Rendering sequences

Rendering sequences

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8/5/2008gr 1/60

Rendering sequences

Introduction

The research project

Research Team

- Gilbert Ritschard, professor of Statistics for social sciences
 U. of Geneva
 main applicant
- Eric Widmer, professor of Sociology,
 U. of Geneva (since September 2007, formerly at U. Lausanne)
 co-applicant
- Alexis Gabadinho (scientific collaborator, 40%)
 Demography
- Nicolas S. Müller (assistant 50%)
 Sociology, Computer Science
- Matthias Studer (assistant 50%)
 Economics, Sociology

Rendering sequences Introduction

The research proje

Research project

The work presented in this seminar is part of the FNS project

- Mining event histories: Towards new insights on personal Swiss life courses
- Project FN 100012-113998
- Start: February 1, 2007 End: January 31, 2009
- It is work in progress

3/5/2008gr 4/60

Rendering sequence Introduction

The research project

Objectives of the project I

- Explore the feasibility and interest of heuristical data mining approaches for discovering interesting knowledge from event history data.
- Develop data mining techniques by adapting existing ones to the specificity of event history data
- Making newly adapted/developed techniques and validation criteria easily accessible to the social scientist end user through a general toolbox for life course data.
- Demonstrate the complementarity of data mining approaches with classical ones through convincing illustrations of the original new insights that they provide.

8/5/2008gr 6/

3/5/2008gr 5/6

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Introduction

The research project

Objectives of the project II

• Discover the most characteristic personal Swiss life course patterns, especially broken life patterns, through an overall in-depth analysis of the retrospective biographical database collected by the Swiss Household Panel.

/5/2008gr 7/60

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Introduction

Objectives of presentation

Evolution tendencies in familial life course trajectories

Sequence analysis techniques permit to test hypotheses about evolution in these familial life trajectories. (Elzinga and Liefbroer, 2007):

- De-standardization: Some states and events of familial life are shared by decreasing proportions of the population, occur at more dispersed ages and their duration is also more scattered.
- De-institutionalization: Social and temporal organization of life courses becomes less driven by normative, legal or institutional rules.
- Differentiation: Number of distinct steps lived by individual increases.

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Objectives of presentation

Objective of this presentation

- Colorize your life courses
- Preliminary results from the analysis of the retrospective Swiss Household Panel (SHP) survey.
- Focus on visualization of life course data.
- Divorce and de-standardization of life Swiss life courses.

8/5/2008gr 9/6

Introduction

Objectives of presentation

Two broad approaches

- Survival analysis (Event history analysis): Focus on one event (divorce)
 - Which factors influence the hazard rate of experimenting the event?
 - What is the importance of these factors?
- Sequence analysis: sequence describing whole life course.
 - Similarity between pairs of state sequences (⇒ cluster analysis).
 - Typical event pattern.
 - Turbulence and other instability measures of a sequence.

