## Bayesian analysis of restricted mean survival time adjusted on covariates using pseudo-observations

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- Usually performed with a Cox model to provide a summary of the treatment effect
- Based on the proportional hazards (PH) assumption
- The presence of **non-PH** doubts the interpretation of a **single reported hazard ratio**
- This case of non-PH becomes more common with the development of immunotherapies<sup>1</sup> (delayed treatment effect)

<sup>&</sup>lt;sup>1</sup>Lin et al. 2020.

For  $\tilde{T}$  the time-to-event variable and  $\tau$  a pre-specified time of interest, the  $\tau$ -RMST is<sup>2</sup>:

$$\mathrm{RMST}(\tau) = E(\tilde{T} \wedge \tau) = \int_0^\tau S(t) dt$$

Royston and Parmar (2011) suggest using the difference in RMST (dRMST) between the two arms:

- As an clinically meaningful measure of the treatment effect
- The **primary measure** when non-PH is observed
- A useful secondary measure when the PH assumption appears to be satisfied

<sup>2</sup>Irwin 1949.

## Real data example: Getug 15 trial

• PH assumption was rejected (p = 0.00022, Grambsch and Therneau test)



Strata - - ADT alone - ADT plus docetaxel

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# One straightforward approach to estimate RMST is to numerically integrate the Kaplan-Meier curve between 0 and $\tau$

However, this approach does not allow for covariate adjustments, which is a **major limitation** because omitting important covariate results in **less precision**<sup>3</sup>

<sup>&</sup>lt;sup>3</sup>Karrison and Kocherginsky 2018.

One approach is to model the survival function and integrate it:

- Piecewise exponential model from Karrison (1987)
- Cox model stratified on the treatment from Zucker (1998)
- $\,\hookrightarrow\,$  Both complex to implement and limited

A more natural approach is to fit a linear model on the RMST directly:

- Using pseudo-observations from Andersen et al. (2004)
- With Inverse Probability of Censoring Weights (IPCW) from Tian et al. (2014)
- $\, \hookrightarrow \, \, \mathsf{Straightforward} \, \, \mathsf{approaches} \,$

In rare diseases or precision medicine, small sample sizes make Bayesian methods attractive<sup>4</sup>:

- Naturally suitable for including prior information (historical data borrowing)
- Provide better interpretation

With small sample sizes, it is particularly needed to adjust the analysis on the prognostic factors used for the randomization

<sup>&</sup>lt;sup>4</sup>Lesaffre et al. 2020.

Bayesian research is limited to two recent nonparametric models on the survival function:

- Zhang and Yin (2023) assign a mixture of Dirichlet processes (MDP) prior No covariates adjustment available
- Chen et al. (2023) overcome this limitation, with another dependent mixture model

Both methods require to model the survival function and are complex to implement

We extended the analysis of pseudo-observations in the Bayesian framework to provide a **straightforward RMST estimation adjusted on covariates** 

Following Andersen et al. (2004), the *i*-th pseudo-observation is computed as:

$$y_{\tau,i} = n \int_0^\tau \widehat{S}(t) dt - (n-1) \int_0^\tau \widehat{S}^{-i}(t) dt$$

where

- $\widehat{S}(t)$ : Kaplan-Meier (KM) estimator at time t of survival probability
- $\widehat{S}^{-i}(t)$ : KM estimator when eliminated *i*-th individual from the data set

Pseudo-observations can be interpreted as the contribution of one individual to the overall estimate.

• Considering the following regression model on the RMST directly:

$$\mu_i = E(\tilde{T}_i \wedge \tau | A_i, Z_i) = \alpha + \delta A_i + \beta_1 Z_{i1} + \dots + \beta_P Z_{iP}$$

where A is the treatment variable,  $Z = (Z_1, \ldots, Z_P)^T$  other variables and  $\beta = (\alpha, \delta, \beta_1, \ldots, \beta_P)^T$  the vector of unknown parameters

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- Assuming completely independent censoring, Overgaard et al. (2017) demonstrate the asymptotic proprieties of pseudo-observations

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$$E(y_{\tau,i}|A_i, Z_i) \approx E(\tilde{T}_i \wedge \tau | A_i, Z_i)$$

 $\implies$  Pseudo-observations are analyzed as an outcome of a generalized linear model

In the frequentist framework:

- Using the **Generalized Estimating Equations**<sup>5</sup> (GEE)
- GEE is a marginal approach that does not require specifying the full distribution
- Only (here) the first moment is specified

In the Bayesian framework:

- Using the Bayesian Generalized Method of Moments<sup>6</sup> (GMM)
- Bayesian GMM can be seen as the Bayesian counterpart of GEE
- Only the mean is specified through the use of a **pseudo-likelihood**

<sup>5</sup>Liang and Zeger 1986. <sup>6</sup>Yin 2009.

