



Network meta-analysis of survival data using fractional polynomials; An example with first line metastatic renal cell cancer treatments

Mihajlović J^{1,2}, Postma MJ¹

¹University of Groningen, Unit of Pharmacoepidemiology and Pharmacoeconomics, Groningen, the Netherlands

²Mihajlović Health Analytics, Novi Sad, Serbia



- First line targeted cancer therapies in treatment of metastatic renal cell cancer (mRCC) enabled an increment in progression-free survival (PFS) from 2 to 6 months
- An improvement in overall survival (OS) was not demonstrated in RCTs, or it was difficult to assess due to “cross-over” confounding
- Most of the evidence is available from registrational RCTs representing comparisons of a treatment of interest with previous therapeutic standard (interferon alpha)



- Network meta-analysis (NMA) synthesizes direct and indirect evidence between ≥ 2 treatments linked by ≥ 2 RCTs
- Frequently NMA of survival data is based on simple adjustment of hazard ratio \rightarrow proportional hazards (PH) assumption (e.g. all published NMAs in mRCC¹)
- Even survival modelling within single treatment appraisals in health economics is commonly founded on PH assumption (e.g. NICE appraisals of 32/45 of cancer drugs²)

1 - Leung HWC et al. Molecular and clinical oncology 2 (2014): 858-864.; Mills et al. BMC Cancer 2009, 9:34

2 - Nicholas R. Latimer, Medical Decision Making, Aug 2013: 743-754.



- What is **wrong** with **PH assumption**?

- Assuming constant ratio of hazards implies constant difference in effectiveness through time

- This is often implausible:
 - if evidence comes from many different RCTs (e.g. NMA)
 - if dealing with terminal disease (e.g. metastatic cancer)
 - if modelling is required far beyond the RCT's horizon (e.g. CEA)



- Relaxing PH assumption can be achieved with **fractional polynomials (FP)**^{1,2}
- Contrary to PH models (effect fixed, one dimensional - HR dependent), FP models estimate the hazard/survival through several parameters

Objective:

The aim is **to apply FP** in NMA of PFS and OS analysis of 1st line targeted cancer therapies for mRCC and **to compare FP and PH** approach in order to identify and explain the potential differences

1 - Royston P, Altman DG. Applied Statistics 1994, 43:429-467.

2 - Jansen JP. BMC Med Res Methodol. 2011;11:61..



1. Systematic literature review

RCTs' selection criteria:

- a. A treatment examined in an RCT must be first line targeted therapy;
- b. PFS and/or OS must be represented by reproducible Kaplan Meier curves accompanied by the numbers of patients at risk at least at two different time points;
- c. The population examined in an RCT should be representative of the general mRCC population;
- d. an RCT must be connected to the rest of RCTs in the NMA through at least one comparator (applied at the end of selection process);



2. Data extraction

- Number of patients at risk (R), number of patients experiencing event (D) and number of censored patients (C) at equal time intervals were needed
- At our disposal were treatment specific KM curves, followed by R per different time intervals (2, 3, 4, 5, 6 or 10 months)
- W/o informationa on C -> Assume constant rate of censoring within a time interval¹ -> improvements of existing method were needed for intervals not dividable by 2 (!)

1. Hoyle MW et Henley W. BMC Medical Research Methodology 2011, 11:139



3A. Survival analysis – FP model

- An FP function of second order can be utilised to estimate natural logarithm of h :

$$\ln (h(t)) = \beta_0 + \beta_1 t^{p1} + \beta_2 t^{p2}$$

- FP model with best fitting powers (DIC) from predefined set (-2,-1, -0.5, 0, 0.5, 1, 2, 3) for all RCTs is selected for further analysis of the effect (β parameter)
- Common parametric curves can be seen as special simplified cases of FP models (e.g. Exponential: $\beta_1 = \beta_2 = 0$; without $p1$ and $p2$; Weibull: $\beta_1 \neq 0$; $\beta_2 = 0$; $p1=0$; without $p2$;))