/5/2008gr 10/60

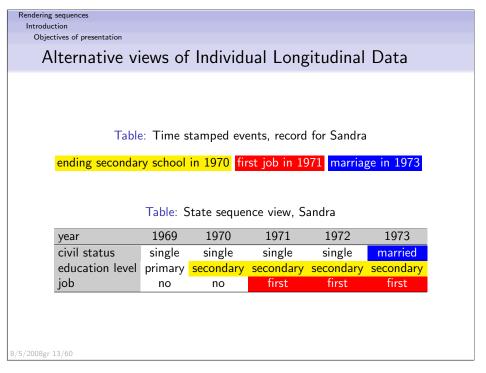
8/5/2008gr 11/6

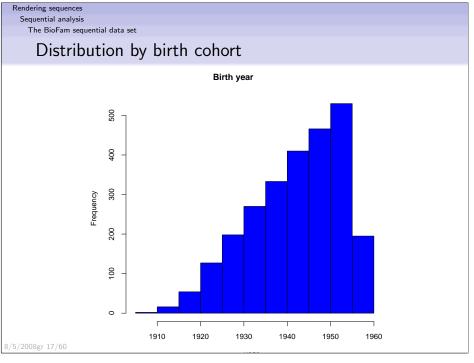
ectives of presentat		
ypology	of methods for life co	urse data
	Issues	
Questions	duration/hazard	state/event sequencing
descriptive	Survival curves:	 Optimal matching
	Parametric	clustering
	(Weibull, Gompertz,)	 Frequencies of given
	and non parametric	patterns
	(Kaplan-Meier, Nelson-	 Discovering typical
	Aalen) estimators.	episodes
causality	 Hazard regression models 	 Markov models
	(Cox,)	 Mobility trees
	 Survival trees 	 Association rules
		among episodes

Rendering sequences

8/5/2008gr 12/60

Rendering sequences
Sequential analysis
The BioFam sequential data set
Presentation of the "BioFam" data
 Data from the retrospective survey conducted in 2002 by the Swiss Household Panel (SHP)
• (with support of Federal Statistical Office, Swiss National
Fund for Scientific Research, University of Neuchatel.)
Retrospective survey: 5560 individuals
 Retained familial life events: Leaving Home, First childbirth,
First marriage and First divorce.
ullet Age 15 to 45 $ ightarrow$ 2601 remaining individuals, born between
1909 et 1957.
8/5/2008gr 16/60





Rendering sequences Sequential analysis

The BioFam sequential data set

Creating sequences

• Example of time stamped data:

individual	LHome	marriage	childbirth	divorce
1	1989	1990	1992	NA

8/5/2008gr 18/60

Rendering sequences Sequential analysis

The BioFam sequential data set

From events to states

Example of transformation:

events:

individual	LHome	marriage	childbirth	divorce
1	1989	1990	1992	NA

states:

individual	 1988	1989	1990	1991	1992	1993	
1	 0	0	1	3	3	6	

Rendering sequences Sequential analysis

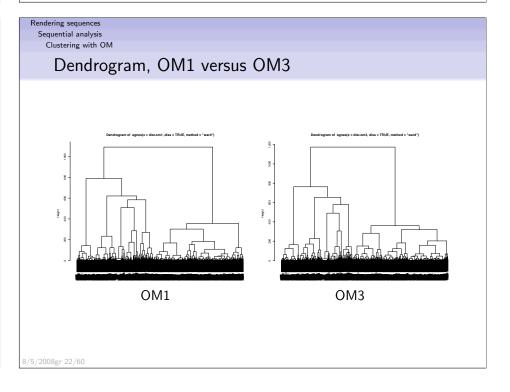
The BioFam sequential data set

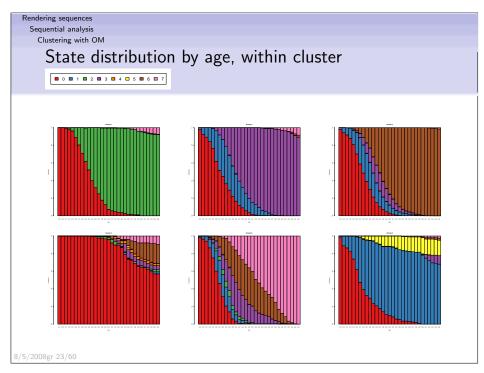
Deriving the states

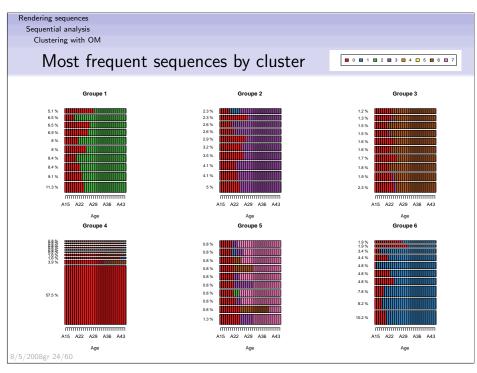
Need one state for each combination of events:

