

# Novel Methodology in Network Meta-analysis of Time-to-event Data using Blended Survival Curves

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## INTRODUCTION

Due to the absence of head-to-head evidence, network meta-analysis (NMA) of parametric survival curves are frequently used to inform the extrapolation of relative treatment effects for multiple interventions while the follow-up of trials are limited. However, conventional methods mainly assume constant treatment effect over time that is implausible, especially in heavily censored data. This study develops a new extrapolation technique called blended survival curves into the NMA setting for evidence synthesis.

## METHODOLOGY

The basic idea of blended survival curves is to mix a flexible model to fit as well as possible the observed data  $S_{obs}$  and a parametric model encoding assumptions on the expected behaviour of underlying long-term survival  $S_{ext}$ .

The “blended” survival curve is obtained as

$$S_{ble}(t|\theta) = S_{obs}(t|\theta_{obs})^{1-\pi(t;\alpha,\beta,a,b)} \times S_{ext}(t|\theta_{ext})^{\pi(t;\alpha,\beta,a,b)}$$

- where:  $\pi(t; \alpha, \beta, a, b) = \Pr(T \leq \frac{t-a}{b-a} | \alpha, \beta) = F_{Beta}(\frac{t-a}{b-a} | \alpha, \beta)$

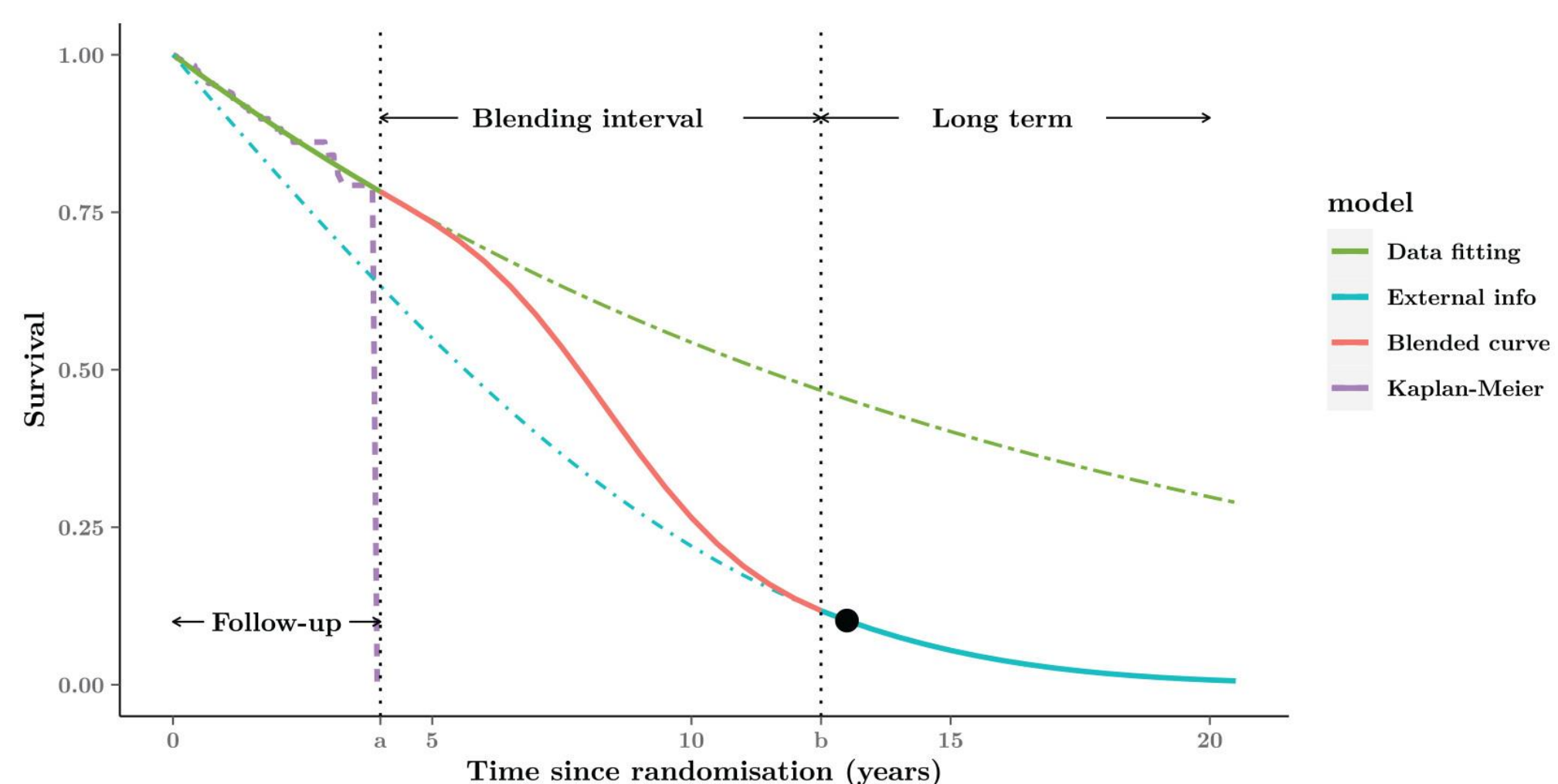


Figure 1: Graphical representation of the blended curve method

The blending hazard function is described as

$$h_{ble}(t) = (1 - \pi(t)) \times h_{obs}(t) + \pi(t) \times h_{ext}(t) + \frac{f_{Beta}(\frac{t-a}{b-a})}{b-a} \times (H_{ext}(t) - H_{obs}(t))$$

