

Multistage modelling of a cardiovascular trial using saddlepoint approximation^{*}

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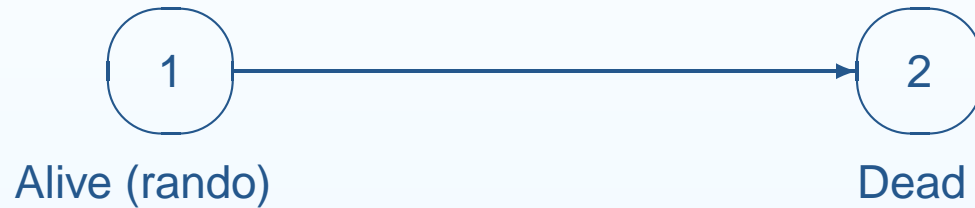
November 2009

Background :

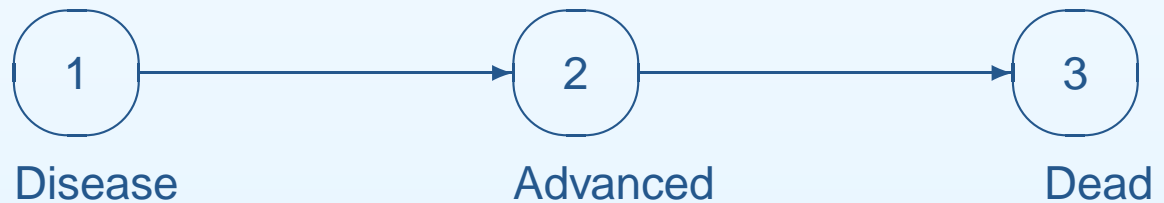
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- **Two-stage illness-death model**



- **Progressive illness disease model**



- Events : progression and death
- Outcomes : time to event T_{12} , T_{23} or $T = T_{12} + T_{23}$
- Std. methods : KM plots, Cox PH...
- Analyse each outcome separately

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- **Diabetic retinopathy flowgraph (with feedback)**
Yau and Huzurbazar, SIM (2003)
 - Type I diabetes for 5+ years
 - longitudinal observational study, n=277
 - 368 transitions, five year follow-up
 - no treatment group
 - fit based on an inverse Gaussian model (using saddlepoint method to estimate survival)

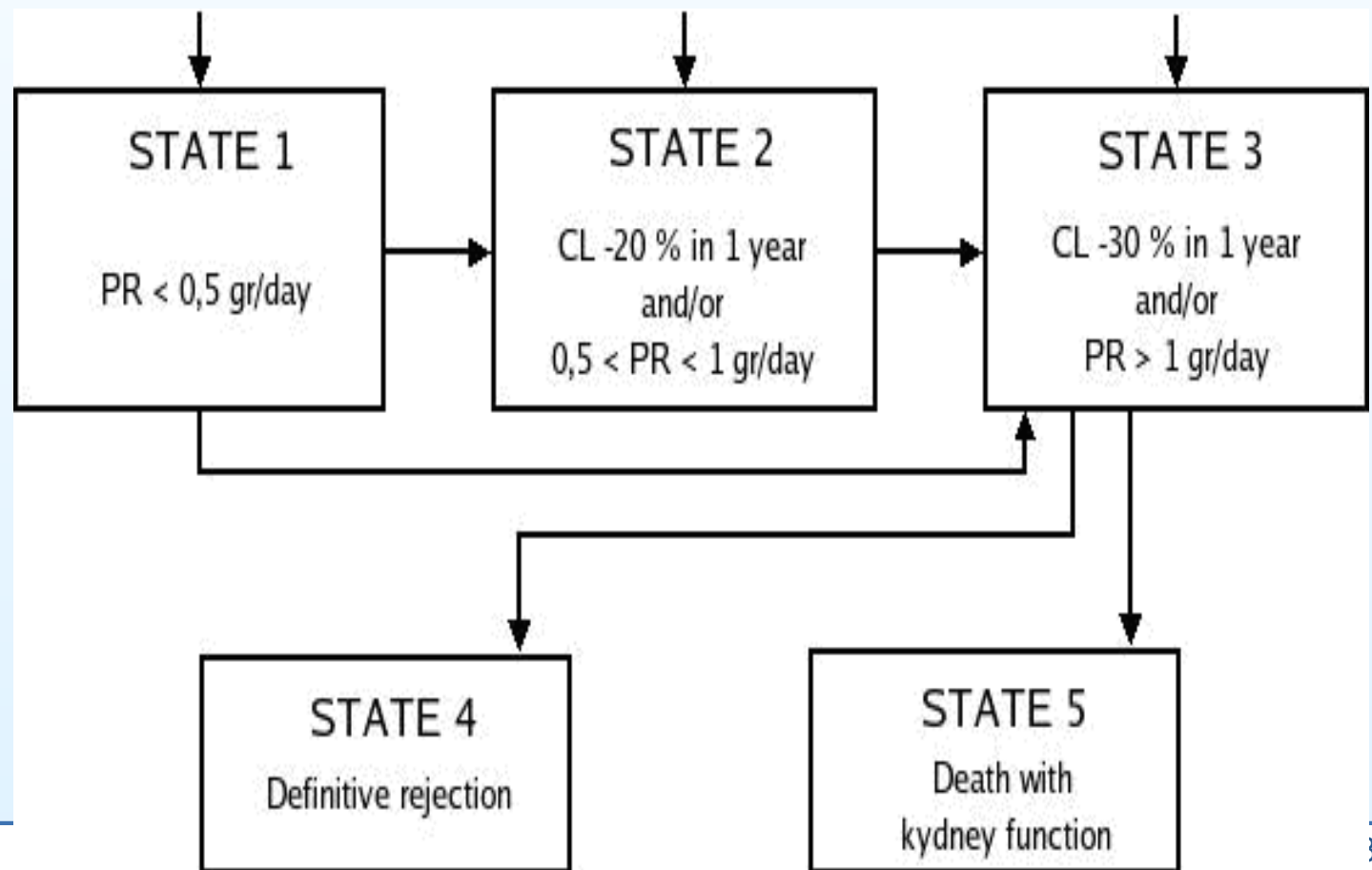
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● **Kidney transplant recipients (Competing Risks)**

see Foucher et al, SM (2007)

- 3-levels of severity, form states based on Creatinine clearance (CL) & Proteinuria (PR)
- 2-terminal states : chronic rejection of the kidney and death.



Standard approach

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RCT reality : *multiple events, possibly recurrent, competing risks* e.g. for LIPID,¹

- **Primary outcome** :
 - CHD death
- **Secondary outcomes** :
 - death from any cause
 - death from cardiovascular causes
 - death from CHD or nonfatal MI
 - MI

LIPID : RCT in patients with CHD history, NEJM (1998).

¹LIPID study group, NEJM, 339 :1349–1357, 1998

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Potential drawbacks

- Each outcome treated separately (multiplicity)
- Recurrent events omitted (time to *first* occurrence)²
- Competing risks issue (poorly dealt with / ignored?)
- Not enough events → combined endpoint

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Alternatively

see the whole process as a multistage disease.

