non-linear time scales
- OMv "warps time" by weighting it differently in different spells
- In turn informed by Sankoff and Kruskal (1983), *Time Warps, String Edits and Macromolecules*
- But time-warping refer to a specific set of algorithms

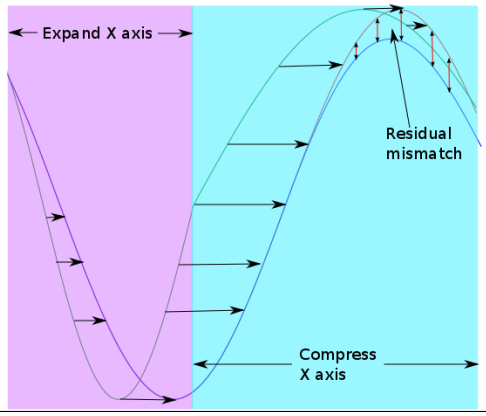
Time warping algorithms

- Formally, time warping is a family of algorithms that do "continuous time-series to time-series correction" while OM *et al* do "string to string correction" (Marteau, 2007)
- Focus on comparing pairs of continuous-time high-dimensional time-series in $\mathbb{R}^n$
- Operates by locally compressing or expanding the time scale of one trajectory to minimise the distance to the other
- Distance is usually Euclidean in $\mathbb{R}^n$ or other simple distance

TWED: Matching 1D series



TWED: Compress and expand



TW algorithms

- TW used widely: was used for speech recognition, signature verification, other machine learning tasks
- Typically used to match a high-dimensional time-series to a "dictionary" of standard elements
- Conceptually it is a continuous time approach but implementations must be discrete – sampling or periodic summaries:
  - e.g., sound sampled at 41 kHz
  - rainfall summarised daily
  - employment history reported monthly
- Kruskal and Liberman (1983) show that the continuous time logic can be faithfully implemented with discretised series

Discrete time-warping

TW with stiffness penalty: TWED

- Violation of the triangle inequality is due to TW usually having no cost to expansion or compression, only to the residual point-by-point distance
- Marteau (2007, 2008) proposes a TW algorithm that has a "stiffness" penalty
- Satisfies the triangle inequality
- Can be programmed very similarly to OM (recursive algorithm)
- Stiffness penalty like but not like *indel* cost – squeezing/stretching, not inserting/deleting
- Point-to-point distance just like substitution

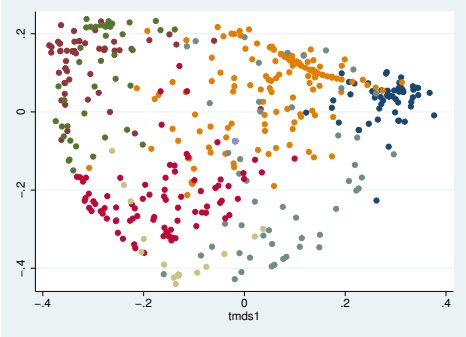
TWED: Recursive algorithm

TW distance, $\delta(A^p, B^q) =$

$$min \begin{cases} \delta(A^{p-1}, B^q) & + d_{LP}(a_p, a_{p-1}) + \gamma d_{LP}(t_{a_p}, t_{a_{p-1}}) + \lambda \\ \delta(A^{p-1}, B^{q-1}) & + d_{LP}(a_p, b_q) + \gamma d_{LP}(t_{a_p}, t_{b_q}) \\ \delta(A^p, B^{q-1}) & + d_{LP}(b_q, b_{q-1}) + \gamma d_{LP}(t_{b_q}, t_{b_{q-1}}) + \lambda \end{cases}$$

(Marteau, 2007)

MDS/Cluster with TWED



(See OM version)

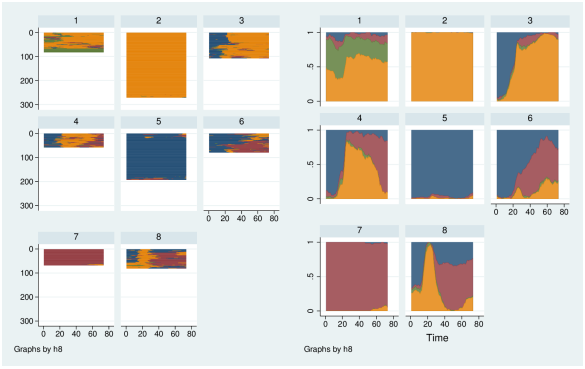
TWED attractive

- TWED has a completely different "narrative" from OM: warping time rather than editing token strings
- Nonetheless, gives results that are not radically different
- More noticeable differences for more complex sequences
- For high values of λ and γ, tends to yield Hamming distance
- For very low values of λ and γ, closer (but still not that close) to X/t
- Distribution in sequence space more like OM than X/t