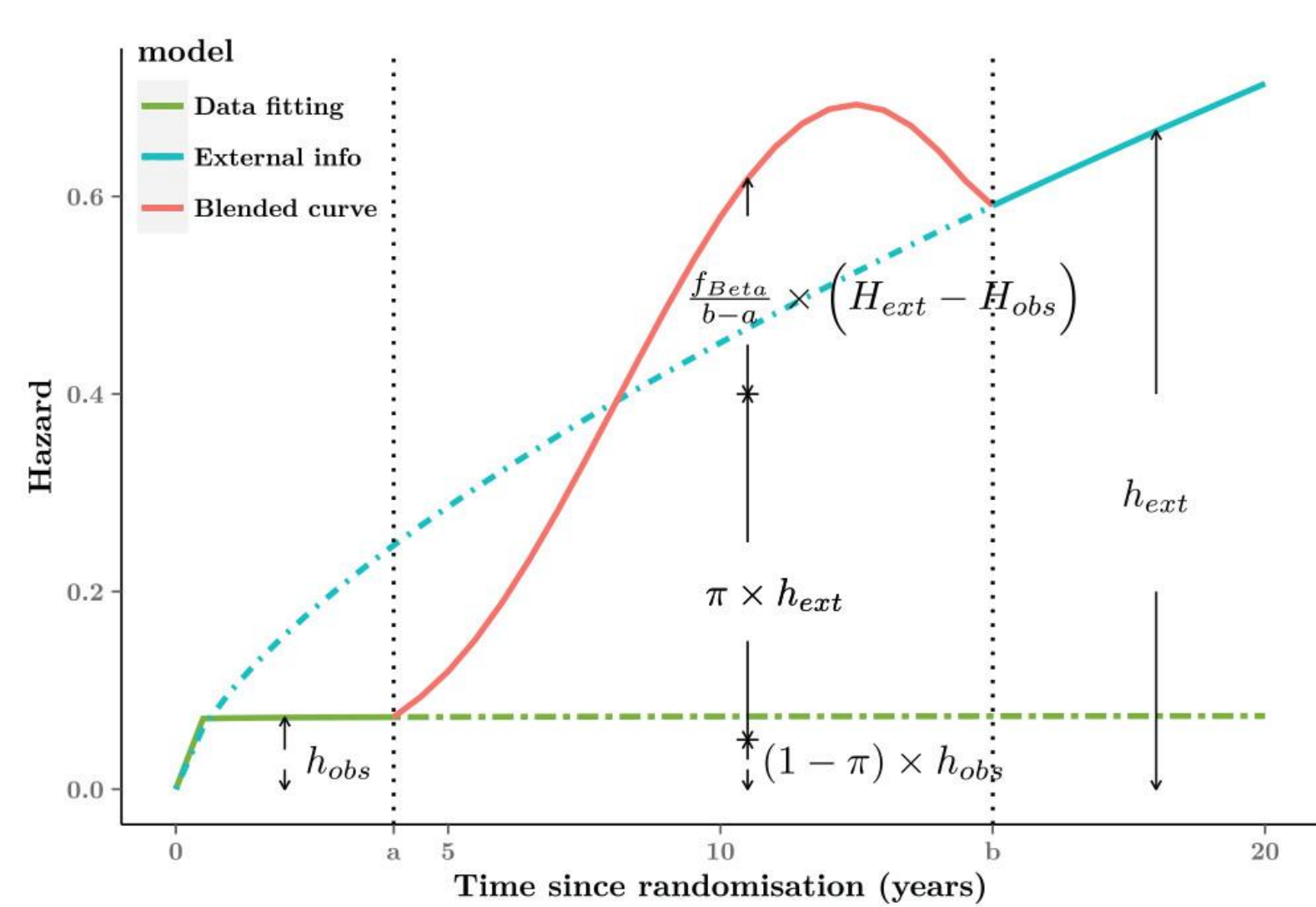


Figure 2: Graphical representation of the blended hazard

While extending the blended method to NMA framework, it has three components: 1) standard NMA for the short-term data; 2) long-term estimate using external evidence; 3) blended process combining two curves.

