

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.

Survival Approaches

- Survival or Event history analysis (Blossfeld and Rohwer, 2002)
 - Focuses on one event.
 - Concerned with duration until event occurs or with hazard of experiencing event.
- Survival curves: Distribution of duration until event occurs
 - $S(t) = p(T \geq t)$.
- Hazard models: Regression like models for $S(t, \mathbf{x})$ or hazard $h(t) = p(T = t \mid T \ge t)$

$$h(t,\mathbf{x}) = g\left(t,\beta_0+\beta_1x_1+\beta_2x_2(t)+\cdots\right)$$

Marriage Survival

Survival Tree The biographical SHP dataset

SHP biographical retrospective survey http://www.swisspanel.ch

- SHP retrospective survey: 2001 (860) and 2002 (4700 cases).
- We consider only data collected in 2002.
- Data completed with variables from 2002 wave (language).

Characteristics of retained data for divorce

(individuals who get married at least once)

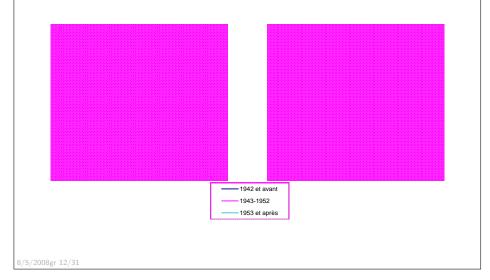
| men | women | Total |
|-------|-------------|-----------|
| 1414 | 1656 | 3070 |
| 231 | 308 | 539 |
| 16.3% | 18.6% | 17.6% |
| | 1414 231 | 1414 1656 |

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Marriage Survival Survival Tree

The biographical SHP dataset

Marriage duration until divorce Survival curves

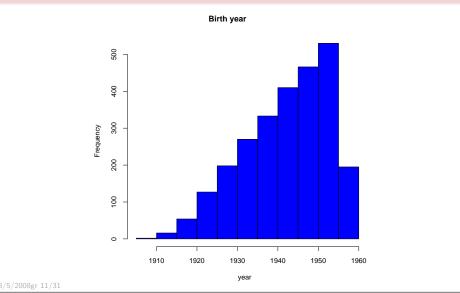


Marriage Survival

Survival Tree

The biographical SHP dataset

Distribution by birth cohort



Marriage Survival Survival Tree The biographical SHP dataset Marriage duration until divorce Hazard model

- Discrete time model (logistic regression on person-year data)
- $\exp(B)$ gives the Odds Ratio, i.e. change in the odd h/(1-h) when covariate increased by 1 unit.

| | | exp(B) | Sig. |
|------------|---------|-------------|-------|
| birthyr | | 1.0088 | 0.002 |
| university | | 1.22 | 0.043 |
| child | | 0.73 | 0.000 |
| language | unknwn | 1.47 | 0.000 |
| | French | 1.26 | 0.007 |
| | German | 1 | ref |
| | Italian | 0.89 | 0.537 |
| Constant | | 0.000000004 | 0.000 |

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Marriage Survival Survival Tree