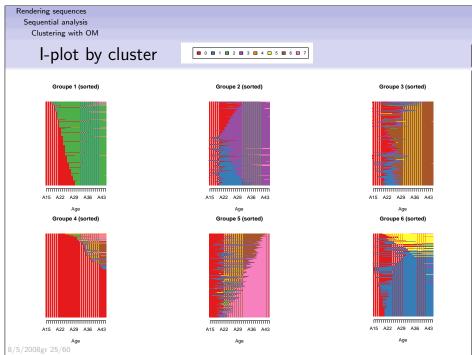
	LHome	marriage	childbirth	divorce
0	no	no	no	no
1	yes	no	no	no
2	no	yes	yes/no	no
3	yes	yes	no	no
4	no	no	yes	no
5	yes	no	yes	no
6	yes	yes	yes	no
7	yes/no	yes	yes/no	yes

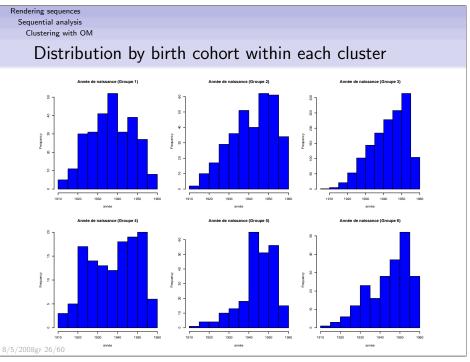
8/5/2008gr 19/60

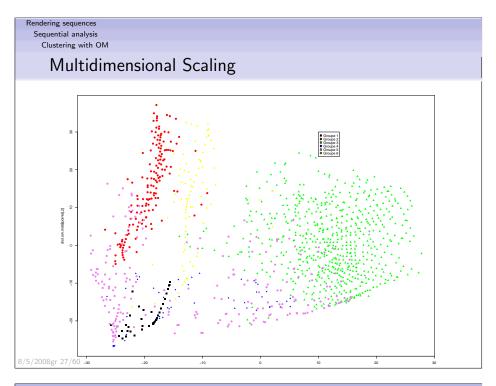












Rendering sequences
Mining frequent sub-sequences
Event sequences

Definitions of event sequences

According to Agrawal and Srikant (1995)

- $I = \{i_1, i_2, ... i_m\}$ set of m distinct events defining an alphabet.
- A transition is a list of non null, not ordered events $(i_1 i_2 ... i_k)$.
- A sequence is an ordered list of transitions.
- A sequence is denoted $\alpha = (\alpha_1 \to \alpha_2 \to ... \to \alpha_q)$, where α_i is a transition.

8/5/2008gr 30/60

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Mining frequent sub-sequences

Event sequences

Sub-sequence (1)

- α is a subsequence of β if each event in α belongs also to β and order between events is preserved.
- We denote it by $\alpha \leq \beta$.
- Ex: $(B \to AC)$ is a subsequence of $(AB \to E \to ACD)$ since $B \subseteq (AB)$ and $(AC) \subseteq (ACD)$.
- A subsequence is said frequent when it is found in a number of sequences that exceeds a minimal threshold support defined by the user.
- ullet A k-sequence is a subsequence composed of k elements.

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Mining frequent sub-sequences

Event sequences

Sub-sequence (2)

- Order of event occurrences matters.
- Simultaneity is also is also taken into consideration.
- Presence/absence of intermediary events is allowed.
- Length of gaps does not matter.

