





Italian Stata Users Group Meeting

November 12, 2015

Assessment of proportional hazards assumption: restricted mean difference as a potential alternative to the hazard ratio for the analysis of time-to-event endpoint on aggregate data

#### Francesca Ghilotti

Background Rationale Objectives

Background

- Survival improvement is an appropriate measure of clinical benefit
- Time-to-event endpoint is the outcome of interest in many oncological clinical studies
- Log-rank and proportional hazards (PH) Cox model are the most common techniques used for analyzing survival time data

Background Rationale Objectives

# Rationale

- The hazards need to be proportional but rarely PH assumption is assessed
- Survival curve convergences and crossings are common in medical research



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Background Rationale Objectives



Conduct a **systematic review** to quantify the phenomenon of survival curve convergences and crossings

Propose the use of **meta-regression** as a method to test the **PH assumption** when only **aggregate data** are available

Propose the use of **restricted mean difference** as a potential alternative to the HR in case of non-PH

Systematic review Estimates of log(HR) and its variance Assessing the PH assumption Assessing the PH assumption RMST



#### Inclusion criteria for the review

- Phase II/III RCTs
- Advanced non-small-cell lung cancer (NSCLC)
- Antitumor therapies
- Time-to-event primary endpoint

Data extraction:

Study design, patient and treatment characteristics, metodological and statistical features

Systematic review Estimates of log(HR) and its variance Assessing the PH assumption Assessing the PH assumption RMST



- Inclusion criteria for the analysis
  - Number of patients at risk reported at each time-point p
  - At least 3 time-points available

Data extraction:

Survival probabilities from the KM curves at p time-points, number of patients at risk

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Estimates of log(HR) and its variance

- Life-table approach
- Censoring uniform within each time interval

$$s_{j,i}^* = s_{j,i-1}^* \cdot \left[ 1 - \frac{d_{j,i}^*}{n_{j,i-1} - (c_{j,i}^*/2)} \right]$$
(1)

$$n_{j,i} = n_{j,i-1} - d_{j,i}^* - c_{j,i}^*$$
(2)

Rearranging (1) e (2) gives the number of events  $d_{j,i}^*$ , the number censored  $c_{i,i}^*$  and the number at risk  $n_{i,i}^*$  during the interval  $[t_{i-1}, t_i)$ 

$[t_{i}]$

Williamson, P.R. Statistics in medicine, 2002 f.ghilotti1@campus.unimib.it

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# Estimates of log(HR) and its variance

Logarithm of the Hazard Ratio whitin the *i*<sup>th</sup> time interval

$$log(HR)_i = rac{(d^*_{2,i} - e^*_{2,i})}{v_i}$$

Variance of the log(HR) whitin the *i*<sup>th</sup> time interval  $var(log(HR)_i) = \frac{1}{v_i}$ 

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Assessing the PH assumption

• GRAPHICAL APPROACH

• log(-log S) plot against time

twoway (scatter ln\_ln1 ln\_t, connect(l)) ///
(scatter ln\_ln2 ln\_t, connect(l))

• Forest plot within each study to visualize the relation between the HR and the time of follow-up

metan ln\_hr se\_hr, fixedi eform label(namevar=t)

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# Assessing the PH assumption

ANALYTICAL APPROACH

#### • Meta-regression to test for a linear trend with time

- Outcome: log(HR) at each time-point
- Explanatory variable: follow-up time
- Inverse-variance weighting

statsby \_b e(chi2) e(df\_m),by(id): vwls ln\_hr t1,sd(se\_hr)

```
rename _eq2_stat_1 chi2
rename _eq2_stat_2 df_m
gen pvalue=chi2tail(df_m, chi2)
gen z=sqrt(chi2)
list if pvalue<0.1</pre>
```

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Association between non-PH and study characteristics

- Type of treatment comparison
  - different mechanism of action
  - same mechanism of action

conventional therapy, biologics, tyrosine-kinase inhibitor (TKI), non-conventional target

- Type of endpoint
  - Overall Survival (OS)
  - Progression Free Survival (PFS)

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Restricted Mean Survival Time (RMST)

- Select a time-point t\*, up to which we wish to compute the RMST
- For a random time-to-event variable T, we estimate:

$$\mu(t^*) = E[\min(T, t^*)] = \int_0^{t^*} S(t) dt$$
 (3)

- Area under the survival curve up to  $t^*$
- Can think of it as the 't\*-year life expectancy'
- Difference in RMST between arms could be used as an alternative to the HR

Royston, P. and Parmar, M.K. Statistics in medicine, 2011 (December 12, 2015) f.ghilotti1@campus.unimib.it November 12, 2015 12/31

Flow-chart

## Flow-chart



Flow-chart Characteristics of the studies PH assumption assessment RMST

Characteristics of the studies included in the review

- Phase: 33% were phase II studies, 67% were phase III
- **Primary endpoint:** 49% OS, 51% PFS
- **Treatment comparisons:** 41% same mechanism of action, 59% different mechanism
- Partecipants: The median number randomized was 332
- Statistical analysis: Log-rank test, Cox model

Only 4 (3%) out of 115 studies reported whether PH assumption was satisfied or not

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Flow-chart Characteristics of the studies **PH assumption assessment** RMST

## PH assumption assessment

For 12 (19%) out of 62 treatment comparisons non-PH was detected

• Two studies in which PH assumption is violated:



Barlesi, F. Journal of clinical oncology, 2013

Flow-chart Characteristics of the studies PH assumption assessment RMST

## PH assumption assessment



Flow-chart Characteristics of the studies PH assumption assessment RMST

#### PH assumption assessment



Barlesi, F. Journal of clinical oncology, 2013

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Flow-chart Characteristics of the studies PH assumption assessment RMST