Methods

- Now β s can be split to represent trial specific baseline (μ) and trial specific treatment effect (δ):

$$\begin{pmatrix} \beta_{0jk} \\ \vdots \\ \beta_{Mjk} \end{pmatrix} = \begin{pmatrix} \mu_{0jb} \\ \vdots \\ \mu_{Mjb} \end{pmatrix} + \begin{pmatrix} \delta_{0jbk} \\ \vdots \\ \delta_{Mjbk} \end{pmatrix}$$

Baseline trt
Active trt

- Each treatment's effect can be estimated through δ that is result of pooled estimates of δ s specific for that treatment across included trials
- To determine the powers of best fitting FP model and to estimate the treatment effects (μ s and δ s), we relied on developed code¹ conducted 50,000 MCMC in WinBugs and R software



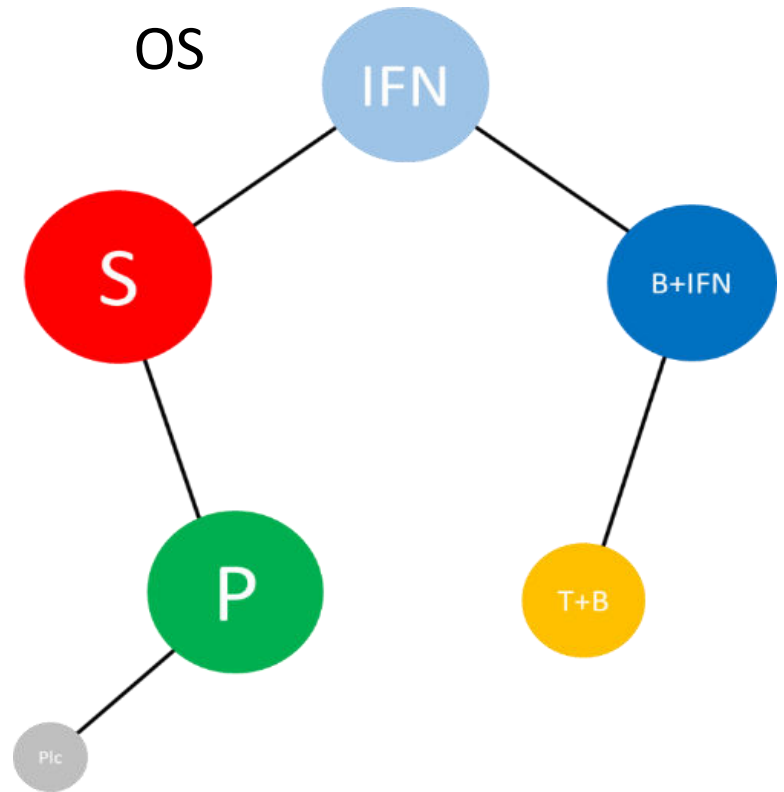
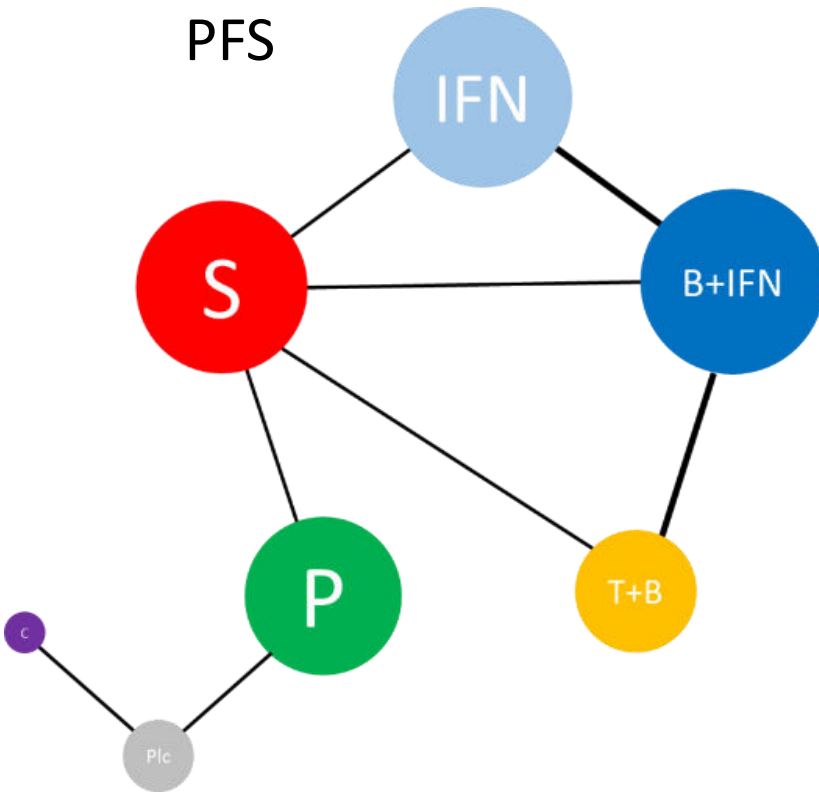
3B. Survival analysis – PH model