8/5/2008gr 32/6

Rendering sequences Mining frequent sub-sequences Considered events Considered events

Code	Description
С	First union
d	Leaving Home
е	First childbirth
m	First marriage
S	Divorce of first marriage

8/5/2008gr 34/60

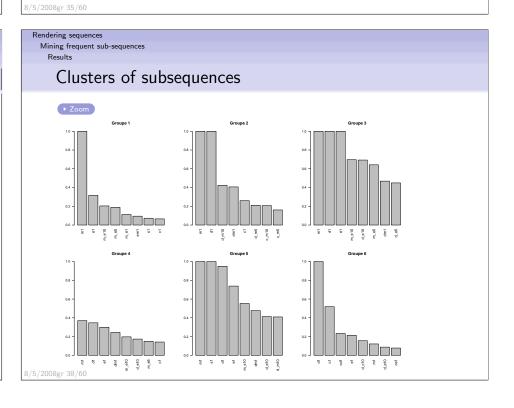
8/5/2008gr 37/60

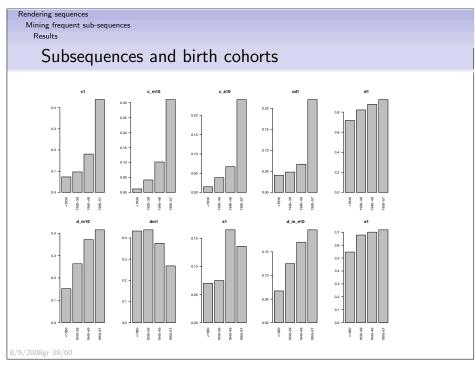
Rendering sequences
Mining frequent sub-sequences
Results
Frequent subsequences

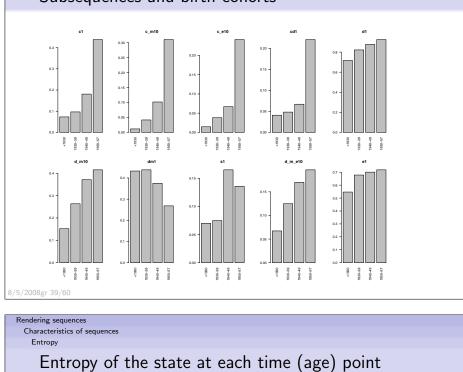
<i>K</i> -sequence	Percentage
m	90.0%
d	85.8%
е	68.1%
m_e10	44.4%
d_e10	43.0%
m_e5	40.1%
dm	36.3%
d_m10	33.1%
d_e5	27.8%
С	22.9%

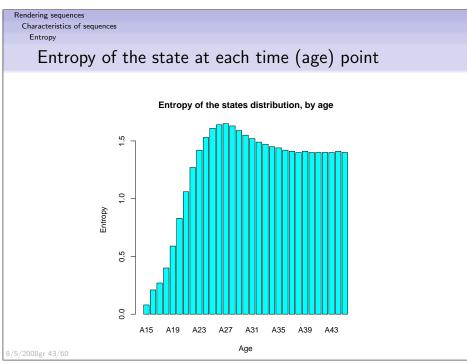
<i>K</i> -sequence	Percentage
dm_e10	19.4%
$d_{-}m5$	19.2%
m_e1	19.1%
em	18.4%
dm_e5	17.5%
d_m_e10	15.5%
c_m10	14.2%
S	12.3%
de	11.3%
c_m5	11.2%

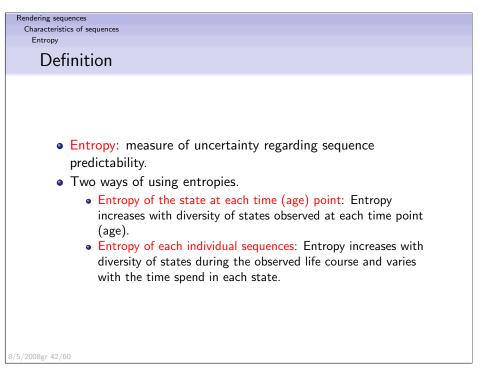
Rendering sequences Mining frequent sub-sequences Considered events Data format individual timestamp events 21 cd 5 28 em 8 16 d 30 С 32 m 8 40 S