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This requires

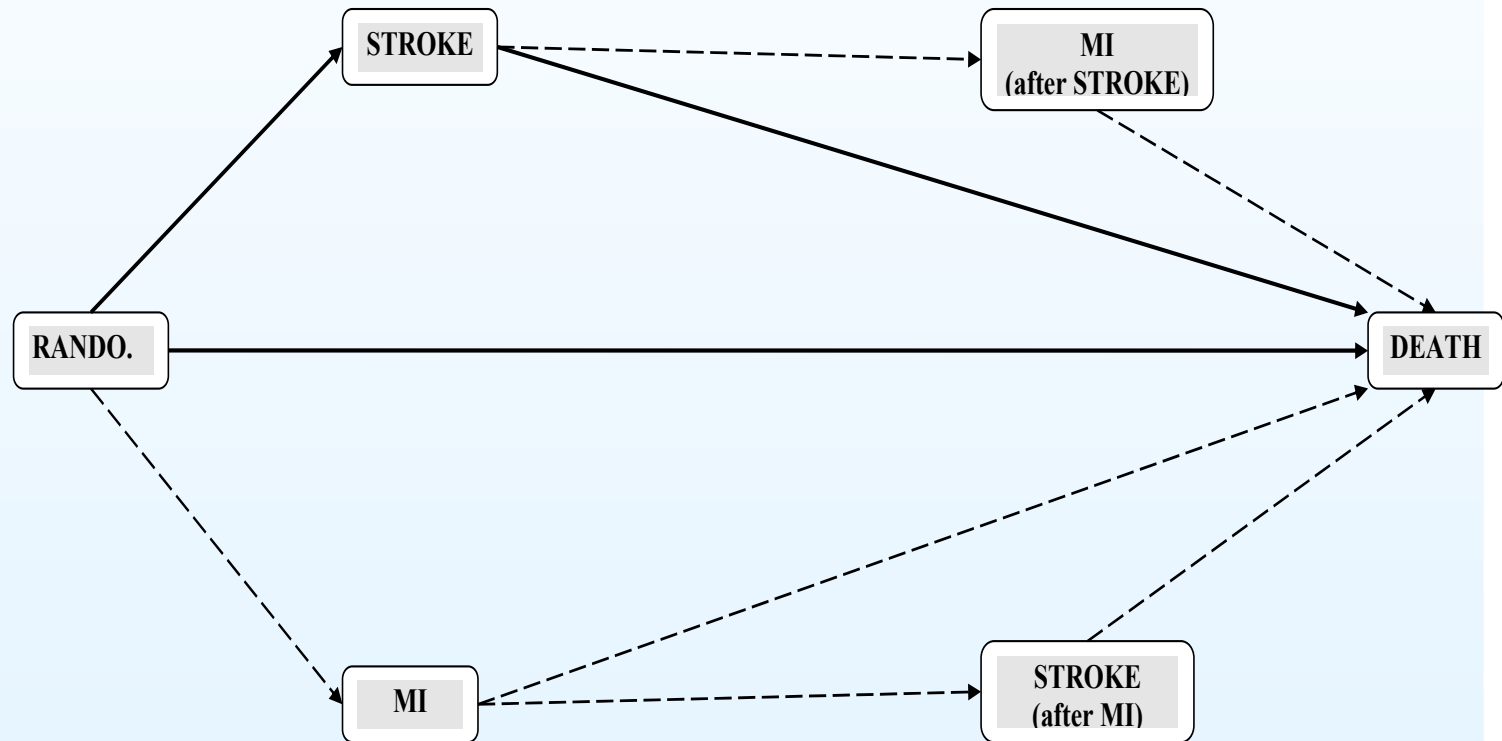
- a multistage model (here semi-Markov)
- a way to fit it / interpret the results

²It is possible to account for these (e.g. WLW analysis)

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- **e.g. LIPID model based on the flowgraph below**



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- Less restrictive assumptions than a Markov model

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- Less restrictive assumptions than a Markov model
- transition times between an initial state and a next state are independent of history prior to first state,
- with distribution that depends only on the adjoining states

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- standard approach : model specified through transition intensity (or cause-specific hazards)

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- Non-constant hazard distributions
- Characterised by a *transmittance matrix* = the product of 2 matrices (elementwise) - Butler (2001-02)

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Applications to RCT ?

Little work so far

- more on observational data (disease pathways)
- difficult to estimate relevant quantities in RCT
- presence of censoring
- mathematical complexity → Saddlepoint technique (SP)

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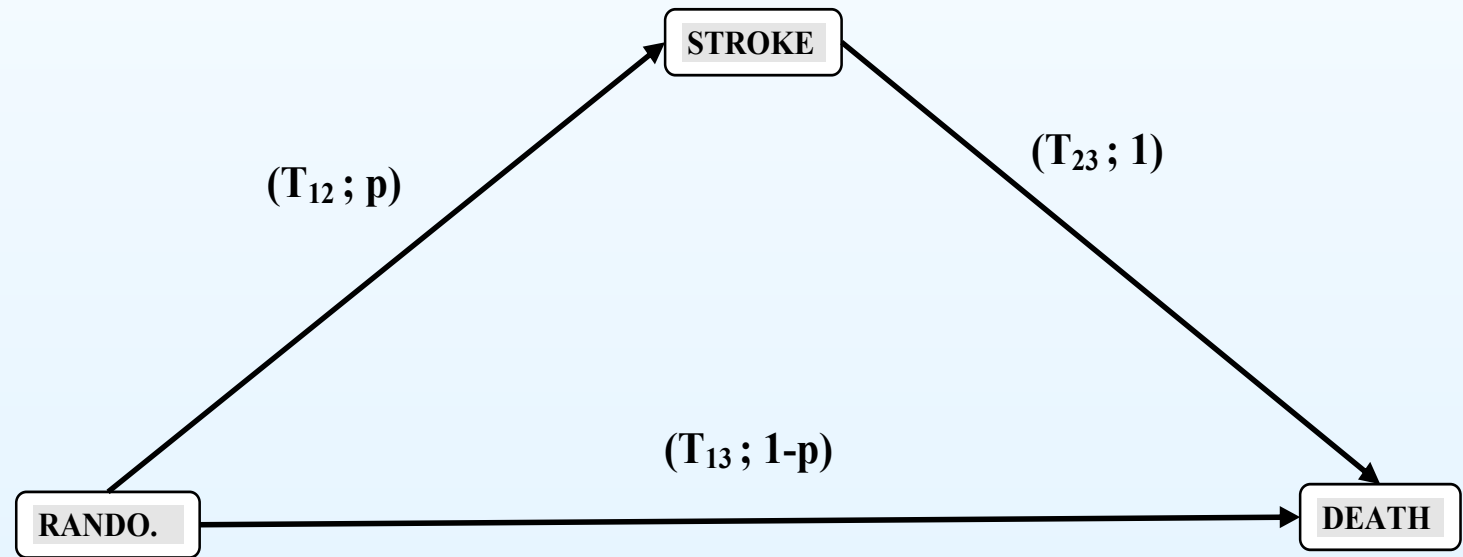
Objectives of this work

- Develop SP methods (Butler's work) for use in RCTs. In particular, account for censoring
- Apply the new methodology to the LIPID data
- Model its primary outcome while accounting for prior events
- Develop its implementation and flexibility
- Comparison with standard approach (HR, survival...)
- Explore the link with competing risks methodology

The model

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Let p_{ij} and T_{ij} for $i, j = 1, 2, 3$ be respectively the transition probability and the transition time from i to j .