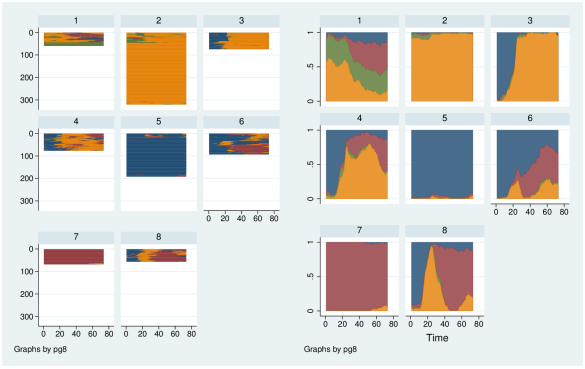
Code to run all the measures

```
use bsseq

set matsize 1000
matrix sm = (0,1,2,3\1,0,1,2\2,1,0,1\3,2,1,0)
matrix fl = (0,1,1,1\1,0,1,1\1,1,0,1\1,1,1,0)

hamming     state1-state72, subs(sm) pwd(ham)
oma         state1-state72, subs(sm) indel(1.5) pwd(om) len(72)
twed        state1-state72, subs(sm) nu(0.5) lambda(0.5) pwd(twd) len(72)

hamming     state1-state72, subs(fl) pwd(haf)
oma         state1-state72, subs(fl) indel(0.5) pwd(of) len(72)
twed        state1-state72, subs(fl) nu(0.5) lambda(0.5) pwd(twf) len(72)
dynhamming state1-state72, pwd(dyn)

preserve
combinprep, state(state) length(l) nspells(nsp) idvar(pid)
combinadd state1-l'r(maxspells)', pws(xtd) nsp(nsp) nstates('r(nels)') rtype(d)
restore
```