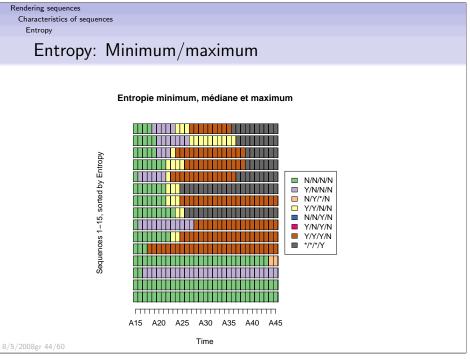


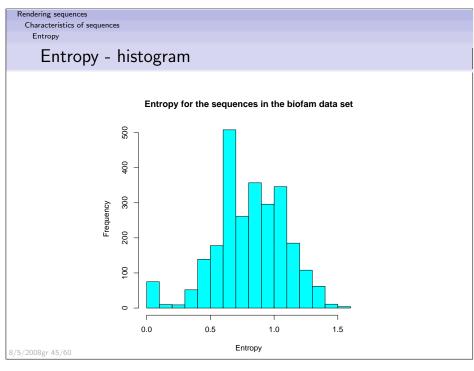


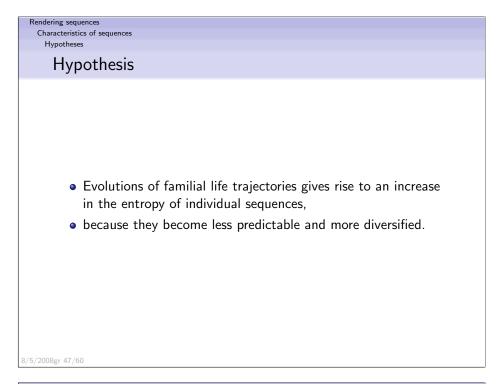


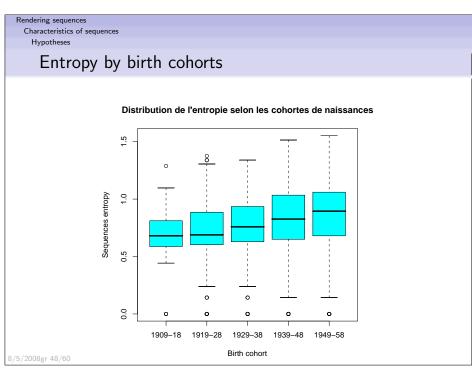


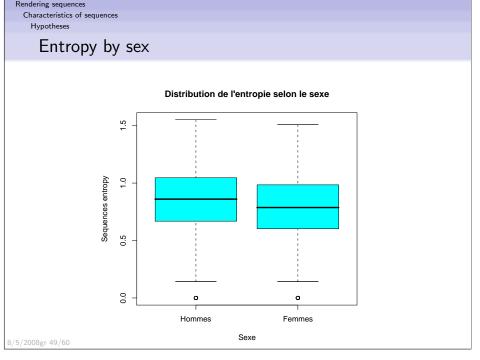












Characteristics of sequences Turbulence Definition

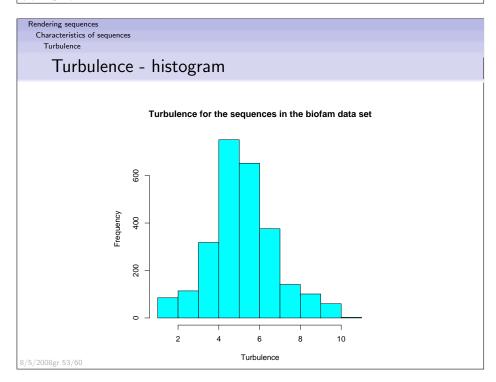
• Turbulence (Elzinga and Liefbroer, 2007): Somewhat similar