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With this simple pattern, the transmittance matrix is defined by,

$$Q(s) = \begin{pmatrix} 0 & p_{12} \cdot M_{12}(s) & p_{13} \cdot M_{13}(s) \\ 0 & 0 & p_{23} \cdot M_{23}(s) \\ 0 & 0 & 0 \end{pmatrix}$$

where $M_{ij}(s) = MGF$ of the transition time from i to j .

e.g. in the case of the *exponential distribution* with mean μ ,

$$M(s) = \frac{1}{1 - \mu s}$$

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Data summary

	placebo($N = 4502$)	pravastatin ($N = 4512$)
<u>Censoring at</u>		
1	3728	3888
2	141	126
<u>Transitions</u>		
$1 \rightarrow 2$	185	151
$1 \rightarrow 3$	589	473
$2 \rightarrow 3$	44	25

Probability transition matrix for placebo group (\mathcal{P}_P) and pravastatin group (\mathcal{P}_T);

$$\mathcal{P}_P = \begin{pmatrix} 0 & 0.239 & 0.761 \\ 0 & 0 & 1 \\ 0 & 0 & 0 \end{pmatrix} \quad \mathcal{P}_T = \begin{pmatrix} 0 & 0.242 & 0.758 \\ 0 & 0 & 1 \\ 0 & 0 & 0 \end{pmatrix}$$

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Fitting a SMP

General idea :

1. estimate parameters³ within transition stages ;
2. form MGF of time through system algebraically from individual stage MGFs using the transmittance matrix ;
3. invert the MGF using saddle-point methods, providing the survival distribution (or hazard) to terminal event.

Butler's method assumes fully observed data (no censoring).
The presence of *censoring* creates an additional difficulty
⇒ we resort to parametric LL techniques to estimate the MGFs and therefore the transmittance matrix

³A nonparametric approach is difficult, but we have an approach !

MGF and saddlepoint

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Butler's work ⁴ leads to explicit MGF for T, time through the system.

$$\begin{aligned}\mathcal{M}_{1m}(s) &:= \frac{(m; 1)\text{-th cofactor } [I_m - \mathcal{Q}(s)]}{(m; m)\text{-th cofactor } [I_m - \mathcal{Q}(s)]} \\ &:= \frac{(-1)^{m+1} \Psi_{m1}(s)}{\Psi_{mm}(s)}\end{aligned}$$

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where Ψ_{ij} is the (i, j) -th minor of $I_m - \mathcal{Q}()$

e.g. 3-node model : $M_T(s) = pM_{12}(s)M_{23}(s) + (1 - p)M_{13}$

⁴proof : see Butler (2000,2001, 2006)

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Let $\mathcal{K}(s) = \ln(\mathcal{M}_{1m})$ be the *cumulant generating fct* of T

The survival function of T is approximated by the

Lugannani-Rice formula :

$$S_T(t) = 1 - \Phi(\hat{w}) - \varphi(\hat{w}) \left(\frac{1}{\hat{w}} - \frac{1}{\hat{u}} \right) \quad t \neq E(T) = \mathcal{K}'(s)$$

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where Φ and φ are respectively the pdf and the cdf of the standard normal distribution, $\hat{w} = \hat{w}(\hat{s})$ and $\hat{u} = \hat{u}(\hat{s})$ depend on \hat{s} according to

$$\hat{w} = \text{sign}(\hat{s}) \sqrt{2\{\hat{s}t - \mathcal{K}(\hat{s})\}},$$

$$\hat{u} = \hat{s} \sqrt{\mathcal{K}''(\hat{s})},$$

and the saddlepoint \hat{s} solves $\mathcal{K}'(\hat{s}) = t$ for $t > 0$.

\mathcal{K}' and \mathcal{K}'' given by a simple algebraic formulas see (Butler 2007).

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Uncensored intervals

Partial likelihood

Transitions

Censored state

see Huzurbazar (2004)

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Uncensored intervals

Partial likelihood

Transitions

$1 \rightarrow 2$

$$L_{12} = \prod_{u=1}^{N_{12}} pf_{12}(x_{u12}, \theta_{12})$$

Censored state

see Huzurbazar (2004)

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Partial likelihood

Transitions

$1 \rightarrow 2$

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$1 \rightarrow 3$

$$L_{13} = \prod_{u=1}^{N_{13}} (1 - p) f_{13}(x_{u13}, \theta_{13})$$

Censored state

see Huzurbazar (2004)

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$$2 \rightarrow 3$$

$$L_{23} = \prod_{u=1}^{N_{23}} f_{23}(x_{u23}, \theta_{23})$$

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Censored state

$$1$$

$$L_1 = \prod_{c=1}^{N_{11}} [p S_{12}(x_{c1}^*) + (1 - p) S_{13}(x_{c1}^*)]$$

see Huzurbazar (2004)

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$$L_2 = \prod_{c=1}^{N_{22}} S_{23}(x_{c2}^*) = \prod_{c=1}^{N_{22}} [1 - F_{23}(x_{c2}^*)]$$

see Huzurbazar (2004)

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$$L(\theta, p) = L_{12} \cdot L_{23} \cdot L_{13} \cdot L_1 \cdot L_2$$

see Huzurbazar (2004)