- We fitted the most common parametric functions over hazard/survival data of a referent treatment and choose the best fitting distribution
- Tested were: Weibull, exponential, lognormal, logistic and loglogistic distributions
- Active treatments' effects were estimated through simple adjustment of HR across all trials as recommended by Bucher et al¹

1. Bucher HC, Guyatt GH, Griffith LE et al. J Clin Epidemiol Vol. 50, No. 6, pp. 683-691, 1997.

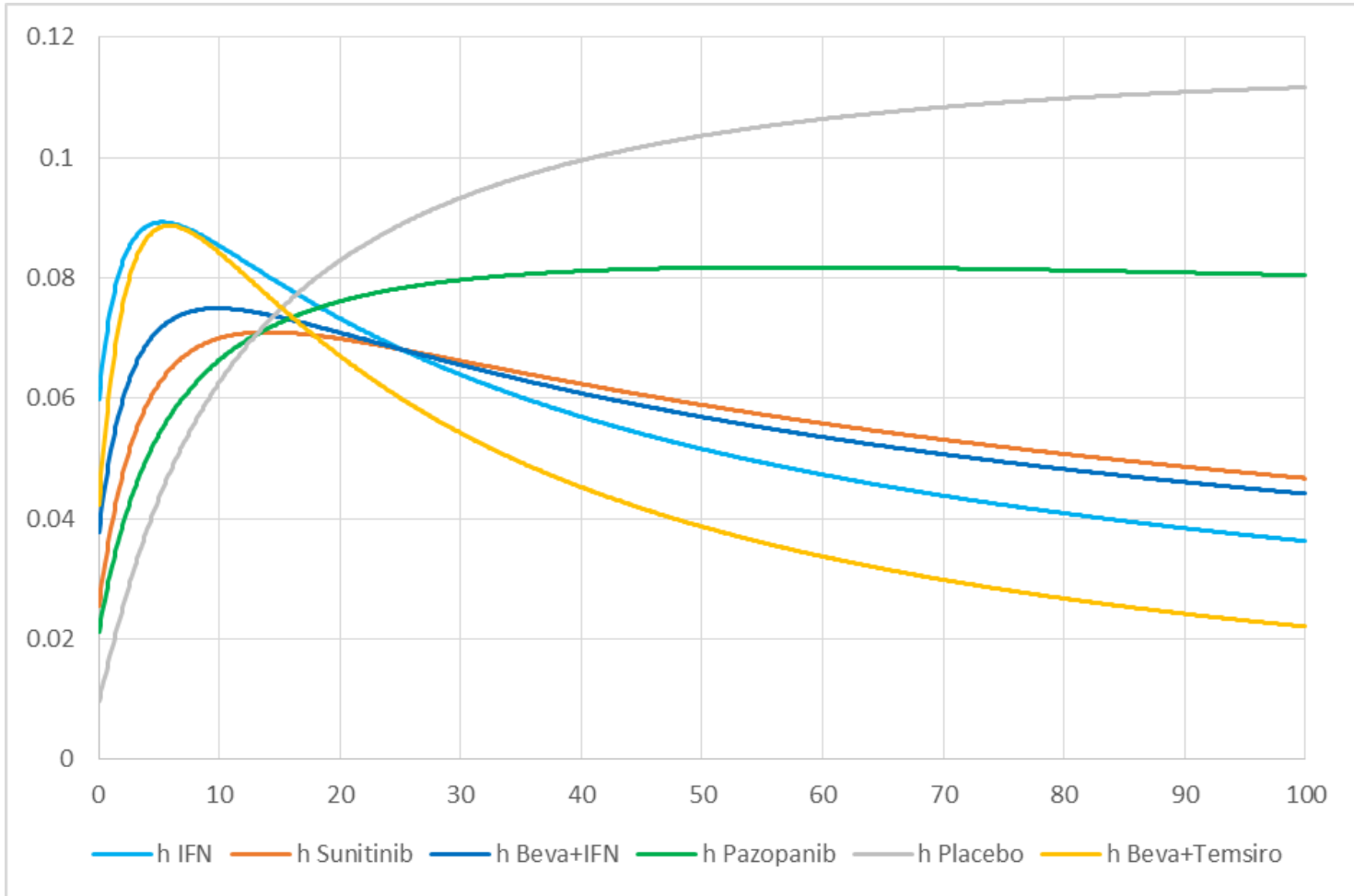


- 11 publications presenting 8 RCTs were included
- 8 publications reported PFS (4,709 pt) and 5 publications OS (3,818 pt)
- 7 compared treatments: sunitinib, pazopanib, interferon alpha (IFN), bevacizumab(beva)+IFN, temsirolimus+beva, cediranib and placebo
- 2 out of 5 OS studies allowed cross-over after progression (sunitinib vs IFN and pazoapnib vs PLC trials)