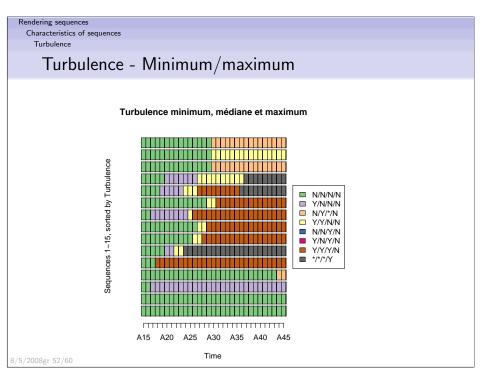
- Turbulence accounts for state sequencing (which is not the case of the entropy).
- Turbulence accounts of the following two elements:
 - number of subsequences:
 x=S,U,M,MC 16 subsequences more turbulent than
 y=S,U,S,C 15 subsequences
 - variance of duration in each state: S/10 U/2 M/132 is less turbulent than S/48 U/48 M/48

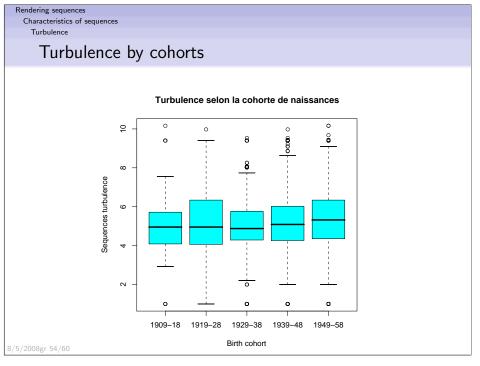
8/5/2008gr 51/60

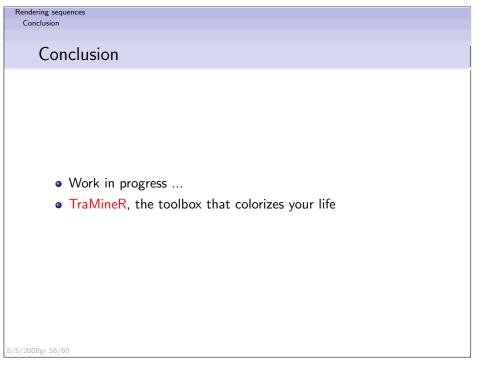
Rendering sequences

to entropy.

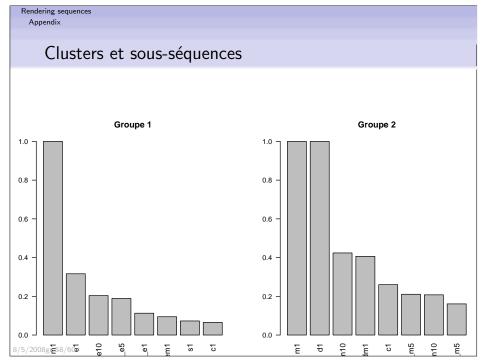


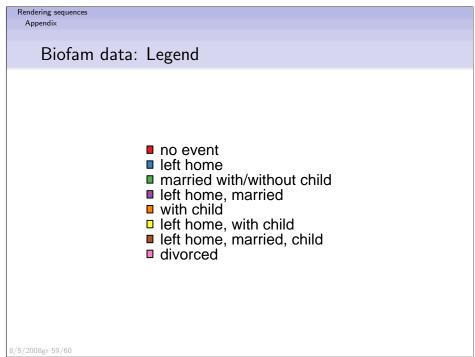












Rendering sequences Appendix

References

Agrawal, R. and R. Srikant (1995). Mining sequential patterns. In P. S. Yu and A. L. P. Chen (Eds.), *Proceedings of the International Conference on Data Engeneering (ICDE), Taipei, Taiwan*, pp. 487–499. IEEE Computer Society. Elzinga, C. H. and A. C. Liefbroer (2007). De-standardization of family-life trajectories of young adults: A cross-national comparison using sequence analysis. *European Journal of Population 23*, 225–250.

8/5/2008gr 60/60