Accurate Sample Size Calculations in Trials with Non-Proportional Hazards

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Introduction

- Non-proportional hazards (NPH) are common in time-to-event (TTE) trials
 - E.g. heterogeneous populations, 'cures', immuno-oncology
- Cox and Log-Rank Test very common analysis even under NPH
 - HR meaningful if viewed as a weighted average over time
 - Both methods powerful under NPH (and often required by FDA/EMA...)
- RMST and landmark analyses are being increasingly investigated as alternatives
 - Other methods are available... (e.g. weighted log-rank test, average HR)
- However there are issues with sample size calculations:
 - Those for Cox/Log-Rank Test assume PH
 - Those for RMST/Landmark methods struggle with censoring
 - Simulations typically recommended....
- Here, accurate analytical methods for NPH planning are presented

Log Rank Test

- Log Rank Test is the Score Test for a basic Cox Model
 - Sample size planning for one works for the other
- Power is typically calculated using the Schoenfeld Formula*:

$$Events = \frac{(Z_{1-\alpha} + Z_{1-\beta})^2}{P_1 P_2 \log(\theta)^2}$$

- However, under NPH, we do not know θ (the HR).
 - Formula also derived under PH: Can it still be used?
- Hard to derive θ directly due to 'dynamic' event-driven weighting scheme
- Instead we use an indirect LRT-based method...

Pike and Peto

• Log-Rank Formula:

$$Z_{LRT} = \frac{O_1 - E_1}{\sqrt{V}}$$

• Two literature-reported methods* use LRT-derived quantities to estimate θ :

$$\ln(\hat{\theta}_{peto}) = \frac{O_1 - E_1}{V}, \quad Var(\ln(\hat{\theta}_{peto})) = 1/V$$

$$\hat{\theta}_{pike} = \frac{O_1 E_2}{O_2 E_1}, \quad Var(\ln(\hat{\theta}_{pike})) = \frac{1}{E_1} + \frac{1}{E_2}$$

- Pike method reported** as more accurate, but conservative → Chosen method
 - Reasonable for $1/3 < \theta < 3$
- Expectations are calculable for all components

Expectations

$$O_j = \sum d_{ij}$$
 $E_j = \sum \frac{n_{ij}d_i}{n_i}$

- To calculate expectations, we consider the distribution functions w.r.t. time:
 - Assuming independence of events, dropout (dr) and administrative censoring (c):

$$d_{j}(t) = N_{j} \left(1 - F_{dr,j}(t)\right) \left(1 - F_{c,j}(t)\right) f_{j}(t) = N_{j} C_{j}^{-}(t) f_{j}(t)$$

$$n_{j}(t) = N_{j} \left(1 - F_{dr,j}(t)\right) \left(1 - F_{c,j}(t)\right) \left(1 - F_{j}(t)\right) = N_{j} C_{j}^{-}(t) S_{j}(t)$$

• Therefore:

$$\mathbf{E}(O_j) = \int_0^T d_j(t) dt
\mathbf{E}(E_j) = \int_0^T \frac{n_j(t)(d_1(t) + d_2(t))}{n_1(t) + n_2(t)} dt \qquad \theta_{pike} = \frac{O_1 E_2}{O_2 E_1}, \quad O = \frac{(Z_{1-\alpha} + Z_{1-\beta})^2}{P_1 P_2 \log(\theta)^2}$$

• → Everything needed to predict HR and hence power

RMST

- Royston & Parmar provided formulae for RMST sample size planning*:
 - $\mu_j = \mathbf{E}(RMST_j) = \int_0^R S_j(t) dt$
 - $\mathbf{V}(RMST_j) = 2 \int_0^R t S_j(t) dt \left\{ \int_0^R S_j(t) dt \right\}^2$
 - $SE(\hat{\mu}_j) = \sqrt{\frac{\varphi^2 V(RMST_j)}{N_j}}$
- However, φ^2 is censoring/recruitment dependent, (1 if no censoring, increasing with censoring).
 - No direct estimation method provided (Suggested to back-estimate from existing trial data).
- Note that $V(RMST_i)$ is an intrinsic property of event distribution
 - Independent censoring does not affect KM plot, only the number at risk
- We therefore need to replace N_j by an effective sample size