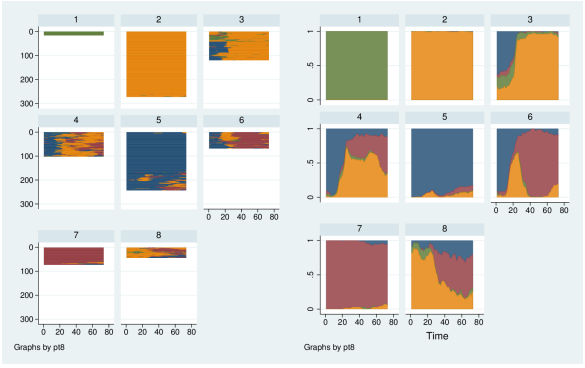

Hamming, linear matrix



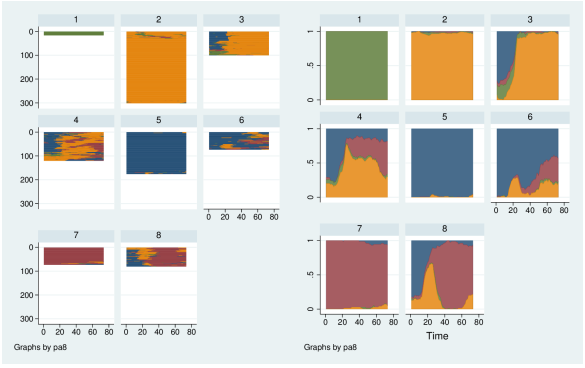
OM, linear matrix



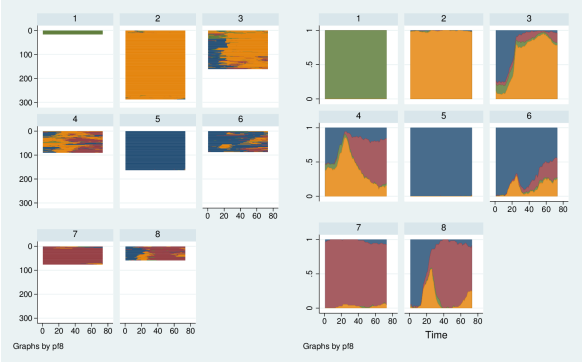
TWED, linear matrix



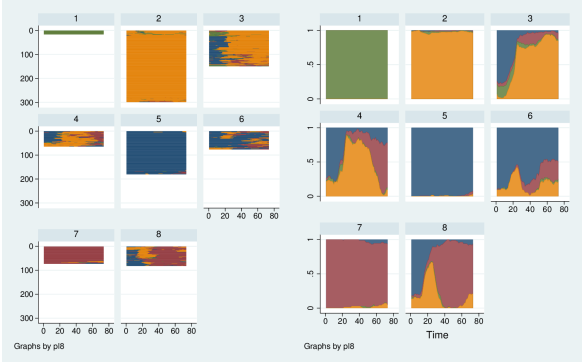
Hamming, flat matrix



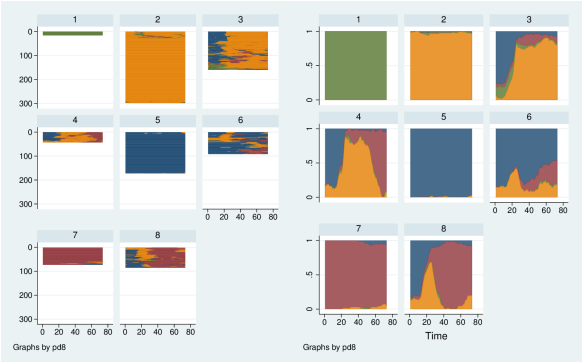
OM, flat matrix



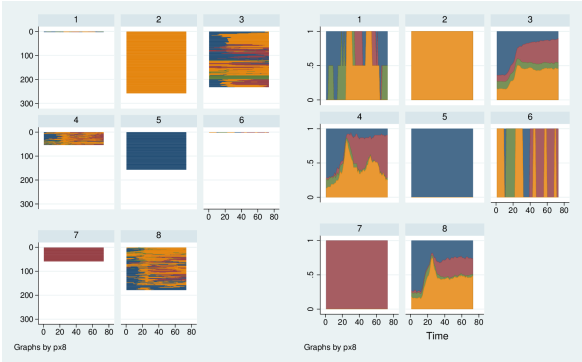
TWED, flat matrix



Dynamic Hamming



X/t



SA and further analysis

- With pairwise distances or a cluster solution we can move on to conventional analysis:
  - Explain the clusters: who goes where?
  - Predict from the clusters: do they have consequences for the future?
- Approaches: tabular, ANOVA, regression, logit
- Using clusters, MDS dimensions or other summaries of the distances

Explaining cluster membership, MVAD data

```
. tab g8 funemp, chi

           |     funemp
        g8 |         0          1 |     Total
-----------+----------------------+----------
         1 |     13.28      11.97 |     13.06
         2 |     22.52      24.79 |     22.89
         3 |      9.41       5.13 |      8.71
         4 |     20.84      18.80 |     20.51
         5 |      8.24      17.09 |      9.69
         6 |      3.03      10.26 |      4.21
         7 |      6.89       5.13 |      6.60
         8 |     15.80       6.84 |     14.33
-----------+----------------------+----------
     Total |    100.00     100.00 |    100.00

          Pearson chi2(7) =  28.5978   Pr = 0.000
```

```
. tab g8 gcse5eq, chi

           |     gcse5eq
        g8 |         0          1 |     Total
-----------+----------------------+----------
         1 |     17.26       5.77 |     13.06
         2 |     29.87      10.77 |     22.89
         3 |      2.21      20.00 |      8.71
         4 |     20.80      20.00 |     20.51
         5 |     13.05       3.85 |      9.69
         6 |      5.75       1.54 |      4.21
         7 |      6.64       6.54 |      6.60
         8 |      4.42      31.54 |     14.33
-----------+----------------------+----------
     Total |       452        260 |       712

          Pearson chi2(7) = 209.0925   Pr = 0.000
```