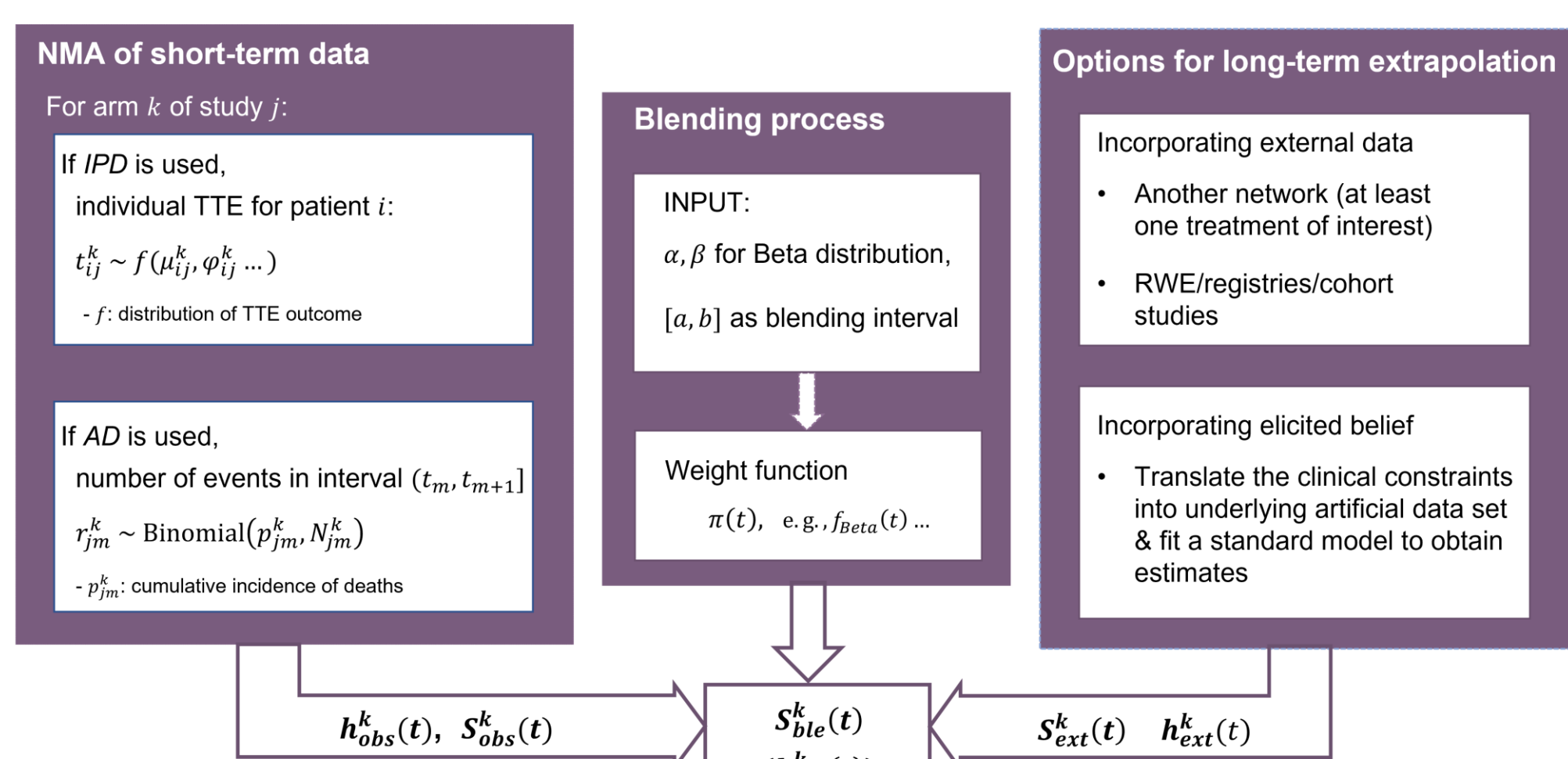