## Bayesian generalized method of moments

• A score vector is defined as

$$U_n(\beta) = \frac{1}{n} \sum_{i=1}^n u_i(\beta)$$

where 
$$u_i(\beta) = \frac{\partial \mu_i}{\partial \beta}(y_{\tau,i} - \mu_i)$$

• And a quadratic inference function<sup>7</sup> is defined using the score vector

$$Q_n(\beta) = U_n^{\mathsf{T}}(\beta) \Sigma_n^{-1}(\beta) U_n(\beta)$$

with  $\sum_n(\beta) = \frac{1}{n^2} \sum_{i=1}^n u_i(\beta) u_i^T(\beta) - \frac{1}{n} U_n(\beta) U_n^T(\beta)$  a  $(P+2) \times (P+2)$  matrix

<sup>7</sup>Qu et al. 2000.

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## Bayesian generalized method of moments

- By the Central Limit Theorem
  - $U_n(\beta) \xrightarrow[n \to +\infty]{d} N(0, \Sigma(\beta))$ , where  $\Sigma(\beta) = \lim_{n \to +\infty} (\Sigma_n(\beta))$

• 
$$Q_n(\beta) \xrightarrow[n \to +\infty]{d} \chi^2_{P+2}$$

- A chi-squared test can be defined<sup>8</sup>, analog to the usual likelihood ratio test, where  $Q_n(\beta)$  behaves like  $-2 \log L(y|\beta)$
- GMM approximates the likelihood for selected moments of the data without specifying the full likelihood<sup>9</sup>

<sup>8</sup>Hansen 1982.
<sup>9</sup>Chernozhukov and Hong 2003.

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## Bayesian generalized method of moments

• The pseudo-likelihood  $\tilde{L}(\beta|y_{\tau})$  is defined as

$$\begin{split} \widetilde{\mathcal{L}}(eta|y_{ au}) \propto \exp\{-rac{1}{2}Q_n(eta)\} \ \propto \exp\{-rac{1}{2}U_n^{ au}(eta)\Sigma_n^{-1}(eta)U_n(eta)\} \end{split}$$

• The posterior probability is estimated as

 $p(eta|y_{ au}) \propto \tilde{L}(eta|y_{ au})p(eta)$ 

- Two-arm randomized clinical trials (experimental vs control)
- Event times  $\sim$  Weibull distribution
- Independently,
  - Censoring times  $\sim$  Uniform distribution
  - Administrative censoring at 8 years
  - $\hookrightarrow \approx 30\%$  of censoring for all scenarios
- Sample sizes: 50, 100, 200, 500

•  $\tau = 5$  years

## Simulation study

**5** scenarios: PH (scenario 1), non-PH: early effect (scenarios 2 and 4), delayed effect (scenarios 3 and 5), with uniform covariate (scenario 4), or normal and Bernoulli covariates (scenario 5)



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## Performance metrics:

Bias, average standard error (ASE), root mean square error (RMSE), and 95% coverage rate estimated for 1000 replicates

## Benchmark methods:

- KM estimator
- Stratified Cox model from Zucker (1998)
- GEE model on pseudo-observations from Andersen et al. (2004)
- IPCW model from Tian et al. (2014)
- Bayesian nonparametric model from Zhang and Yin (2023)

## Bayesian GMM:

NUTS algorithm in Stan

• chains = 3, burn-in = 1000, iteration = 2000, priors:  $\beta \sim N(\mu = 0, \sigma^2 = 10)$ 

## Results without covariates adjustment: scenarios 1-3 (n = 200)



The Bayesian GMM gave valid estimations of the dRMST, with similar performances compared to the other approaches

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## Model misspecification: omitting prognostic variables (scenario 4: early effect)

n	Methods	Adjustment variable	Bias	$ASE^1$	RMSE <sup>2</sup>	95% coverage rate	
200	Frequentist						
	KM estimator	-	-0.0056	0.257	0.266	93.8	
	Zucker (1998)	-	-0.0104	0.258	0.264	93.8	
	Zucker (1998)	$Z_1$	-0.0133	0.239	0.243	93.9	
	Andersen et al. (2004)	-	-0.0056	0.258	0.266	93.8	
	Andersen et al. (2004)	$Z_1$	-0.0088	0.246	0.251	93.9	
	Bayesian						
	Zhang and Yin (2023)	-	-0.0058	0.256	0.266	93.8	
	GMM	-	-0.0070	0.259	0.263	94.5	
	GMM	<i>Z</i> <sub>1</sub>	-0.0033	0.250	0.249	94.6	

<sup>1</sup> ASE = Average Standard Error, <sup>2</sup> RMSE = Root Mean Square Error Prognostic variable  $Z_1 \sim U([0, 2])$ 

## Other settings:

- Omitting prognostic variables also results in less precision with a delayed treatment effect (scenario 5)
- Similar results were observed for other sample sizes (n = 50, 100, 500)