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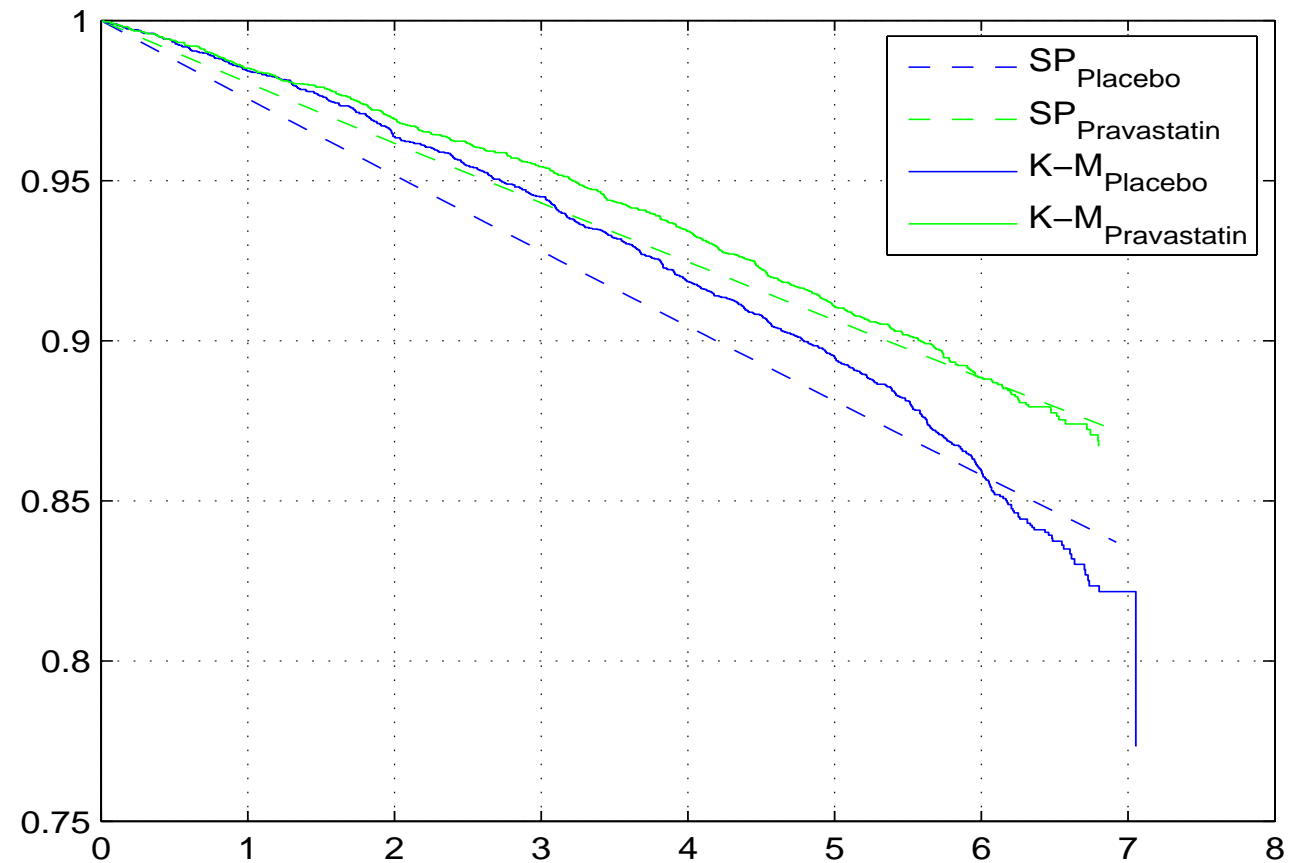
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Markov model : KM survival and SP model with exponential distributions of time in each state



LHRD

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Linear hazard rate distribution (LHRD)

popular for modelling the life-length of a system or component (reliability theory)

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hazard function

survival function

$$h(t) = \alpha$$

$$S(t) = \exp[-t \alpha]$$

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hazard function

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$$h(t) = \alpha + \frac{1}{\beta^2}t \quad S(t) = \exp \left[-t \alpha - \frac{1}{2\beta^2}t^2 \right]$$

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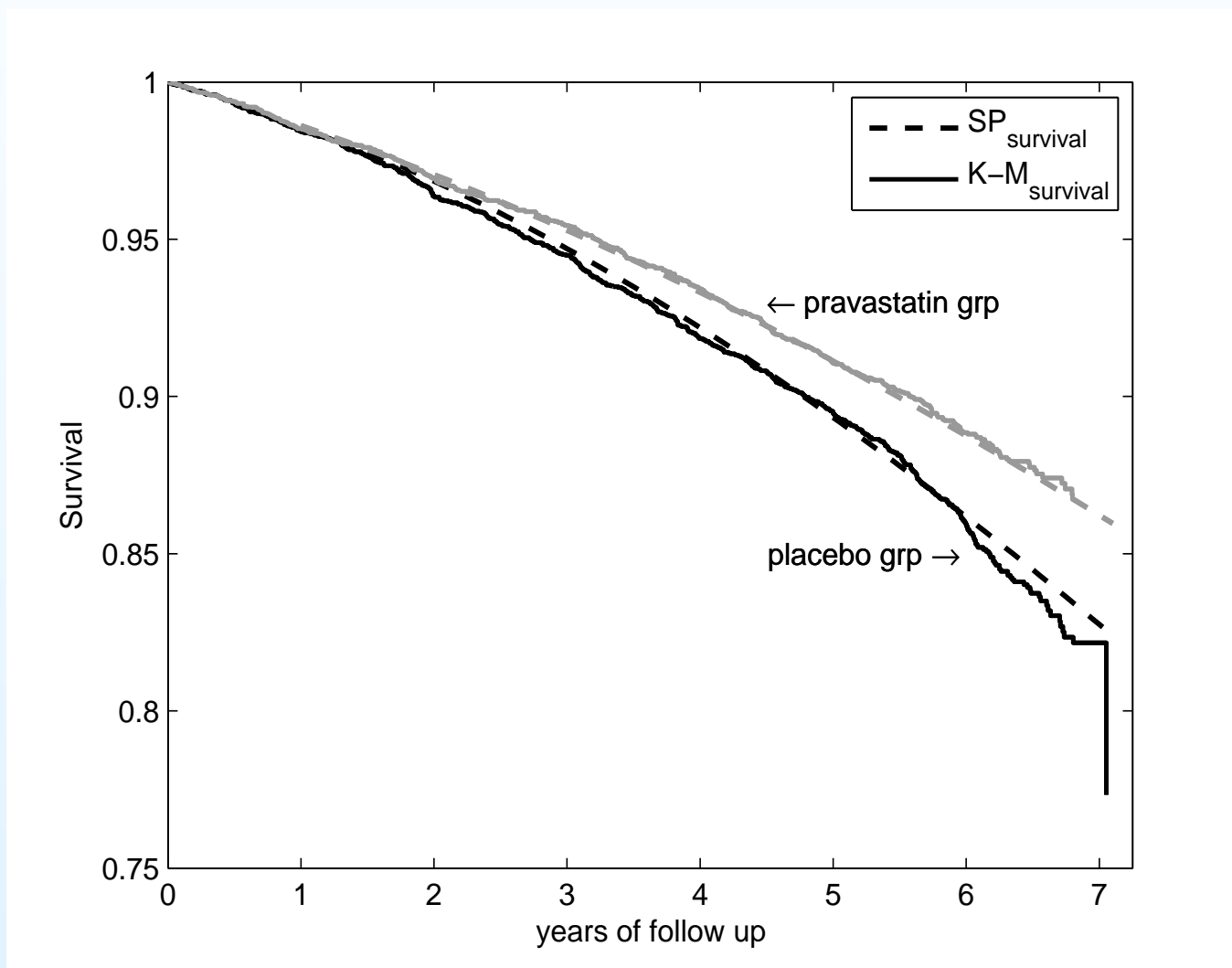
$$h(t) = \alpha + \frac{1}{\beta^2}t \quad S(t) = \exp \left[-t \left(\alpha + \frac{1}{2\beta^2}t \right) \right]$$