Association between covariates and clustering

- Where we have outcome variables, we may want to see how well they are predicted by the cluster solution
- Here one question is whether the cluster solution has additional explanatory power over and above simple summaries such as cumulated duration
- Example using Mothers' data
  - use sequence analysis/clustering of first 48 months to predict working in month 72
  - Nested model test: does cluster solution have predictive power after taking account of cumulated duration and state in month 48

Stata code

```
use bsseq
matrix subs = (0,1,2,3\ ///
               1,0,1,2\ ///
               2,1,0,1\ ///
               3,2,1,0)
oma state1-state48, subs(subs) indel(1.5) pwd(pwd) len(48)
clustermat wards pwd, add
cluster gen g8=groups(8)
cumuldur state1-state48, cdstub(cd) nstates(4)

gen working = inlist(state72,1,2)
logit working cd* i.state48
est store base
logit working cd* i.state48 i.g8
lrtest base
```

Beating cumulated duration

```
Logistic regression                             Number of obs     =        940
                                                LR chi2(13)       =     692.23
Log likelihood =  -304.3196                     Pseudo R2         =     0.5321
------------------------------------------------------------------------------
     working |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         cd1 |   .0567982   .0303362     1.87   0.061    -.0026595     .116256
         cd2 |   .0448847   .0257596     1.74   0.081    -.0056033    .0953726
         cd3 |  -.0250336    .023572    -1.06   0.288    -.0712338    .0211667
         cd4 |           0  (omitted)
             |
     state48 |
Part time..  |  -.6516304   .4752393    -1.37   0.170    -1.583082    .2798214
 Unemployed  |   -1.42019   .7612029    -1.87   0.062     -2.91212    .0717405
Non-emplo~d  |   -1.91716    .476274    -4.03   0.000     -2.85064   -.9836802
             |
          g8 |
           2 |   1.383836   1.482716     0.93   0.351    -1.522235    4.289906
           3 |   .9581697   .8137579     1.18   0.239    -.6367663    2.553106
           4 |   1.408097   .5815145     2.42   0.015     .268349    2.547844
           5 |   1.633173    .746909     2.19   0.029     .1692583    3.097088
           6 |   .6102612   1.210328     0.50   0.614    -1.761939    2.982461
           7 |   1.660886   .8701866     1.91   0.056    -.0446485     3.36642
           8 |   2.953757   1.329375     2.22   0.026     .3482298    5.559284
       _cons |  -1.357889   .5485839    -2.48   0.013    -2.433093   -.2826838
------------------------------------------------------------------------------

. lrtest base
Likelihood-ratio test                           LR chi2(7)  =     21.78
(Assumption: base nested in .)                  Prob > chi2 =    0.0028
```


MDS and modelling

- It may make sense to model with the MDS dimensions

```
set matsize 1000
mdsmat pwd, dim(3)
matrix dim=e(Y)
svmat dim
logit working cd* i.state48 dim*
lrtest base
```


MDS dimensions and model

```
Logistic regression                             Number of obs     =        940
                                                LR chi2(9)        =     680.39
                                                Prob > chi2       =     0.0000
Log likelihood = -310.23558                     Pseudo R2         =     0.5230

------------------------------------------------------------------------------
     working |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         cd1 |  -.2089523   .7153776    -0.29   0.770    -1.611067    1.193162
         cd2 |   -.066477   .4688012    -0.14   0.887    -.9853105    .8523564
         cd3 |  -.0511365   .2315928    -0.22   0.825    -.5050501    .4027771
         cd4 |           0  (omitted)
             |
     state48 |
Part time..  |   -1.15598   .4838525    -2.39   0.017    -2.104314   -.2076468
 Unemployed  |  -1.808753   .7752256    -2.33   0.020    -3.328167   -.2893387
Non-emplo~d  |  -2.050996   .5259212    -3.90   0.000    -3.081782   -1.020209
             |
        dim1 |  -4.520051   11.43535    -0.40   0.693    -26.93293    17.89283
        dim2 |   1.239288   .6851007     1.81   0.070    -.1034849     2.58206
        dim3 |  -1.502881    .567547    -2.65   0.008    -2.615252    -.390509
       _cons |   5.161245   15.96924     0.32   0.747    -26.13789    36.46038
------------------------------------------------------------------------------

. lrtest base

Likelihood-ratio test                           LR chi2(3)  =      9.94
(Assumption: base nested in .)                  Prob > chi2 =    0.0191
```


