

Methods for adjusting survival estimates in the presence of treatment crossover – a simulation study

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Please note: results subject to minor changes – re-running due to minor errors in data generating model

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Extensions

- Allow the treatment effect to change over time, based upon a timedependent covariate
 - Generate a time-dependent covariate that represents the continuous progression of the disease – as this increases, the relative treatment effect falls
 - → This involves relaxing the equal treatment effect assumption
- Allow the treatment crossover decision to be based upon timedependent covariates, rather than baseline characteristics
- Include 'observational-based' methods
 - IPCW
 - SNM with g-estimation



Data Generation (1)

- Used a two-stage Weibull model to generate underlying survival times and a time-dependent covariate (called 'CEA')
- Longitudinal model for CEA (for *i*th patient at time *t*):

 $cea_i(t) = \beta_{0i} + \beta_1 * log(t) + \beta_2 * log(t) * trt_i + \beta_4 badprog_i$

where $\beta_{0i} \sim N(\beta_0, \sigma_0^2)$

 β_{0i} is the random intercept

- β_1 is the slope for a patient in the control arm
- $\beta_1 + \beta_2$ is the slope for a patient in the treatment arm (all
- β₄ is the change in the intercept for a patient with bad prognosis compared to a patient without bad prognosis
- Picked parameter values such that CEA increased over time, more slowly in the experimental group, and was higher in the badprog group



Data Generation (2)

- The survival hazard function was based upon a Weibull (see Bender et al 2005):
 - $h(t) = \lambda \gamma t^{\gamma-1} \exp(X\beta)$
- In our case,

 $X\beta = \delta_1 * trt_i + \delta_2 * badprog_i + \alpha * (cea(t))$

where δ_1 is the log hazard ratio (the treatment effect)

- δ_2 is the impact of a bad prognosis baseline covariate on survival
- α is the coefficient of CEA, indicating its effect on survival
- We used this to generate our survival times
- → So, CEA has an effect on survival



Data Generation (3)

• We then estimated the treatment effect over time (in terms of an acceleration factor) based upon Collett's HR to AF formula:

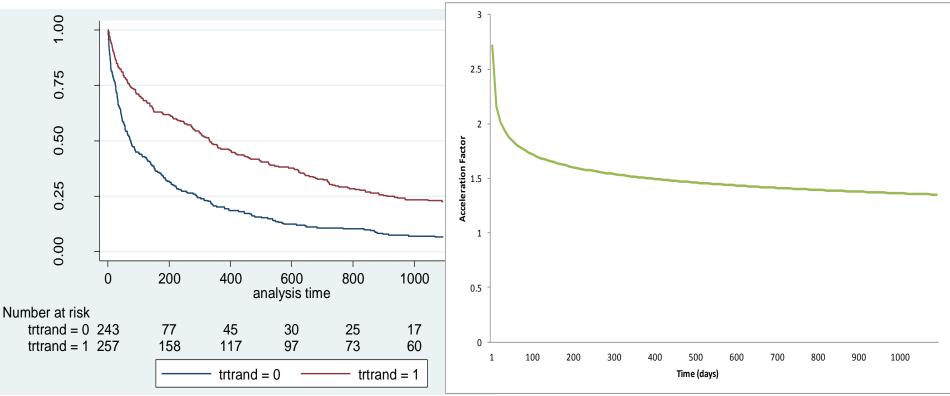
$$AF = \exp\left(\frac{-(\delta_1 + \alpha\beta_2 * \log(t))}{\gamma}\right)$$

- We used this to 'inflate' survival times of crossover patients, based upon the time-point at which they started receiving the experimental treatment
- NOTE: This equation is wrong
- Collett's formula is only applicable when there are proportional hazards, and we do not have proportional hazards due to our time-dependent covariate
- → Working on this
- Note unlikely to change our results as we are still doing what we intended applying a lower treatment effect to crossover patients



Data Generation (4)

• We then selected parameter values in order that 'realistic' datasets were created:



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Data Generation (5)

We made several assumptions about the 'crossover mechanism':