Results – hazard rates OS



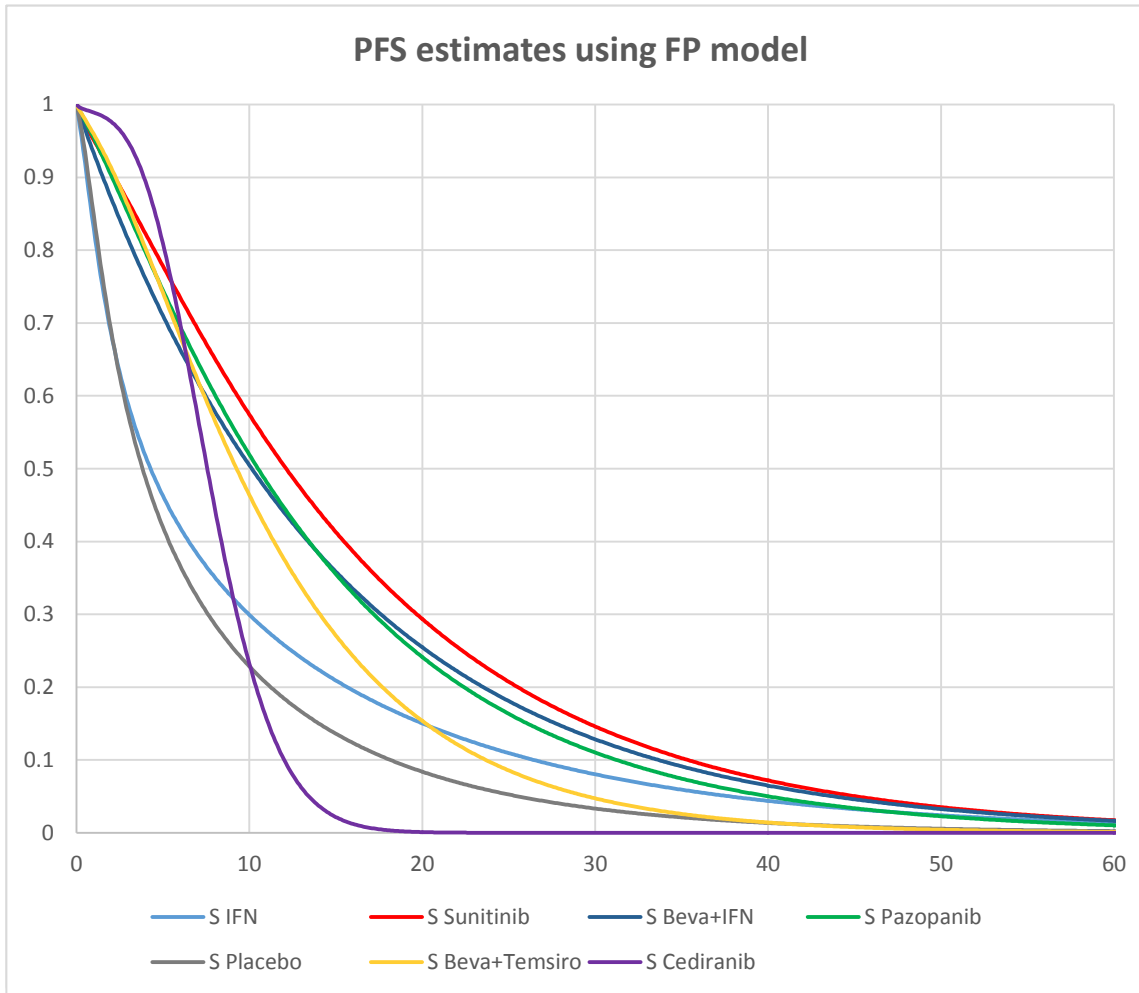


Results – median survival estimates

| | Progression free survival | | | Overall survival | | |
|-------------------|----------------------------|---------------------|---------------------|----------------------------|---------------------|---------------------|
| | RCTs' estimates (mnths) | FP model (mnths) | PH model (mnths) | RCTs' estimates (mnths) | FP model (mnths) | PH model (mnths) |
| IFN | 5.0-5.4 | 4.3 | 6 | 17.4-21.8 | 16.6 | 18.2 |
| Sunitinib | 8.2-11.0 | 12.1 | 12.6 | 26.4-29.3 | 21.4 | 22.4 |
| Bevacizumab+IFN | 8.5-16.8 | 10.1 | 7.3 | 18.3-25.5 | 19.7 | 21.5 |
| Pazopanib | 8.4-9.2 | 10.5 | 12.1 | 22.9-28.4 | 22 | 24.5 |
| Placebo | 2.8-4.2 | 3.8 | 5 | 20.5 | 20.7 | 22.4 |
| Temsirolimus+Beva | 8.2-9.1 | 9.3 | 6.6 | 25.8 | 17.4 | 21.5 |
| Cediranib | 12.1 | 7.6 | 11.6 | | | |