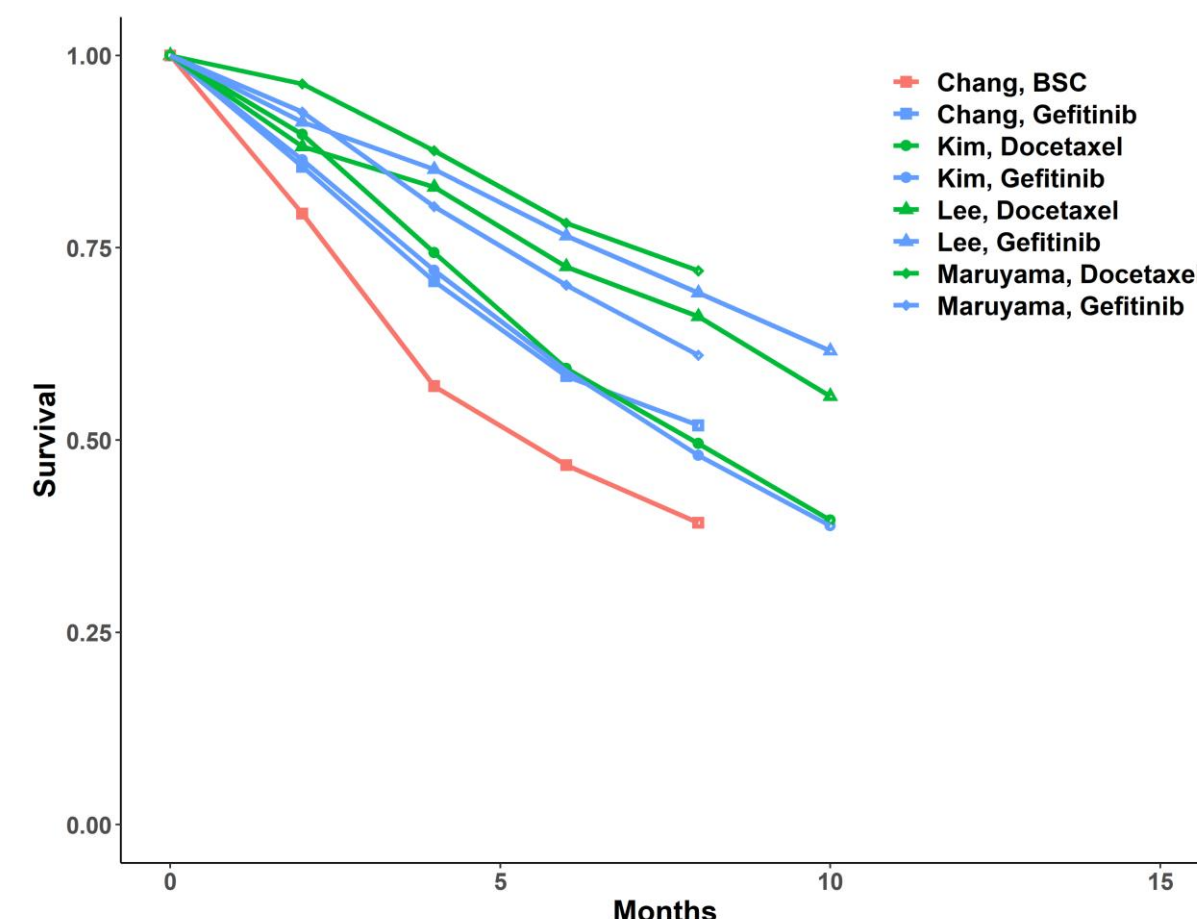