- 1. Crossover could only occur after disease progression (disease progression was approximately half of OS, calculated for each patient using a beta(5,5) distribution)
- 2. Crossover could only occur at 3 'consultations' following disease progression
 - These were set at 21 day intervals
 - Probability of crossover highest at initial consultation, then falls in second and third
- 3. Crossover probability depended on time-dependent covariates:
 - CEA value at progression (high value reduced chance of crossover)
 - Time to disease progression (high value increased chance of crossover)
 - This was altered in scenarios to test a simpler mechanism where probability only depended on CEA
- → Given all this, CEA was a time-dependent confounder



Scenarios

Variable	Value	Alternative
Sample size	500	×
Number of prognosis groups (prog)	2	×
Probability of good prognosis	0.5	×
Probability of poor prognosis	0.5	×
Maximum follow-up time	3 years (1095 days)	×
Multiplication of OS survival time due	Log hazard ratio = 0.5	×
to bad prognosis group		
Survival time distribution	Alter parameters to test two levels of disease	\checkmark
	severity	
Initially assumed treatment effect	Alter to test two levels of treatment effect	\checkmark
Time-dependence of treatment effect	Treatment effect received depends upon CEA at	\checkmark
	time of crossover. However set α to zero in some	
	scenarios. Also include additional treatment effect	
	decrement in crossover patients in some scenarios	
	to approximate a continued reduction in treatment	
	effect over time in these patients	
Probability of switching treatment	Test two levels of treatment crossover proportions	\checkmark
over time		
Prognosis of crossover patients	Test three crossover mechanisms in which different	\checkmark
	groups become more likely to cross over	





Variable	Value	Alternative
Sample size	500	×
Number of prognosis groups (prog)	2	×
Probability of good prognosis	0.5	×
Probability of poor prognosis	0.5	×
Maximum follow-up time	3 years (1095 days)	×
Multiplication of OS survival time due	Log hazard ratio = 0.5	×
to bad prognosis group		
Survival time distribution	Alter parameters to test two levels of disease severity	✓ (2)
Initially assumed treatment effect	Alter to test two levels of treatment effect	✓
Time-dependence of treatment effect	Treatment effect received depends upon CEA at time of crossover. However set α to zero in some scenarios. Also include additional treatment effect decrement in crossover patients in some scenarios to approximate a continued reduction in treatment effect over time in these patients	✓
Probability of switching treatment over time	Test two levels of treatment crossover proportions	V
Prognosis of crossover patients	Test three crossover mechanisms in which different groups become more likely to cross over	V





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Survival time distribution	Alter parameters to test two levels of disease	✓ (2)
	severity	
Initially assumed treatment effect	Alter to test two levels of treatment effect	✓ (4)
Time-dependence of treatment effect	Treatment effect received depends upon CEA at	\checkmark
	time of crossover. However set α to zero in some	
	scenarios. Also include additional treatment effect	
	decrement in crossover patients in some scenarios	
	to approximate a continued reduction in treatment	
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Probability of switching treatment	Test two levels of treatment crossover proportions	\checkmark
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Variable	Value	Alternative
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Maximum follow-up time	3 years (1095 days)	×
Multiplication of OS survival time due to bad prognosis group	Log hazard ratio = 0.5	×
Survival time distribution	Alter parameters to test two levels of disease severity	✓ (2)
Initially assumed treatment effect	Alter to test two levels of treatment effect	√ (4)
Time-dependence of treatment effect	Treatment effect received depends upon CEA at time of crossover. However set α to zero in some scenarios. Also include additional treatment effect decrement in crossover patients in some scenarios to approximate a continued reduction in treatment effect over time in these patients	✓ (8)(12)
Probability of switching treatment over time	Test two levels of treatment crossover proportions	 ✓
Prognosis of crossover patients	Test three crossover mechanisms in which different groups become more likely to cross over	V