MGF has a close form

Results

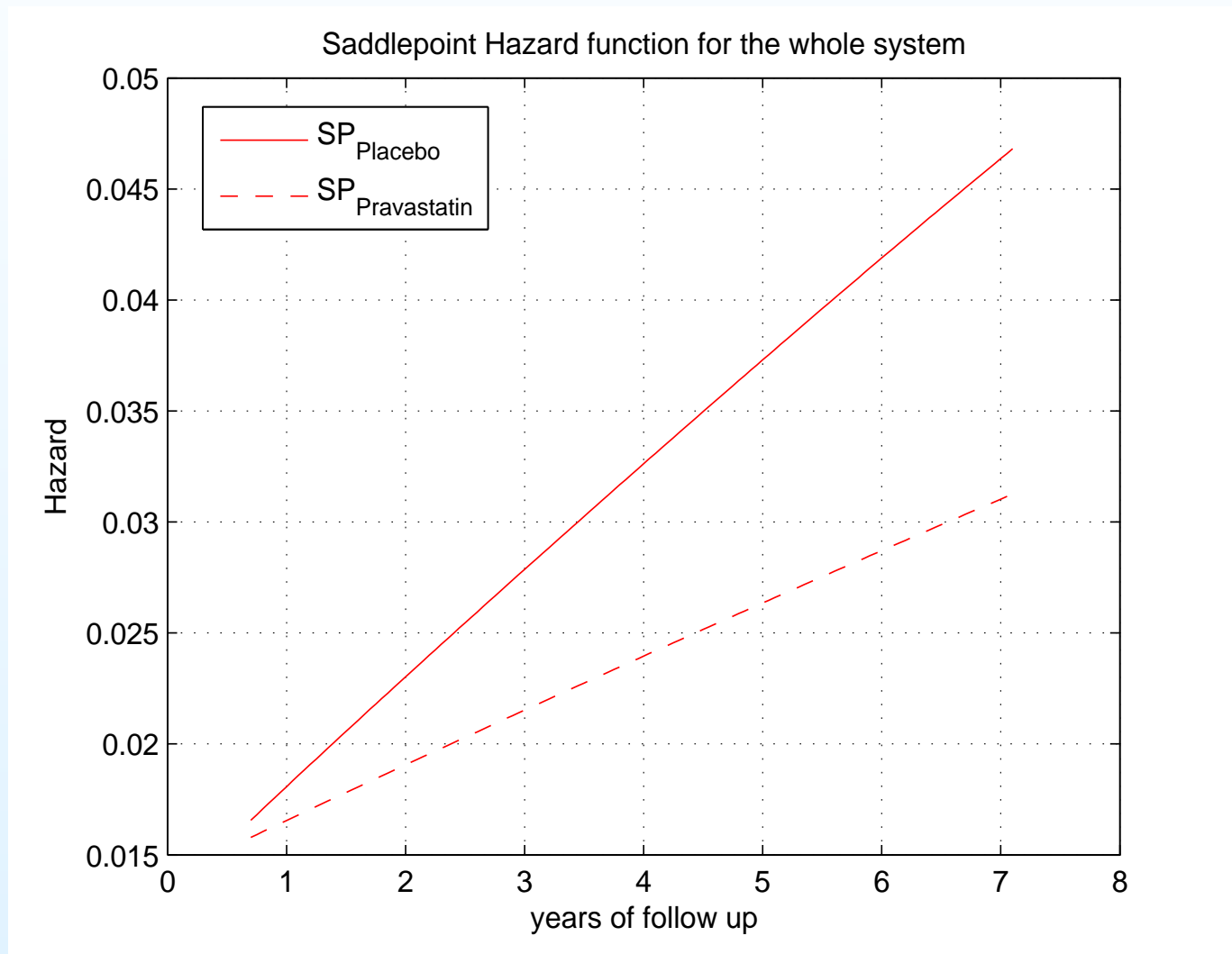
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Overall survival curve with stroke as intermediate endpoint



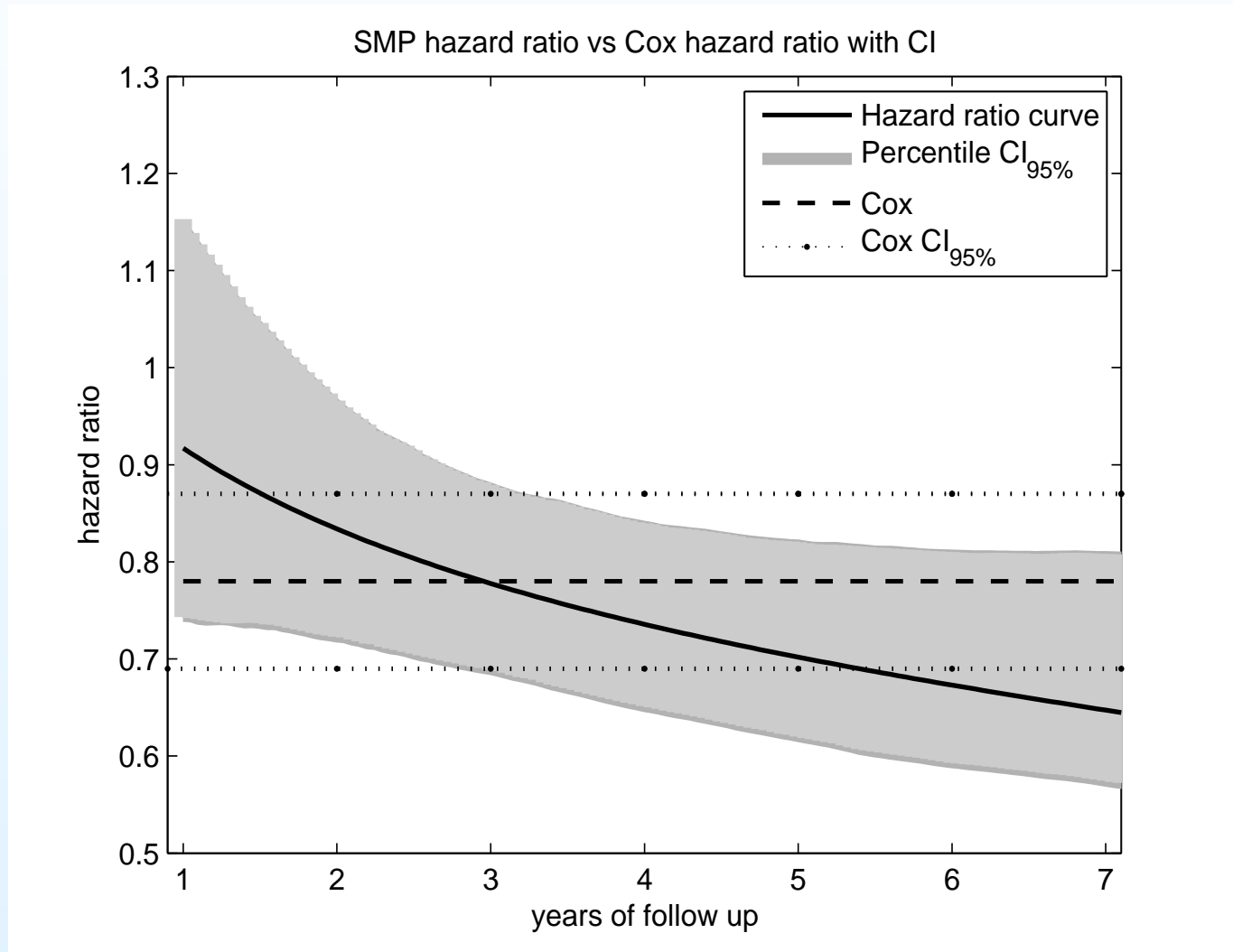
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Hazards for T (irrespective of the path)