Survival Tree Principle

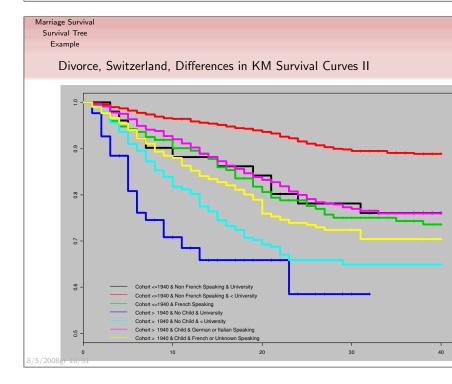
Survival trees: Principle

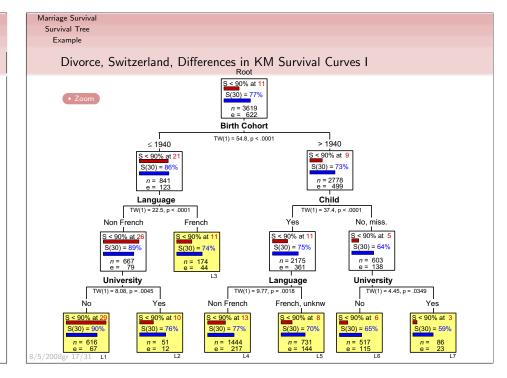
- Target is survival curve or some other survival characteristic.
- Aim: Partition data set into groups that
- differ as much as possible (max between class variability)
 - Example: Segal (1988) maximizes difference in KM survival curves by selecting split with smallest *p*-value of Tarone-Ware Chi-square statistics

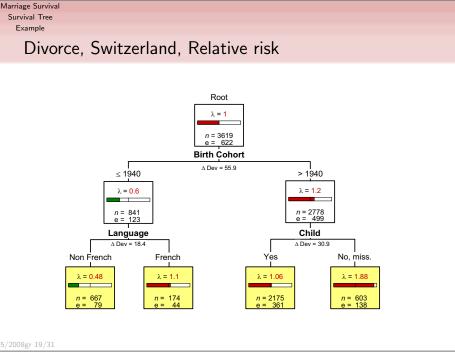
$$TW = \sum_{i} \frac{w_i \left(d_{i1} - \mathsf{E}(D_i) \right)}{\left(w_i^2 \operatorname{var}(D_i) \right)^{1/2}}$$

- are as homogeneous as possible (min within class variability)
 - Example: Leblanc and Crowley (1992) maximize gain in deviance (-log-likelihood) of relative risk estimates.

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Marriage Survival Survival Tree

Example

Hazard model with interaction

- Adding interaction effects detected with the tree approach
- improves significantly the fit (sig $\Delta \chi^2 = 0.004$)

| | | exp(B) | Sig. |
|--------------------|---------|--------|-------|
| born after 1940 | | 1.78 | 0.000 |
| university | | 1.22 | 0.049 |
| child | | 0.94 | 0.619 |
| language | unknwn | 1.50 | 0.000 |
| | French | 1.12 | 0.282 |
| | German | 1 | ref |
| | Italian | 0.92 | 0.677 |
| b_before_40*French | | 1.46 | 0.028 |
| b_after_40*child | | 0.68 | 0.010 |
| Constant | | 0.008 | 0.000 |
| - | | | |

Marriage Survival Growing a tree with party

Creating duration and censor variables from sequences

- Duration until marriage.
- The seqfpos() function of TraMineR returns first occurrence of state.

```
data(biofam)
svar <- 10:25
durmax <- length(svar)
# seqfpos returns the position of first occurrence of the provided state
   data,s:e means that we consider the sequence defined in data between columns s and e
  states considered are
       2 (married without leaving home)
       3 (married and leaved home)
       6 (married with child)
       7 (divorced)
# If divorce occurs before any marriage, we assume marriage and divorce the same year
fmar <- data.frame(s2=seqfpos(biofam,svar,2), s3=seqfpos(biofam,svar,3),</pre>
   s6=seqfpos(biofam,svar,6), s7=seqfpos(biofam,svar,7))
# creating duration variable as min value of the 4 states
fmar <- data.frame(fmar,fpos=apply(fmar,1,min,na.rm=TRUE))</pre>
# create the censor variable mar
fmar <- data.frame(fmar,mar=(fmar$fpos!=Inf))</pre>
# Setting duration to sequence length for censored cases.
fmar$fpos[fmar$fpos==Inf] <- durmax</pre>
```

Marriage Survival

Survival Tree Social Science Issues

Issues with survival trees in social sciences

- Dealing with time varying predictors
 - Segal (1992) discusses few possibilities, none being really satisfactory.
 - Huang et al. (1998) propose a piecewise constant approach suitable for discrete variables and limited number of changes.
 - Room for development ...
- Ø Multi-level analysis
 - How can we account for multi-level effects in survival trees, and more generally in trees?
 - Conjecture: Should be possible to include unobserved shared effect in deviance-based splitting criteria.