Variable	Value	Alte	ernative
Sample size	500	×	
Number of prognosis groups (prog)	2	×	
Probability of good prognosis	0.5	×	
Probability of poor prognosis	0.5	×	
Maximum follow-up time	3 years (1095 days)	×	
Multiplication of OS survival time due to bad prognosis group	Log hazard ratio = 0.5	×	
Survival time distribution	Alter parameters to test two levels of disease severity	~	(2)
Initially assumed treatment effect	Alter to test two levels of treatment effect	 ✓ 	(4)
Time-dependence of treatment effect	Treatment effect received depends upon CEA at time of crossover. However set α to zero in some scenarios. Also include additional treatment effect decrement in crossover patients in some scenarios	√	(8) (12)
	to approximate a continued reduction in treatment effect over time in these patients		
Probability of switching treatment over time	Test two levels of treatment crossover proportions	✓	(24)
Prognosis of crossover patients	Test three crossover mechanisms in which different groups become more likely to cross over	✓	





Variable	Value	Alternativ	е
Sample size	500	×	
Number of prognosis groups (prog)	2	×	
Probability of good prognosis	0.5	×	
Probability of poor prognosis	0.5	×	
Maximum follow-up time	3 years (1095 days)	×	
Multiplication of OS survival time due to bad prognosis group	Log hazard ratio = 0.5	×	
Survival time distribution	Alter parameters to test two levels of disease severity	✓ (2)	
Initially assumed treatment effect	Alter to test two levels of treatment effect	√ (4)	
Time-dependence of treatment effect	Treatment effect received depends upon CEA at time of crossover. However set α to zero in some	✓ (8)	
	scenarios. Also include additional treatment effect decrement in crossover patients in some scenarios to approximate a continued reduction in treatment effect over time in these patients	(12)	
Probability of switching treatment over time	Test two levels of treatment crossover proportions	✓ (24)	
Prognosis of crossover patients	Test three crossover mechanisms in which different groups become more likely to cross over	✓ (72)	

This combined to 72 scenarios

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Variable	Value	Alternative
Sample size	500	×
Number of prognosis groups (prog)	2	×
Probability of good prognosis	0.5	×
Probability of poor prognosis	0.5	×
Maximum follow-up time	3 years (1095 days)	×
Multiplication of OS survival time due	Log hazard ratio = 0.5	×
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Survival time distribution	Alter parameters to test two levels of disease	\checkmark
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over time		
Prognosis of crossover patients	Test three crossover mechanisms in which different	\checkmark
	groups become more likely to cross over	



Performance measures

Similar to James' study...

- We used bias as our primary performance measure
- Also assessed coverage

However, because our treatment effect is time-dependent there is not a 'true' HR or AF

- Therefore we used restricted mean survival as our true measure. We estimated the truth from our survivor function equations
- This is highly relevant for the context of economic evaluation
- But means that we had to estimate restricted mean survival for each crossover method – not just the adjusted HR or AF



Estimating survival

Three broad approaches assessed (all estimated out to 3 years):

1. 'Survivor function' approach

Apply treatment effect to survivor function (or hazard function) estimated for experimental group \rightarrow calculate AUC

2. 'Extrapolation' approach

Extrapolate counterfactual dataset to required time-point (only relevant for RPSFTM/IPE approaches) \rightarrow calculate AUC

3. 'Shrinkage' approach

Use estimated acceleration factor to 'shrink' survival times in crossover patients in order to obtain an adjusted dataset \rightarrow calculate AUC (only relevent for AF-based approaches)



Methods

Naive methods

- ITT
- Exclude crossover patients (PPexc)
- Censor crossover patients (PPcens)
- Treatment group as a time-dependent covariate (TDCM)
- Treatment crossover as a time-dependent indicator (XOTDCM)



Methods

Complex methods

- RPSFTM with log-rank test (with and without covariates)
- IPE algorithm (Weibull and exponential versions, with and without covariates)
- IPCW
- SNM with g-estimation
- Two-stage Weibull method (Weib 2m)