MDS correlated?

```
. corr cd* dim*
(obs=940)

             |      cd1      cd2      cd3      cd4     dim1     dim2     dim3
-------------+---------------------------------------------------------------
         cd1 |   1.0000
         cd2 |  -0.2586   1.0000
         cd3 |  -0.1879  -0.0914   1.0000
         cd4 |  -0.7082  -0.4017  -0.1321   1.0000
        dim1 |  -0.8801  -0.2130   0.1039   0.9471   1.0000
        dim2 |   0.3202  -0.5932  -0.2478   0.1919  -0.0000   1.0000
        dim3 |  -0.1299   0.1803   0.3282  -0.1219   0.0000  -0.0000   1.0000
```


Studer et al's discrepancy

- Studer et al. (2011) propose a method for treating distances matrices analogously to SS in regression and ANOVA
- The average distance to the centre of the whole matrix is the analogue of total sum of squares
- With a grouping variable, the distance to the centre for each groups is the residual sum of squares
- This allows a pseudo-R^2 and a pseudo-F test
- Permutation is used to approximate the sampling distribution of pseudo-F

Discrepancy and MVAD

```
use mvad

matrix md = (0, 1, 1, 2, 1, 3\ ///
             1, 0, 1, 2, 1, 3\ ///
             1, 1, 0, 2, 1, 2\ ///
             2, 2, 2, 0, 1, 1\ ///
             1, 1, 1, 1, 0, 2\ ///
             3, 3, 2, 1, 2, 0)
matrix rownames md = E F H S T U
matrix colnames md = E F H S T U

set matsize 1000
oma state*, subs(md) indel(1.5) pwd(oma) length(72)
discrepancy funemp, dist(oma) idvar(id) niter(1000) dcg(d2c)
```


Discrepancy results

```
. discrepancy funemp, dist(oma) idvar(id) niter(100) dcg(d2c)

Discrepancy based R2 and F, 100 permutations for p-value

             | pseudo R2   pseudo F    p-value
-------------+------------------------------
      funemp |   .007956   5.694094        .17

------------------------------------------------------------
   funemp |      N(d2c)     min(d2c)    mean(d2c)    max(d2c)
----------+-------------------------------------------------
        0 |          595    .2215114     .463736    1.919831
        1 |          117    .2757618    .5502117    1.518995
------------------------------------------------------------
```


Multiple domains

- Lifecourse analysis recognises the interrelatedness of domains
- Somewhat hard to handle in many approaches: a potential strength of SA?
- In practice, not very well developed; most research on single domains
- Some work (Dijkstra and Taris (1995), Pollock (2007), Gauthier et al. (2010))

Combined distance versus combining distances

- How to proceed?
- Conduct parallel analyses and combine results?
- Combine domains into a single variable?
- The former is easy but will be less sensitive to the synchronisation of domains
- The latter involves a large state space and problem in defining distances
- However, better sensitivity to cross-domain features makes it attractive

Combine by cross-tabulation

- The simplest approach is to create a new state space that is the cross-tabulation of the two (or more) domains
- This yields a large number of states, one for each combination
- How then to determine costs?

Determining costs

- Simplest strategy is to sum across the domains
- In short, $d^{AB}_{ik,jl} = d^{A}_{i,j} + d^{B}_{k,l}$
- There may be justification for imposing other patterns, for instance,
  - imposing a ceiling
  - changing d^A for certain values in domain B
  - weighting the domains differentially
- Note that with two different substitution matrices it can be difficult to weight equally
  - equalise by max substitution cost?
  - equalise by average substitution cost?
  - equalise by average substitution cost weighted by occurrence in the data?