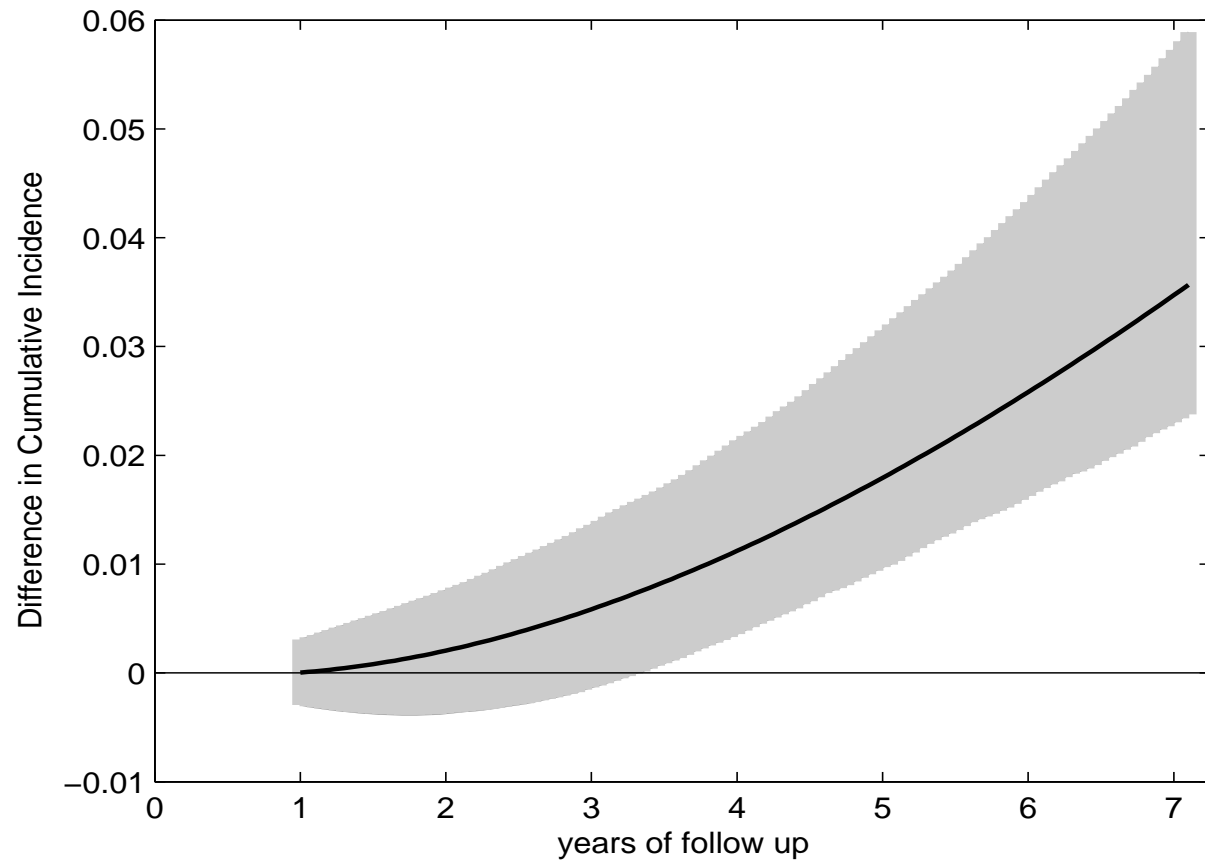
- Background:
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Overall hazard ratio function



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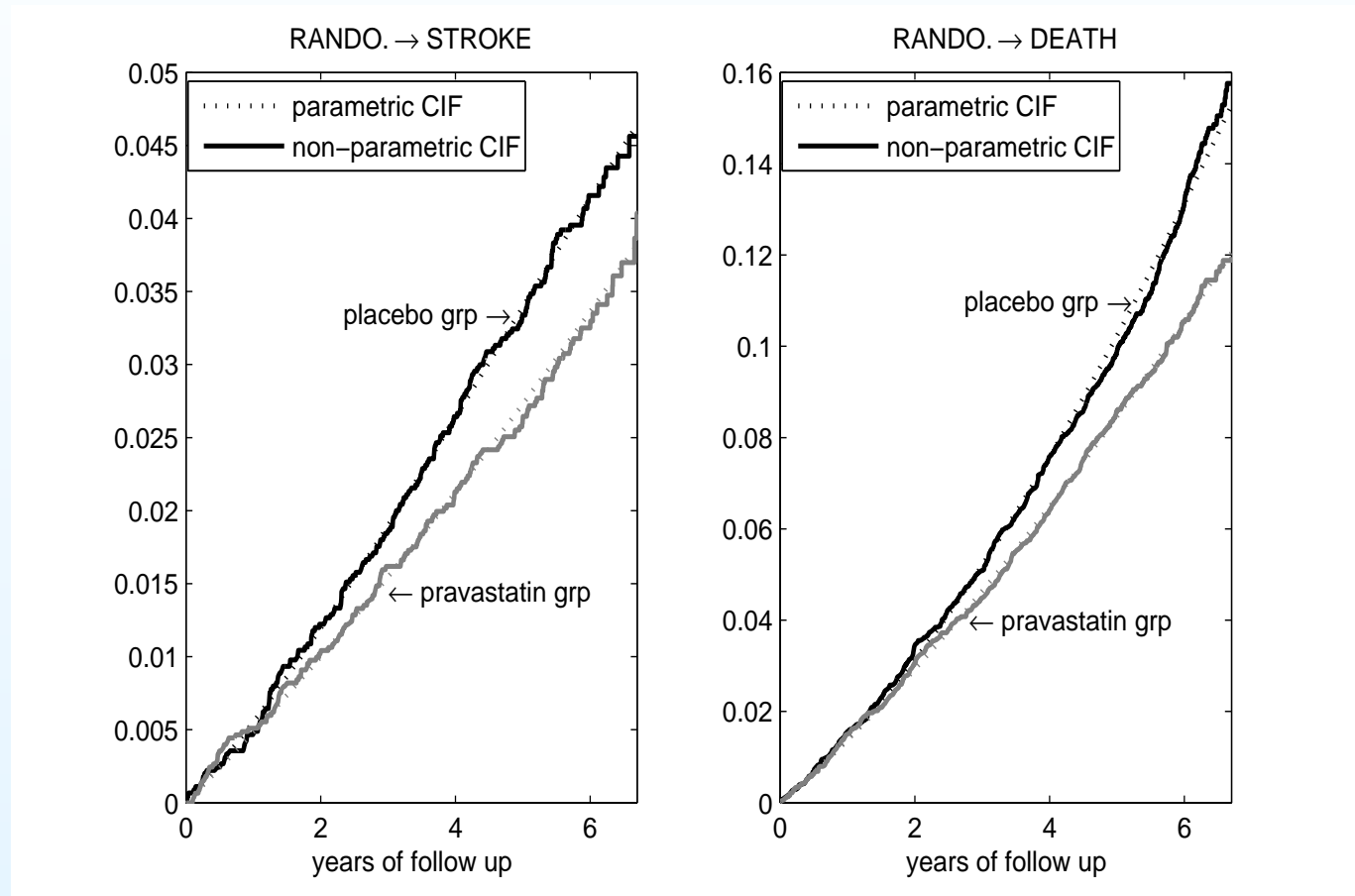
Absolute treatment benefit (Lagakos et al. NEJM 2006)