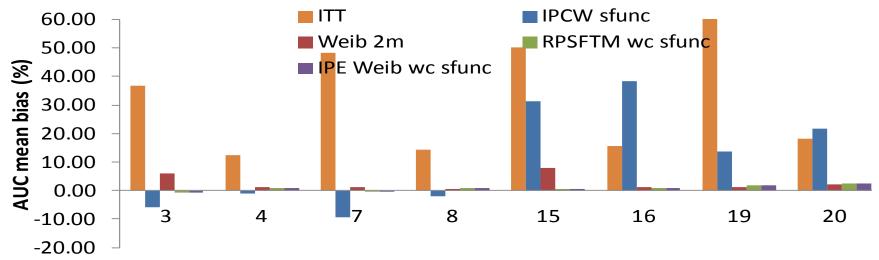
Note, we did not include:

- Walker et al's method due to poor performance in James' study
- Loey and Goetghebeur's method as only for all-or-nothing compliance
- Law and Kaldor's method as fundamentally flawed
- And only included log-rank test version of RPSFTM 27/02/2012 © The University of Sheffield



Results (1)

 Randomisation-based methods worked very well when the treatment effect was not time-dependent, eg:

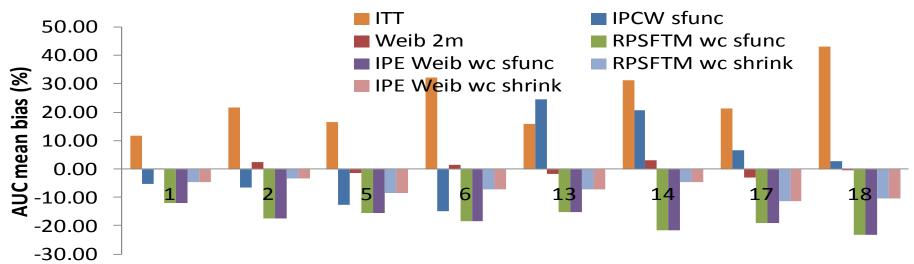


- IPCW method performed poorly when crossover proportion was very high
- SNM method performed poorly
- Naive methods performed poorly
- Two-stage Weibull produced low bias



Results (2)

 Randomisation-based methods produced large bias when the treatment effect was time-dependent, eg:

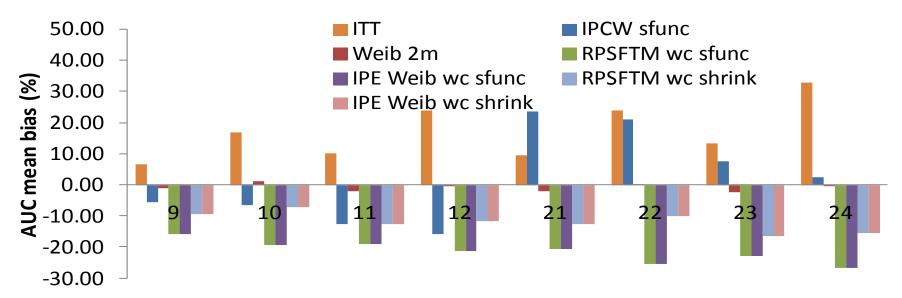


- RPSFTM/IPE 'shrinkage' approach performed better, but this is flawed
- IPCW method performed better than randomisation-based approaches providing crossover proportion was less than 90%, but still gave considerable bias



Results (3)

 When there was an additional treatment effect decrement in crossover patients, indicating a particularly strong time-dependent treatment effect, the randomisation-based methods performed even less well:



 IPCW is unaffected by this, and becomes more likely to produce least bias (excluding two-stage Weibull approach)



Conclusions

- RPSFTM / IPE survivor function methods produce very low levels of bias when the treatment effect is not time-dependent
- When the treatment effect (in terms of an AF) is 20-30% lower in crossover patients RPSFTM / IPE survivor function approaches produce high levels of bias (>10%)
 - 'Shrinkage' approaches perform with lower bias but these methods are flawed
- When the treatment effect decrement is >30% IPCW produces less bias than any RPSFTM / IPE variant, providing <90% of at-risk patients crossover
 - But significant bias remains
- Where applicable, two-stage methods are worthy of consideration
- 'Survivor function' approaches generally produce lower bias than 'extrapolation' approaches, due to the loss of information associated with recensoring and the effect of this on the extrapolation