Figure 3: Framework of NMA modelling structure

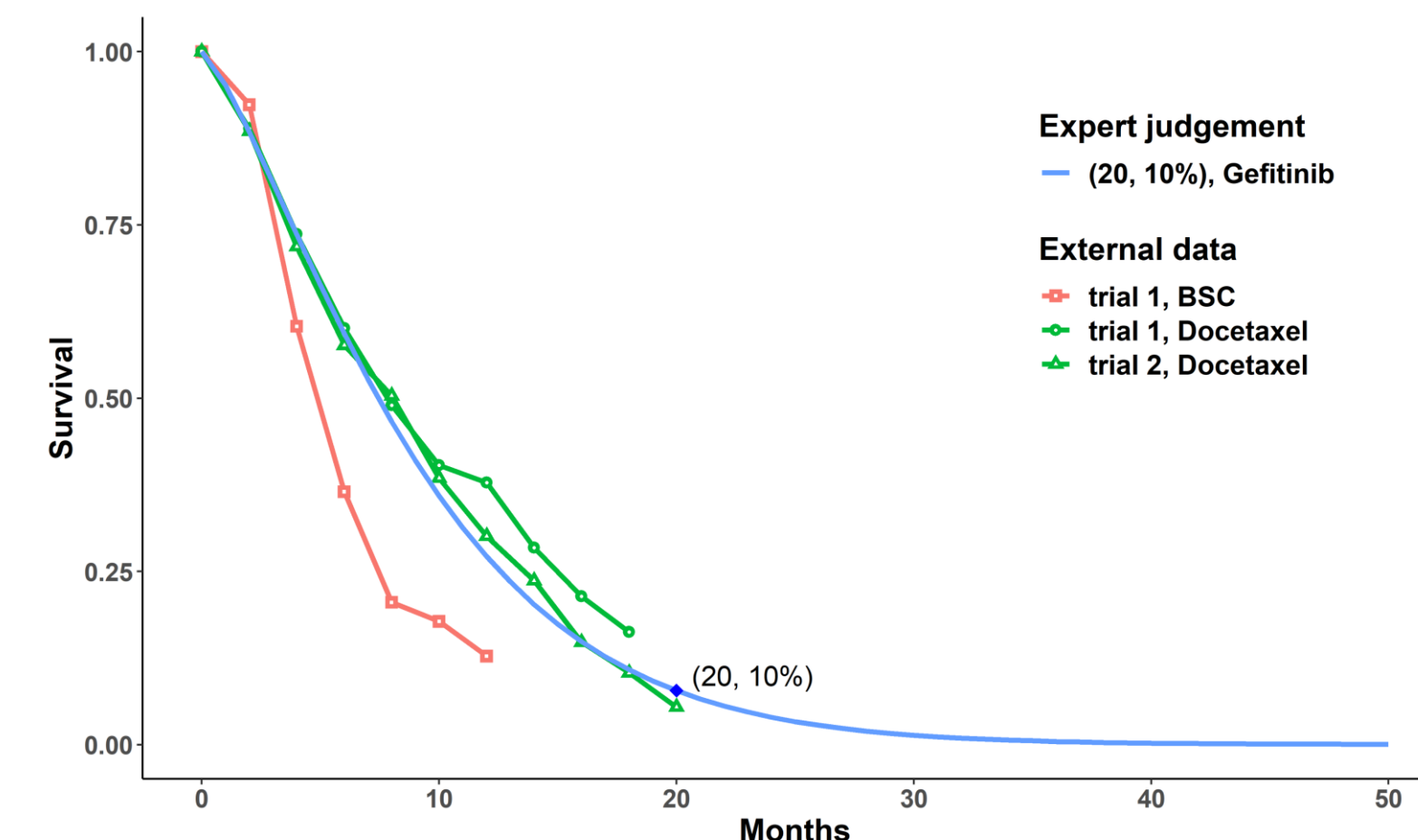
## ILLUSTRATIVE EXAMPLE

To test blended method, four NSCLC trials were used comparing gefitinib with best-supportive care (BSC) (1 study) and gefitinib with docetaxel (3 studies).