Implementation

- We take a simple case (four parity levels and five employment statuses)
- First step is to create the interaction or crosstabulation of the states

```
// Reshape long to work on all months simultaneously
reshape long parx emp, i(pid) j(month)

// Create a variable that is the interaction of the two
gen cross = emp+(parx-1)*5

// Verify the state interaction variable
tab cross
table parx emp, c(mean cross)

// Back to wide, fix the variable order
reshape wide parx emp cross, i(pid) j(month)
order pid parx* emp* cross*
```


Create the substitution cost matrix

- We have two substitution cost matrices, 4x4 and 5x5:

```
matrix spar = (0,1,2,3\ ///      matrix semp = (0,1,2,3,3\ ///
               1,0,1,2\ ///                     1,0,1,2,2\ ///
               2,1,0,1\ ///                     2,1,0,1,1\ ///
               3,2,1,0)                         3,2,1,0,1\ ///
                                                3,2,1,1,0)
```

- Both have a max of 3, otherwise perhaps divide each by its max

Combine into 20x20

```
// Use Mata to combine the two matrices
mata:
spar = st_matrix("spar")
semp = st_matrix("semp")

// each element becomes a 5x5 block
sparx = spar # J(1,5,1) # J(5,1,1)

// replicate the 5x5 matrix 4x4 times
sempx = semp
for (i=2; i<=4; i++) {
  sempx = sempx,semp
}
sempxy = sempx
for (i=2; i<=4; i++) {
  sempxy = sempxy\sempx
}

// The combined matrix is the element-wise sum; return it from Mata to Stata
st_matrix("mcsa", sempxy :+ sparx)
end
```


The combined matrix

```
symmetric mcsa[20,20]
     c1 c2 c3 c4 c5 c6 c7 c8 c9c10c11c12c13c14c15c16c17c18c19c20
 r1  0
 r2  1  0
 r3  2  1  0
 r4  3  2  1  0
 r5  3  2  1  1  0
 r6  1  2  3  4  4  0
 r7  2  1  2  3  3  1  0
 r8  3  2  1  2  2  2  1  0
 r9  4  3  2  1  2  3  2  1  0
r10  4  3  2  2  1  3  2  1  1  0
r11  2  3  4  5  5  1  2  3  4  4  0
r12  3  2  3  4  4  2  1  2  3  3  1  0
r13  4  3  2  3  3  3  2  1  2  2  2  1  0
r14  5  4  3  2  3  4  3  2  1  2  3  2  1  0
r15  5  4  3  3  2  4  3  2  2  1  3  2  1  1  0
r16  3  4  5  6  6  2  3  4  5  5  1  2  3  4  4  0
r17  4  3  4  5  5  3  2  3  4  4  2  1  2  3  3  1  0
r18  5  4  3  4  4  4  3  2  3  3  3  2  1  2  2  2  1  0
r19  6  5  4  3  4  5  4  3  2  3  4  3  2  1  2  3  2  1  0
r20  6  5  4  4  3  5  4  3  3  2  4  3  2  2  1  3  2  1  1  0
```


Dyadic SA

- SA typically uses all-pair-wise distances, or distance to special cases
- Dyadic SA is also useful: distance between a specific pair
  - Couple time-diaries
  - Couple labour market histories
  - Mother–daughter fertility histories, etc.

Research questions

- Allows testing hypotheses about dyadic similarity
  - Are couples' time-use patterns or life-course histories aligned
  - Are fertility patterns inherited?
  - Under what conditions are dyadic distances smaller or larger?
  - How do couples arrange joint lifecourses?

Similarity and difference

- Couples may coordinate their lives under very different gender constraints
- Fertility patterns may be similar within the constraints of different cohort patterns of fertility
- The relationship between sequences may not be one of replication
  - some daughters may completely reject their mother's fertility pattern

Literature

- Off-scheduling (Lesnard, 2008) Dyadic in concept but actually creates combined sequences
- Robette et al. (2015): Mother–daughter labour market careers
- Fasang and Raab (2014): Intergenerational fertility; notes that focus on similarity ignores heterogeneity
- Raab et al. (2014): Jun 13 2015 15:18:18 Sibling dyads, fertility

Practical issues

- We can calculate dyadic distances with standard software
- For efficiency it might better to just calculate dyads' distances
- But the cost of calculating all pairs is relatively small, and offers an advantage:
  - Compare dyadic distances with distances to all others

Strategy: Begin with dyad-ordered data

	Dyad	1	1	2	2	3	3	4	4
Type		M	D	M	D	M	D	M	D
M	1	11	12	13	14	15	16	17	18
D	1	21	22	23	24	25	26	27	28
M	2	31	32	33	34	35	36	37	38
D	2	41	42	43	44	45	46	47	48
M	3	51	52	53	54	55	56	57	58
D	3	61	62	63	64	65	66	67	68
M	4	71	72	73	74	75	76	77	78
D	4	81	82	83	84	85	86	87	88