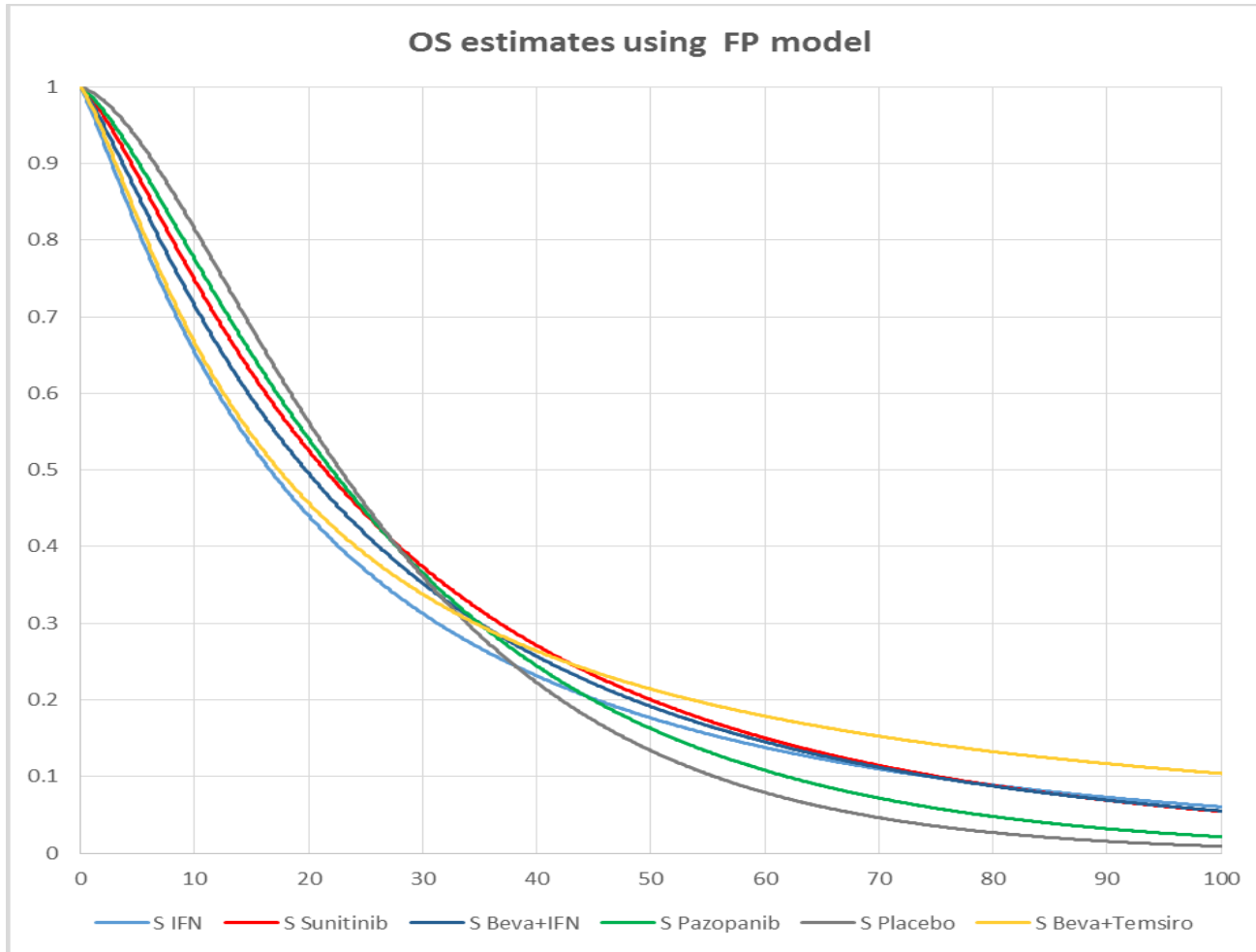


Results – PFS estimates (PH vs FP model)





Results – OS estimates (PH vs FP model)





1. **PH assumption was violated** in NMA of PFS and OS estimations
2. **Median survival estimates were almost always lower with FP vs PH model** (PH overestimates ?)
3. **Sunitinib was the most effective treatment on PFS** in both models (heavily overestimated in long term by PH)
4. **Unclear effect on OS in both models** (FP – sunitinib; PH – pazopanib), impact of cross over



Future research

- Resolving issues on models' uncertainty
- Transferring effectiveness NMA data to CEA in settings of Serbia and the Netherlands

Questions?



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