RMST

- On day 1, effective sample size is N_i but decreases over time due to censoring
- The overall effective sample size can be viewed as a **weighted average** of the changing **effective sample size over time**, using the **point variance function** as the weighting.
- We therefore derive:
 - Variance contribution at time x (by differentiation): $dV(x) = 2S(x)(x \int_0^x S(t) dt)$
 - Effective sample size at time x: $N_{eff}(x) = \frac{N \int_0^x c^{-}(t)f(t)dt}{F(x)}$
- Then:

$$N_{eff} = \frac{2N}{V(RMST)} \int_0^R \frac{S(x) \left(x - \int_0^x S(t) dt\right) \int_0^x C^-(t) f(t) dt}{F(x)} dx \text{ and } \mathbf{SE}(\mu_j) = \sqrt{\frac{V(RMST_j)}{N_{eff,j}}}$$

• Following Royston et al., sample size may then be calculated using standard approaches

Landmark

• Landmark analysis is typically performed using a normal approximation and **Greenwood's formula*** to calculate variance:

$$V(\hat{S}(t)) = \hat{S}(t)^2 \sum_{i: t_i \le t} \frac{d_i}{n_i(n_i - d_i)}$$

- We can again calculate expectations based upon distribution functions, similar to O and E
 - $(n_i d_i) \xrightarrow{\delta t \to 0} n(t)$ since the 'point' number of events tends to 0

$$V(S(t)) = \frac{S(t)^{2}}{N} \int_{0}^{T} \frac{f(t)}{S(t)^{2} C^{-}(t)} dt$$

- Note: This also corresponds more directly to Tsiatis' formula**
- Standard normal-approximation based methods may then be applied

^{*}Greenwood M Reports on Public Health and Medical Subjects. 1926, 33: 1–26.

^{**} Tsiatis A Annals of Statistic 1981 9, 93-108

GESTATE

- These are complex integrals where any distributions could be specified. Problems!
 - Most integrals **not analytically-solvable**
 - Don't want to limit distribution choice; particular issue for NPH
 - Combinatorics become prohibitive with even a handful of distribution types

• Solutions:

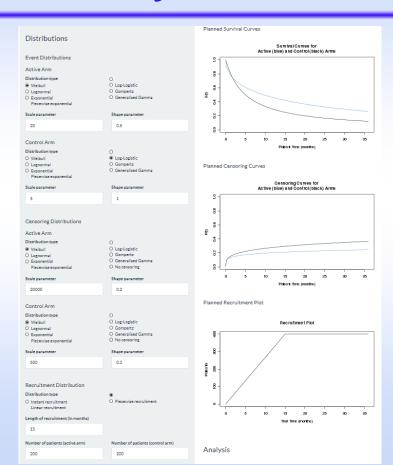
- Numerical integration; most relevant integrals evaluable
- **Generic formula coding**; no distribution-specific code
- **Object-oriented programming**; distributions are from interchangeable **Curve** objects
- **Self-writing code**; integration functions written at run-time
- To implement this, an R package has been written: GEneralised Survival Trial Assessment Tool Environment (GESTATE).
- Core code can handle any 'well-behaved' distribution, or combination of distributions
 - Adding new distributions is straightforward

Simulation

- Curve architecture also allows for a generalised simulation approach:
 - Wide variety of event, censoring and recruitment distributions supported
 - Shared inputs/syntax with analytic approach simple to validate
 - Note: still relies on independent censoring
- Designed to be straightforward to use
 - Automatic analysis and summary functions covering each analysis method
 - Parallel processing options included for speed

- Interactive R Shiny UI written
 - •Real-time plots of S(t), censoring CDF and recruitment input distributions
 - •Analytic and simulation approaches run through same interface
 - •Exportable outputs
- Inputs for an example are displayed:
 - Weibull active event curve,
 - Log-logistic control event curve
 - Differential Weibull censoring between arms.
- Analysis performed after 36 months
 - Restriction time: 30 months
 - Landmark analysis: 30 months
- 20,000 simulations performed

R Shiny UI



Example

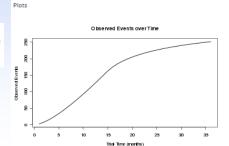
Simulation Summary:

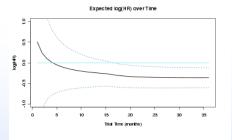
Analytic Properties:

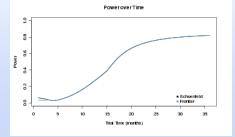
					Log-	Log-	Observed	Observed	Observed	Failed	Log-		Mean		RMST		RMST		RMST			Landmark	Survival	Landmark	Survival	Landmark	Landmark		
		Log(HR)	Cox	Cox	Rank	Rank	Events	Events	Events	(Log-	Rank		Assessment	RMST	(Active)	RMST	(Control)	RMST	Difference	Failed	RMST	Survival	(Active)	Survival	(Control)	Survival	Survival	Failed	Landmark
log(HR)	HR	SE	Z-value	P-Value	Z-Value	P-Value	(Active)	(Control)	(Total)	Rank)	Power	Simulations	Time	(Active)	SE	(Control)	SE	Difference	SE	(RMST)	Power	(Active)	SE	(Control)	SE	Difference	Delta SE	(Landmark)	Power
-0.3691	0.6914	0.12793	-2.8787	0.002	-2.8993	0.0019	117.0942	134.6266	251.721	0	0.8282	20000	36	13.8469	0.9493	9.7385	0.827	4.1084	1.259	0	0.9016	0.2934	0.0382	0.1433	0.0315	0.1501	0.0496	0	0.8526

134.698 117.055 251.753 0.6958 -0.3627 0.1245 0.8206

Values																						
Below is a table (based on Schoe												ne of the sar	nple size rei	quired to re	ach the pre	-specified	oower if all par	rameters othe	r than patient	numbers are ke	ot the same	
Assessment	Patients	Events	Events	Events	Hazard	Log	Log (HR)	Power	Power	Estimated Required	RMST	RMST	RMST	RMST	RMST	RMST	Landmark	Landmark	Landmark	Greenwood	Landmark	
Time	Recruited	(Control)	(Active)	(Total)	Ratio	(HR)	SE	(Schoenfeld)	(Frontier)	SS	(Control)	(Active)	Delta	SE	Power	Failure	(Control)	(Active)	Delta	Delta SE	Power	
1	27	1.065	1.681	2.747	1.6642	0.5093	1.225	0.062	0.0303	23596	0.9116	0.8627	-0.0489	0.1282	0.0572	1	NA	NA	NA	NA	NA	
2	53	3.75	4.545	8.295	1.2676	0.2371	0.696	0.0528	0.0292	36053	1.6824	1.6244	-0.058	0.2159	0.0454	1	NA	NA	NA	NA	NA	
3	80	7.573	8.081	15.654	1.1024	0.0975	0.5055	0.0386	0.0376	113023	2.35	2.3272	-0.0229	0.2876	0.03	1	NA	NA	NA	NA	NA	
4	107	12.244	12.114	24.357	1.0093	0.0092	0.4051	0.0264	0.0261	8127360	2.9389	2.9856	0.0467	0.3485	0.0339	1	NA	NA	NA	NA	NA	
5	133	17.57	16.546	34.116	0.9489	-0.0524	0.3423	0.0354	0.0343	179197	3.4657	3.6082	0.1424	0.4015		1	NA	NA	NA	NA	NA	
6	160	23.417	21.315	44.732	0.9065	-0.0982	0.299	0.0514	0.0499	39013	3.9423	4.2002	0.2579	0.4484	0.0831	1	NA	NA	NA	NA	NA	
7	187	29.689	26.373	56.063	0.8751	-0.1334	0.2671	0.0721	0.0701	16845	4.3773	4.7658	0.3885	0.4905	0.1214	1	NA.	NA	NA	NA	NA	
8	213	36.313	31.687	68	0.8509	-0.1615	0.2425	0.0978	0.0954	9482	4.7776	5.308	0.5304	0.5286		1	NA	NA	NA	NA	NA	
9	240	43.234	37.228	80.461	0.8317	-0.1843	0.2229	0.1285	0.1257	6153	5.1481	5.8291	0.681	0.5634		1	NA	NA	NA	NA	NA	
10	267	50.407	42.974	93.381	0.8162	-0.2031	0.2069	0.1639	0.1608	4363	5.4931	6.3312	0.8381	0.5954	0.2904	1	NA	NA	NA	NA	NA	
11	293	57.798	48.907	105.706	0.8033	-0.219	0.1935	0.2036	0.2002	3285	5.8158	6.8158	1	0.625	0.3594	1	NA	NA	NA	NA	NA	
12	320	65.38	55.012	120.392	0.7926	-0.2325	0.1821	0.2468	0.2432	2585	6.1189	7.2843	1.1654	0.6526	0.4309	1	NA	NA	NA	NA	NA	
13	347	73.128	61.275	134.403	0.7835	-0.244	0.1723	0.2927	0.289	2101	6.4047	7.7379	1.3332	0.6783		1	NA	NA	NA	NA	NA	
14	373	81.023	67.685	149.709	0.7757	-0.254	0.1638	0.3405	0.3367	1753	6.675	8.1777	1.5027	0.7025		1	NA	NA	NA	NA	NA	
15	400	89.05	74.232	163.281	0.769	-0.2627	0.1562	0.3892	0.3855	1492	6.9315	8.6045	1.673	0.7253	0.6356	1	NA	NA	NA	NA	NA	
16	400	96.129	79.225	175.354	0.7539	-0.2825	0.1507	0.4644	0.4606	1202	7.1754	9.0192	1.8437	0.7534	0.687	1	NA	NA	NA	NA	NA	
17	400	101.695	83.155	184.85	0.7406	-0.3003	0.1468	0.5324	0.5286	1009	7.408	9.4224	2.0144	0.7861	0.7265	1	NA	NA	NA	NA	NA	
18	400	106.218	86.527	192.745	0.7304	-0.3141	0.1436	0.5873	0.5837	884	7.6303	9.8148	2.1846	0.8211	0.7582	1	NA	NA	NA	NA	NA	
19	400	109.983	89.507	199.49	0.7226	-0.3249	0.1411	0.631	0.6276	799	7.8431	10.1971	2.354	0.8572	0.7841	1	NA.	NA	NA	NA	NA	
20	400	113.169	92.188	205.357	0.7166	-0.3333	0.139	0.6657	0.6626	737	8.0472	10.5696	2.5225	0.8941		1	NA	NA	NA	NA	NA	
21	400	115.907	94.63	210.537	0.7119	-0.3399	0.1372	0.6935	0.6907	692	8.2433	10.933	2.6897	0.9313	0.8233	1	NA	NA	NA	NA	NA	
22	400	118.289	96.871	215.16	0.7081	-0.3451	0.1356	0.7161	0.7135	657	8.432	11.2876	2.8556	0.9687	0.8384	1	NA	NA	NA	NA	NA	
23	400	120.38	98.945	219.324	0.7052	-0.3493	0.1343	0.7344	0.7321	629	8.6138	11.6338	3.02	1.0062	0.8511	1	NA.	NA	NA	NA	NA	
24	400	122.232	100.872	223.104	0.7029	-0.3526	0.133	0.7495	0.7474	607	8.7893	11.9721	3.1928	1.0437		1	NA.	NA	NA	NA	NA	
25	400	123.884	102.674	226.558	0.7011	-0.3552	0.1319	0.762	0.7601	589	8.9588	12.3027	3.3439	1.081	0.8715	1	NA.	NA	NA	NA	NA	
26	400	125.367	104.361	229.728	0.6996	-0.3573	0.131	0.7726	0.7708	574	9.1227	12.626	3.5033	1.1182	0.8796	1	NA.	NA	NA.	NA	NA	