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Marriage Survival Growing a tree with party

Growing a survival tree with party

Creting the survival object
library(survival)
surv.fmar <- Surv(fmar\$fpos,fmar\$mar)</pre>

covariate data frame

coho1 <- (biofam\$birthyr < 1940)*"<1940" coho2 <- (biofam\$birthyr >=1940 & biofam\$birthyr < 1950) coho3 <- (biofam\$birthyr >=1950) coho = coho1 + 2*coho2 + 3*coho3 lang <- biofam\$plingu02 sex <- biofam\$sex</pre>

covariates <-data.frame(sex,lang,coho1,coho2,coho3)</pre>

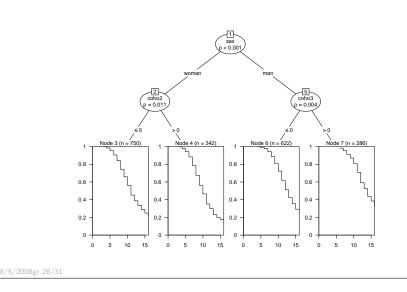
library(party)
stree <- ctree(surv.fmar ~ .,data=covariates)
plot(stree,legend)</pre>

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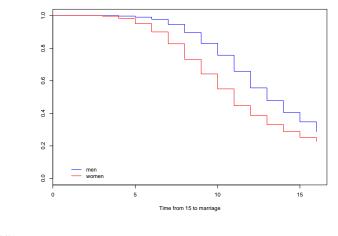
Marriage Survival

Growing a tree with party

Obtained survival tree for time to marriage



Growing a tree with party Generated survival curves



Fleming-Harrington Survival Curves, Time to Marriage

Marriage Survival Growing a tree with party

Generating survival curves

Creting the survival object
library(survival)
surv.fmar <- Surv(fmar\$fpos,fmar\$mar)</pre>

surv.fmar <- Surv(fmar\$fpos,fmar\$mar)</pre>

K-M survival curve

sf.fmar <- survfit(surv.fmar)
summary(sf.fmar)
plot(sf.fmar)</pre>

Fleming-Harrington survival curve

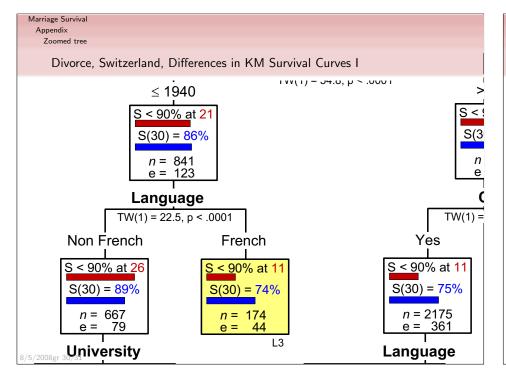
sf.fmar.fh <- survfit(surv.fmar ~ biofam\$sex,type="fleming-harrington")
summary(sf.fmar.fh)</pre>

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Marriage Survival



| Marriage Survival |
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| Appendix |
| Zoomed tree |
| References |
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| Blossfeld, HP. and G. Rohwer (2002). <i>Techniques of Event History Modeling,</i> <i>New Approaches to Causal Analysis</i> (2nd ed.). Mahwah NJ: Lawrence Erlbaum. |
| Huang, X., S. Chen, and S. Soong (1998). Piecewise exponential survival trees with time-dependent covariates. <i>Biometrics</i> 54, 1420–1433. |
| Leblanc, M. and J. Crowley (1992). Relative risk trees for censored survival data. <i>Biometrics 48</i> , 411–425. |
| Segal, M. R. (1988). Regression trees for censored data. <i>Biometrics</i> 44, 35–47. |
| Segal, M. R. (1992). Tree-structured methods for longitudinal data. <i>Journal of the American Statistical Association 87</i> (418), 407–418. |
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