Link with CR

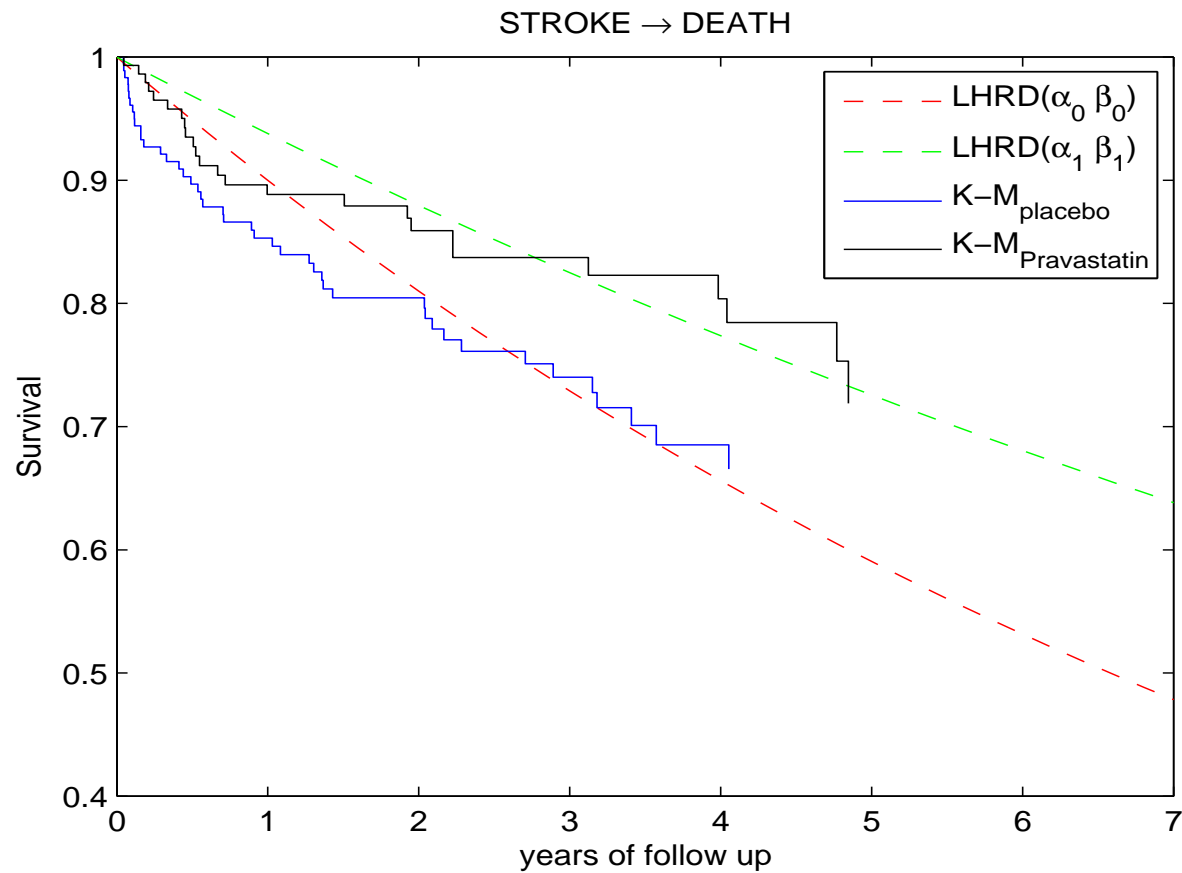
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Components $1 \rightarrow 2$ and $1 \rightarrow 3$



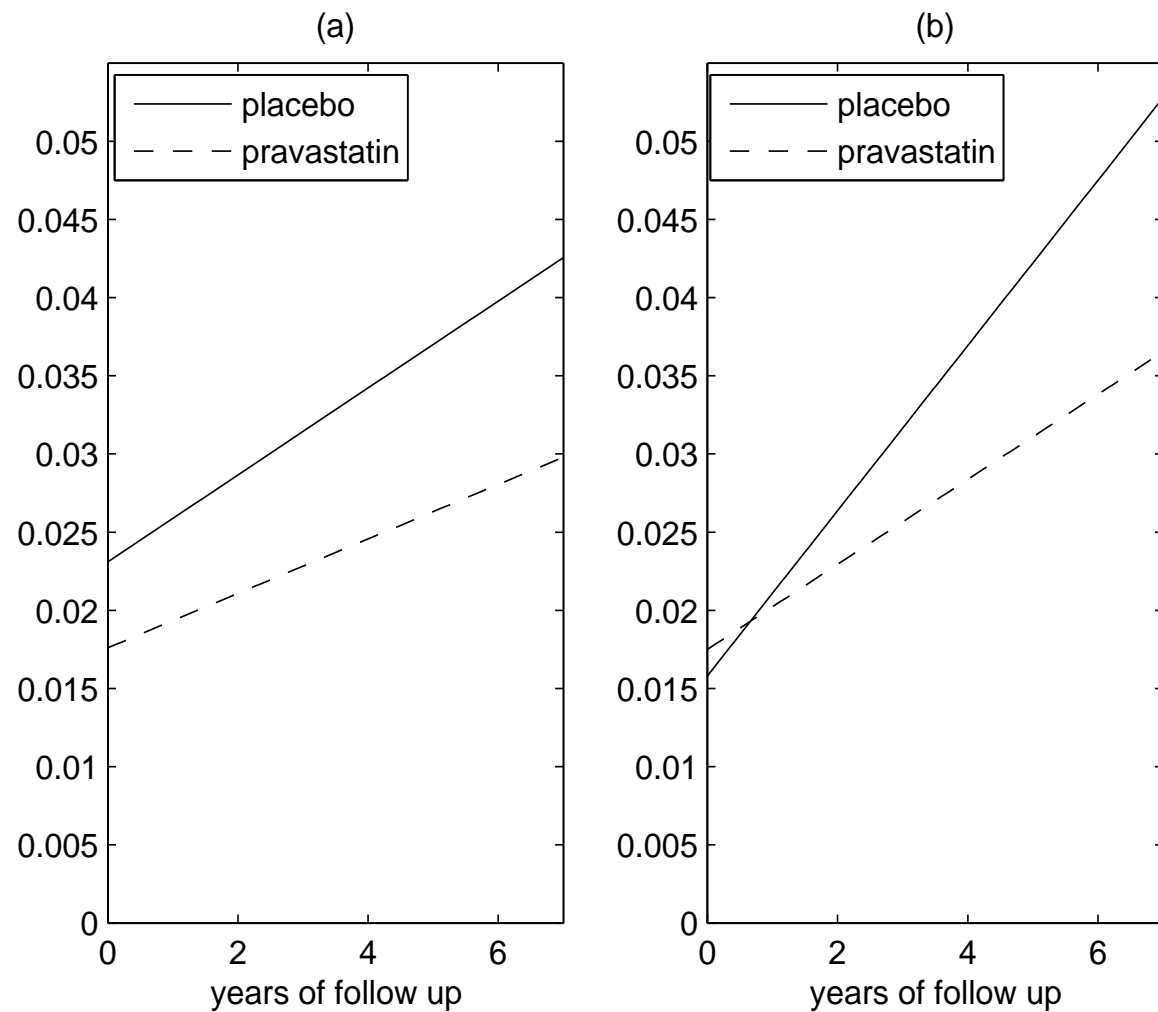
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Component 2 \rightarrow 3