Example

	Events	HR	Log-Rank Power	RMST 30 Δ (months)	RMST 30 Δ SE (months)	RMST Power	ΔS(30)	ΔS(30) SE	ΔS(30) Power
Simulation	251.72	0.691	82.8%	4.108	1.259	90.2%	0.150	0.0496	85.3%
Analytic	251.75	0.696	82.0%	4.122	1.255	90.7%	0.151	0.0497	85.9%

- Properties are a good match between simulation and analytic approaches
- HR of 0.69 accurately predicted for this time of assessment (36 months)
 - For comparison, HR at 12 months predicted to be 0.79
- RMST and landmark standard errors accurately calculated, despite high censoring:
 - Overall, 37% censoring
 - Without any dropout, 308.6 events predicted (18.5% events censored due to dropout)
 - For comparison, binomial-derived SE would be 0.0406
- Powers are close, although in 2-3 σ range for Monte Carlo error

Discussion

- Methods work well for most cases, but have a few limitations:
 - HR calculation becomes less accurate as planned HR moves further from 1
 - Limitation of the Pike approximation
 - Power calculation becomes less accurate for all three methods the more extreme the non-proportional hazards
 - The normal assumptions start breaking down:
 - Variance becomes correlated with point estimate
 - Properties may be predicted well, but power less so
- For RMST it is important to calculate the probability of analysis 'failure' (due to undefined analysis curve at point of restriction)
 - Also implemented analytically, but not shown here

Summary

- Accurate numerical-integration methods for prediction of many time-to-event trial properties under Non-Proportional Hazards have been presented
- Prediction of the Cox hazard ratio at a given assessment time is demonstrated
- Direct, analytic power calculations under censoring are presented for RMST and Landmark analyses
- The GESTATE R package has been written to implement these methods in a uniquely flexible fashion, allowing for simple input of complex assumption combinations
 - It also separately includes simulation functionality
- The GESTATE package should be publically available later in 2018.

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