## Model misspecification: adding unrelated variables (scenario 4: early effect)

n	Methods	Adjustment variable	Bias	$ASE^1$	$RMSE^2$	95% coverage rate	
200	Frequentist						
	Zucker (1998)	-	-0.0104	0.258	0.264	93.8	
	Zucker (1998)	$Z_1$	-0.0133	0.239	0.243	93.9	
	Zucker (1998)	$Z_1, X_1$	-0.0128	0.239	0.245	93.9	
	Zucker (1998)	$Z_1$ , $X_1$ , $X_2$ , $X_3$	-0.0117	0.239	0.248	93.8	
	Andersen et al. (2004)	-	-0.0056	0.258	0.266	93.8	
	Andersen et al. (2004)	$Z_1$	-0.0088	0.246	0.251	93.9	
	Andersen et al. (2004)	$Z_1, X_1$	-0.0074	0.246	0.251	93.9	
	Andersen et al. (2004)	$Z_1$ , $X_1$ , $X_2$ , $X_3$	-0.0068	0.246	0.254	93.7	
	Bayesian						
	GMM	-	-0.0070	0.259	0.263	94.5	
	GMM	$Z_1$	-0.0033	0.250	0.249	94.6	
	GMM	$Z_1, X_1$	-0.0014	0.253	0.249	94.3	
	GMM	Z <sub>1</sub> , X <sub>1</sub> , X <sub>2</sub> , X <sub>3</sub>	-0.0008	0.261	0.252	95.3	

 $^{1}$  ASE = Average Standard Error,  $^{2}$  RMSE = Root Mean Square Error

Prognostic variable  $Z_1 \sim U([0, 2])$ , other variable  $X_1 \sim N(0, 1)$ ,  $X_2 \sim B(0.5)$ ,  $X_3 \sim U([0, 2])$ Bayesian analysis of restricted mean survival time adjusted on covariates using pseudo-observations

## Other settings:

- No bias nor variance inflation was observed for the frequentist approaches with a delayed treatment effect (scenario 5)
- Similar results were observed for other sample sizes for the frequentist approaches (n = 50, 100, 500)
- Higher variance for the Bayesian GMM with  $n\,=\,50$  and 1-3 unrelated covariates

**Phase 3 randomized clinical trial:** comparing an androgen-deprivation therapy alone or with docetaxel in non-castrate metastatic prostate cancer (n = 384, 25% of censoring)

Outcome of interest: Prostate-Specific Antigen (PSA) progression-free survival

## **Covariates adjustment:**

- Gleason score (< 8 vs.  $\geq$  8 )
- European Cooperative Oncology Group performance status (0 vs. 1-2)
- Concentration of alkaline phosphatase (Normal vs. Abnormal)
- Presence of bone metastases (Yes vs. No)

## Estimation of the difference of 5-RMST between the two treatment groups



Bayesian analysis of restricted mean survival time adjusted on covariates using pseudo-observations

Quantiles

$\widehat{eta}$	SD	2.5%	25%	50%	75%	97.5%	
5.63	0.55	4.53	5.27	5.63	5.99	6.73	
-0.19	0.18	-0.53	-0.30	-0.19	-0.07	0.15	
-0.55	0.18	-0.90	-0.68	-0.56	-0.44	-0.21	
-1.25	0.18	-1.60	-1.37	-1.24	-1.12	-0.89	
-0.49	0.27	-1.01	-0.68	-0.49	-0.31	0.04	
0.58	0.17	0.25	0.46	0.58	0.69	0.91	
	$\widehat{\beta}$ 5.63 -0.19 -0.55 -1.25 -0.49 0.58	$\widehat{\beta}$ SD5.630.55-0.190.18-0.550.18-1.250.18-0.490.270.580.17	$\begin{array}{ c c c c c c c c }\hline\hline & & & & & & \\ \hline \hline & & & & & \\ \hline & & & &$	$\begin{array}{ c c c c c c c c }\hline\hline & & & & & & & & & & & & & & & & & & $	$\begin{array}{ c c c c c c c c c c }\hline\hline & & & & \\\hline\hline & & & \\\hline\hline & & & \\\hline\hline & & & \\\hline\hline & & & \\\hline & & & \\ \hline \\ \hline$	$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	

## Getug 15: Estimation of the difference of 5-RMST with the Bayesian GMM



The mean of the posterior samples is 0.58 year (95% credible interval: 0.24-0.92).
 On average, receiving docetaxel in addition to ADT increases the lifetime without PSA progression during the next 5 years by 0.58 year compared to receiving ADT alone.

## Getug 15: Estimation of the difference of 5-RMST with the Bayesian GMM



We propose a **Bayesian** approach for analyzing RMST adjusted on covariates:

- Combining the flexibility of pseudo-observations:
  - To fit a straightforward linear model, without specifying any model on the survival function
  - To estimate not only the treatment effect but also the covariate effects
- With the Bayesian GMM:
  - To allow for including prior information in the analysis
  - To benefit from the advantages of the Bayesian interpretation

## **Perspectives:**

• Extend this approach to the joint analysis of RMST at multiple time points

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