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Cause-specific hazards



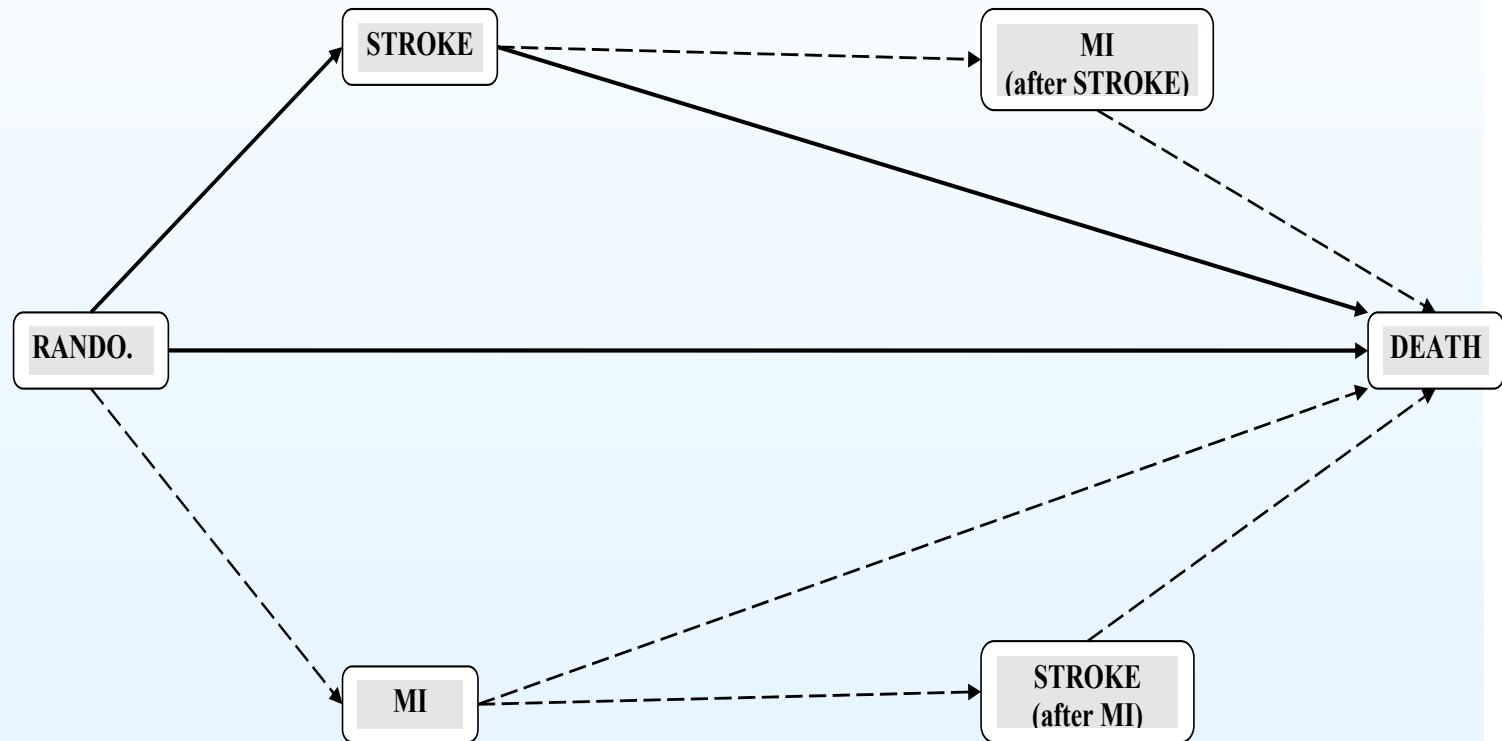
Assumptions

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- Censored observations in a known stage have the same distribution of time to the next event as individuals not censored (**Uninformative censoring**)
- Information on all states visited
- Waiting times in different stages are **independent**
- Waiting times to future events depend only on the current health state, not on the history leading to this health state. (**lack of memory of past history**)

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- **e.g. LIPID model based on the flowgraph below**



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Conclusions

- ◆ We have used SP methods in a trial context to aggregate information from a structured flowgraph model.

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- ◆ We have used SP methods in a trial context to aggregate information from a structured flowgraph model.
- ◆ By use of a SMP in LIPID data we found evidence of a **cumulating benefit of treatment** with time, not consistent with a fixed proportional hazard ratio model.

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- ◆ **Interpretation and inference is possible** with SP methodology in flowgraph data for RCTs.

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- ◆ By use of a SMP in LIPID data we found evidence of a **cumulating benefit of treatment** with time, not consistent with a fixed proportional hazard ratio model.
- ◆ Standard approaches to survival analysis **had not identified this cumulative** effect.
- ◆ **Interpretation and inference is possible** with SP methodology in flowgraph data for RCTs.
- ◆ **Potential** in many applications (*models can be developed in a blinded fashion !*)

Future work

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◆ non-parametric version

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Future work

◆ non-parametric version

◆ adjustment for covariates

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- ◆ adjustment for covariates
- ◆ other applications

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- ◆ adjustment for covariates
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- ◆ 2+ final states (competing risks)

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Open questions

- ◆ more complex models including
 - more stages ?
 - loops ?
 - competing risks ?
- ◆ Stroke - Death : time difference ?
- ◆ prediction beyond FU ?

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Future work

- ◆ application to other trials
- ◆ health economics
- ◆ theory ?
- ◆ covariates
- ◆ non-parametric estimation of the MGF (with censoring)