#### PH assumption assessment



Mok, T.S. New England Journal of Medicine, 2009

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Introduction Methods Results

Discussion

Flow-chart Characteristics of the studies PH assumption assessment RMST

### PH assumption assessment





Flow-chart Characteristics of the studies PH assumption assessment RMST

#### PH assumption assessment





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Flow-chart Characteristics of the studies **PH assumption assessment** RMST

#### PH assumption assessment

• Two studies in which PH assumption is satisfied:





Flow-chart Characteristics of the studies PH assumption assessment RMST

## PH assumption assessment





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Gridelli, C. Journal of thoracic oncology, 2007

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Quoix, E. The Lancet, 2011

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Flow-chart Characteristics of the studies PH assumption assessment RMST

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Flow-chart Characteristics of the studies **PH assumption assessment** RMST

## PH assumption results

#### Table: Association between non-PH and study characteristics

	PH assumpt	Fisher's	
	No	Yes	exact test
<b>Treatments</b> Same treatment comparison Different treatment comparison	20 (100%) 30 (71%)	0 (0%) 12 (29%)	0.006
Primary endpoint OS PFS	23 (92%) 27 (73%)	2 (8%) 10 (27%)	0.101

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Flow-chart Characteristics of the studies PH assumption assessment RMST

Table: Comparison between the RMST results and the results reported by authors

	RMST results		Median Results			HR Results	
Study	RMST diff <sup>a</sup>	p-value test Z	Median (control)	Diff (HR) <sup>b</sup>	Diff (KM) <sup>c</sup>	HR	p-value
Wu	6.66	< 0.001	5.6	14.4	8.1	0.28	< 0.001
Solomon	6.13	< 0.001	7.0	8.56	3.9	0.45	< 0.001
Seto	5.13	< 0.001	9.7	8.26	6.3	0.54	0.002
Shaw	3.33	0.004	3.0	3.12	4.7	0.49	< 0.001
Barlesi	2.37	< 0.001	3.7	4.01	3.7	0.48	< 0.001
Lee	1.23	0.15	3.4	1.26	-0.1	0.73	0.04 <sup>§</sup>
Jänne	0.82	0.61	5.2	1.30	4.2	0.80	0.21 <sup>§</sup>
Reck	0.76	0.018	2.7	0.72	0.8	0.79	0.002
Belani	0.65	0.73	7.1	0.88	0.9	0.89	0.36

<sup>a</sup> Restricted Mean Survival Time difference (months)

<sup>b</sup> Median difference derived from HR (months)

<sup>c</sup> Median difference derived from KM curve (months)

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Pros and Cons Next steps

# Pros and Cons

- **New!** Assess the PH assumption using aggregate data
- Conclusions are in line with the log-log plots and with the results reported by authors

- Data constrained by the quality of figures
- Assumption about the mechanism of censoring
  - Only studies with patients at risk reported

Pros and Cons Next steps

## Future research

- Compare the conclusions obtained with individual patient data (IPD) and with aggregate data
- Investigate how many time-points are needed

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Pros and Cons Next steps

# Thank you for your attention!

Joined work with: Rino Bellocco <sup>1</sup> Eliana Rulli <sup>2</sup> Valter Torri <sup>2</sup>

1 Karolinska Institutet, University of Milano-Bicocca 2 Mario Negri Institute for Pharmacological Research

## Appendix

Numbers at risk during a time interval are:

$$n_{j,i}^{*} = \frac{(n_{j,i-1} + n_{j,i}) \cdot s_{j,i-1}^{*}}{(s_{j,i-1}^{*} + s_{j,i}^{*})}$$
(4)

Number of events during a time interval is:

$$d_{j,i}^{*} = \frac{(n_{j,i-1} + n_{j,i}) \cdot (s_{j,i-1}^{*} - s_{j,i}^{*})}{(s_{j,i-1}^{*} + s_{j,i}^{*})}$$
(5)

Numbers censored during a time interval are:

$$c_{j,i}^{*} = \frac{2 \cdot (n_{j,i-1} \cdot s_{j,i}^{*} - n_{j,i} \cdot s_{j,i-1}^{*})}{(s_{j,i-1}^{*} + s_{j,i}^{*})}$$
(6)



Appendix



$$log(HR)_{i} = \frac{(d_{2,i}^{*} - e_{2,i}^{*})}{v_{i}}$$
(7)  
$$var(log(HR)_{i}) = \frac{1}{v_{i}}$$
(8)

where

$$e_{2,i}^{*} = (d_{2,i}^{*} + d_{1,i}^{*}) \cdot \frac{(n_{2,i}^{*})}{(n_{2,i}^{*} + n_{1,i}^{*})}$$
(9)  
$$v_{i} = (d_{2,i}^{*} + d_{1,i}^{*}) \cdot \frac{n_{2,i}^{*} \cdot n_{1,i}^{*}}{(n_{2,i}^{*} + n_{1,i}^{*})^{2}}$$
(10)

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## Appendix

The area under the curve for group j was estimated by:

$$\mu_{j} = \sum_{i=1}^{p} \mu_{j,i} = \sum_{i=1}^{p} \frac{(s_{j,i-1}^{*} + s_{j,i}^{*}) \cdot (t_{i} - t_{i-1})}{2}$$
(11)

To estimate the variability of this quantity the formula reported by Klein was used:

$$V(\mu_j) = \sum_{i=1}^{p} \left[ \int_{t_i}^{t^*} S(t) dt \right]^2 \cdot \frac{d_i}{n_i \cdot (n_i - d_i)}$$
(12)

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