### Incorporating external information

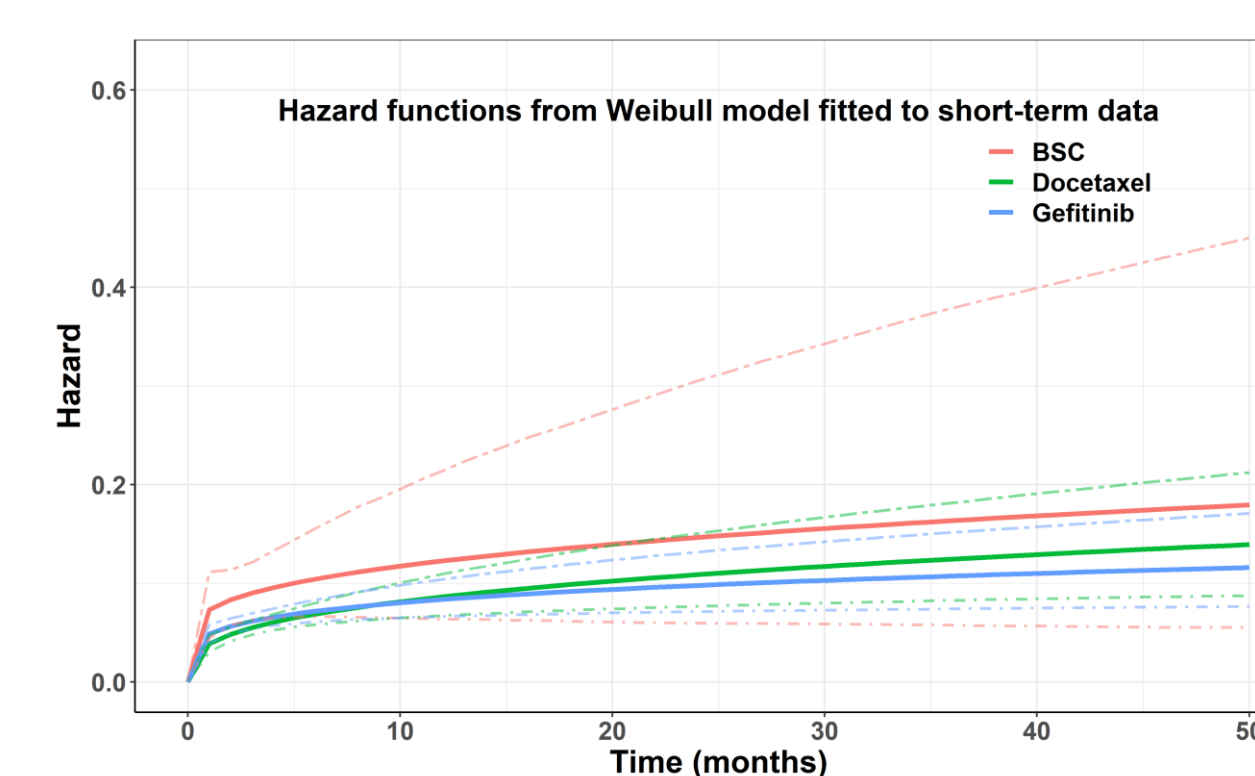
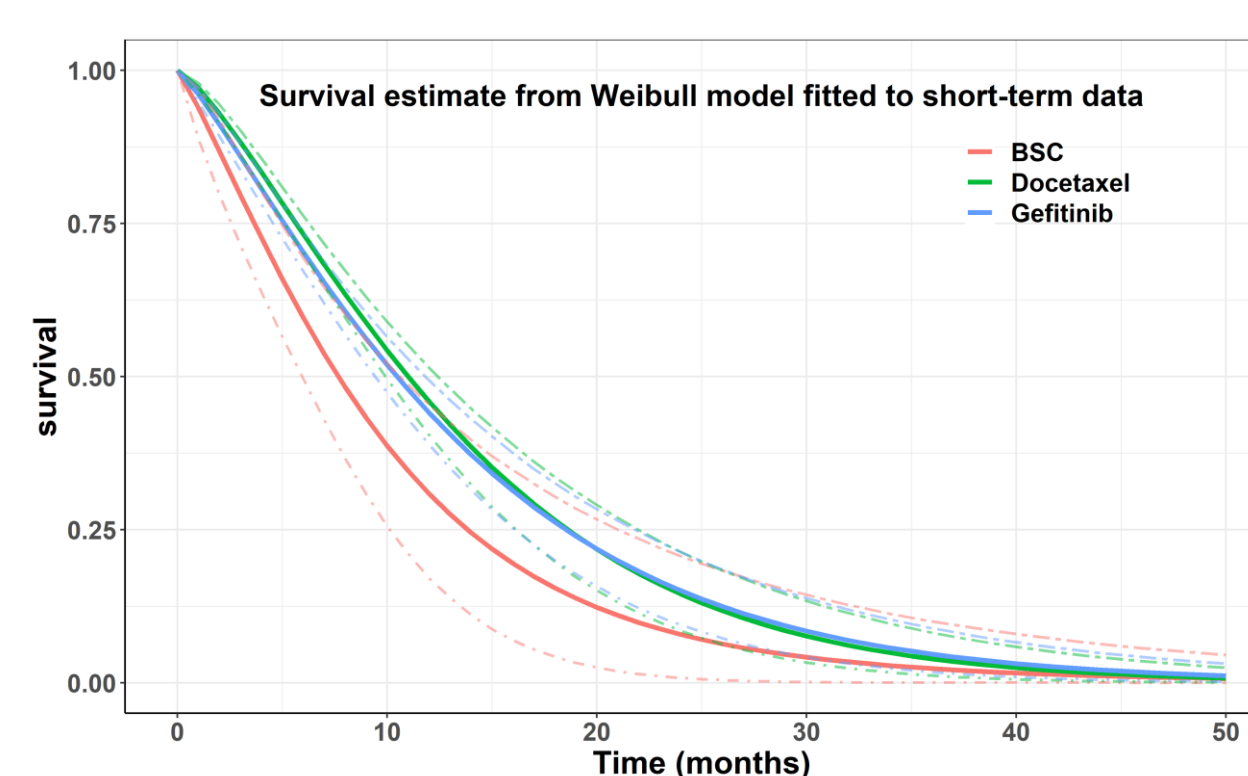
- External data:** Other trials were identified (BSC: 1 study; docetaxel: 2 studies) with relatively longer follow-up until 20 months.
- Expert judgement:** clinical opinion is assumed for arm gefitinib, that 10% of the cohort would be alive beyond 20 months.