Sort by types

	Dyad	1	2	3	4	1	2	3	4
Type		D	D	D	D	M	M	M	M
D	1	22	24	26	28	21	23	25	27
D	2	42	44	46	48	41	43	45	47
D	3	62	64	66	68	61	63	65	67
D	4	82	84	86	88	81	83	85	87
M	1	12	14	16	18	11	13	15	17
M	2	32	34	36	38	31	33	35	37
M	3	52	54	56	58	51	53	55	57
M	4	72	74	76	78	71	73	75	77

Submatrices

- Two submatrices, with distances from each mother to each daughter (and transpose)
- Distance from mother to her own daughter on diagonal (and transpose)
- Use distance from mother to all daughters to assess whether distance to own daughter is unusual

Submatrices

	Pair	1	2	3	4
Type		M	M	M	M
D	1	21	23	25	27
D	2	41	43	45	47
D	3	61	63	65	67
D	4	81	83	85	87

	Pair	1	2	3	4
Type		D	D	D	D
M	1	12	14	16	18
M	2	32	34	36	38
M	3	52	54	56	58
M	4	72	74	76	78

Extract diagonals and other information

- The main info is on the diagonals: the dyad distances (repeated across the two submatrices since distance is symmetric)
- Other summaries are also interesting
  - mean distance of each daughter to all mothers (and vice versa)
  - variance, standard deviation of this distance
  - z-score of dyad distance relative to all distances
  - rank of dyad distance compared with all distances

Abbott, A. (1984). Event sequence and event duration: Colligation and measurement. *Historical Methods*, 17(4):192–204.

Abbott, A. (2000). Reply to Levine and Wu. *Sociological Methods and Research*, 29(1):65–76.

Abbott, A. (2001). *Time Matters: On Theory and Method*. University of Chicago Press, Chicago.

Abbott, A. and Forrest, J. (1986). Optimal matching methods for historical sequences. *Journal of Interdisciplinary History*, XVI(3):471–494.

Abbott, A. and Hrycak, A. (1990). Measuring resemblance in sequence data: An optimal matching analysis of musicians' careers. *American Journal of Sociology*, 96(1):144–85.

Abbott, A. and Tsay, A. (2000). Sequence analysis and optimal matching methods in sociology. *Sociological Methods and Research*, 29(1):3–33.

Aisenbrey, S. and Fasang, A. E. (2010). New life for old ideas: The 'second wave' of sequence analysis – bringing the 'course' back into the life course. *Sociological Methods and Research*, 38(3):420–462.

Barban, N. and Billari, F. (2012). Classifying life course trajectories: A comparison of latent class and sequence analysis. *Journal of the Royal Statistical Society Series C*, 61(5):765–784.

Billari, F. C., Fürnkranz, J., and Prskawetz, A. (2006). Timing, sequencing and quantum of life course events: A machine learning approach. *European Journal of Population*, 22:37–65.

Blair-Loy, M. (1999). Career patterns of executive women in finance: An optimal matching analysis. *American Journal of Sociology*, 104(5):1346–1397.

Blanchard, P., Bühlmann, F., and Gauthier, J.-A., editors (2014). *Advances in Sequence Analysis: Theory, Method, Applications*. Springer, Berlin.

Dijkstra, W. and Taris, T. (1995). Measuring the agreement between sequences. *Sociological Methods and Research*, 24(2):214–231.

Elzinga, C. H. (2003). Sequence similarity: A non-aligning technique. *Sociological Methods and Research*, 32(1):3–29.

Elzinga, C. H. (2005). Combinatorial representations of token sequences. *Journal of Classification*, 22(1):87–118.

Elzinga, C. H. (2010). Complexity of categorical time series. *Sociological Methods and Research*, 38(3):463–481.

Fasang, A. and Raab, M. (2014). Beyond transmission: Intergenerational patterns of family formation among middle-class american families. *Demography*, 51(5):1703–1728.

Gabadinho, A. (2014). Package 'pst'. probabilistic suffix trees and variable length Markov chains. Technical report, CRAN.

Gauthier, J.-A., Widmer, E. D., Bucher, P., and Notredame, C. (2010). Multichannel sequence analysis applied to social science data. *Sociological Methodology*, 40(1):1–38.

Halpin, B. (2013). Sequence analysis. In Baxter, J., editor, *Oxford Bibliographies in Sociology*. Oxford University Press, New York.

Halpin, B. (2014a). SADI: Sequence analysis tools for Stata. Working Paper WP2014-03, Dept of Sociology, University of Limerick, Ireland.

Halpin, B. (2014b). Three narratives of sequence analysis. In Blanchard, P., Bühlmann, F., and Gauthier, J.-A., editors, *Advances in Sequence Analysis: Theory, Method, Applications*. Springer, Berlin.

Halpin, B. (2016). Cluster analysis stopping rules in stata. Working Paper WP2016-01, Department of Sociology, University of Limerick.

Halpin, B. and Chan, T. W. (1998). Class careers as sequences: An optimal matching analysis of work-life histories. *European Sociological Review*, 14(2).

Han, S.-K. and Moen, P. (1999). Work and family over time: A life course approach. *Annals of the American Academy of Political and Social Science*, 562:98–110.

Kruskal, J. B. and Liberman, M. (1983). The symmetric time-warping problem. In Sankoff and Kruskal (1983), pages 125–161.

Lesnard, L. (2006). Optimal matching and social sciences. Document du travail du Centre de Recherche en Économie et Statistique 2006-01, Institut Nationale de la Statistique et des Études Économiques, Paris.

Lesnard, L. (2008). Off-scheduling within dual-earner couples: An unequal and negative externality for family time. *American Journal of Sociology*, 114(2):447–90.

Lesnard, L. (2010). Setting cost in optimal matching to uncover contemporaneous socio-temporal patterns. *Sociological Methods and Research*, 38(3):389–419.

Lesnard, L. and de Saint Pol, T. (2009). Patterns of workweek schedules in France. *Social Indicators Research*, 93:171–176.

Levine, J. H. (2000). But what have you done for us lately? Commentary on Abbott and Tsay. *Sociological Methods and Research*, 29(1):34–40.

Lovaglio, P. G. and Mezzanzanica, M. (2013). Classification of longitudinal career paths. *Quality and Quantity*, 47(2):989–1008.

Marteau, P.-F. (2007). Time Warp Edit Distance with Stiffness Adjustment for Time Series Matching. *ArXiv Computer Science e-prints*.

Marteau, P.-F. (2008). Time Warp Edit Distance. *ArXiv e-prints*.

Pollock, G. (2007). Holistic trajectories: A study of combined employment, housing and family careers by using multiple-sequence analysis. *Journal of the Royal Statistical Society: Series A*, 170(1):167–183.

Raab, M., Fasang, A. E., Karhula, A., and Erola, J. (2014). Sibling similarity in family formation. *Demography*, 51(6):2127–2154.

Robette, N., Bry, X., and Éva Lelièvre (2015). A "global interdependence" approach to multidimensional sequence analysis. *Sociological Methodology*, Online advance copy.

Sankoff, D. and Kruskal, J. B., editors (1983). *Time Warps, String Edits and Macromolecules*. Addison-Wesley, Reading, MA.

Stovel, K. (2001). Local sequential patterns: The structure of lynching in the Deep South, 1882–1930. *Social Forces*, 79(3):843–880.

Stovel, K., Savage, M., and Bearman, P. (1996). Ascription into achievement. *American Journal of Sociology*, 102(2):358–99.

Studer, M. and Ritschard, G. (2014). A comparative review of sequence dissimilarity measures. Working Paper 2014-33, LIVES, Geneva.

Studer, M., Ritschard, G., Gabadinho, A., and Müller, N. S. (2011). Discrepancy analysis of state sequences. *Sociological Methods and Research*, 40(3):471–510.

Wu, L. L. (2000). Some comments on "Sequence analysis and optimal matching methods in sociology: Review and prospect". *Sociological Methods and Research*, 29(1):41–64.

Wuerker, A. (1996). The changing careers of patients with chronic mental illness: A study of sequential patterns in mental health service utilization. *The Journal of Behavioral Health Services and Research*, 23(4):458–470.