## RESULTS

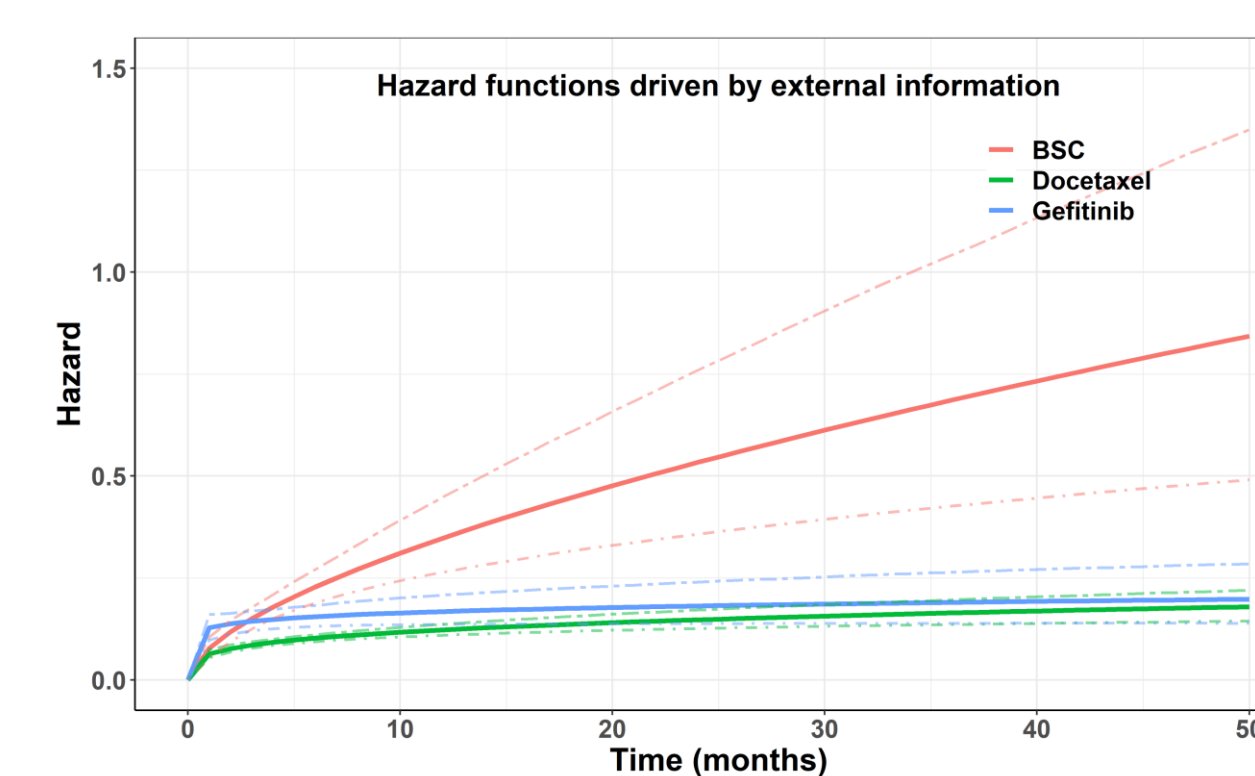
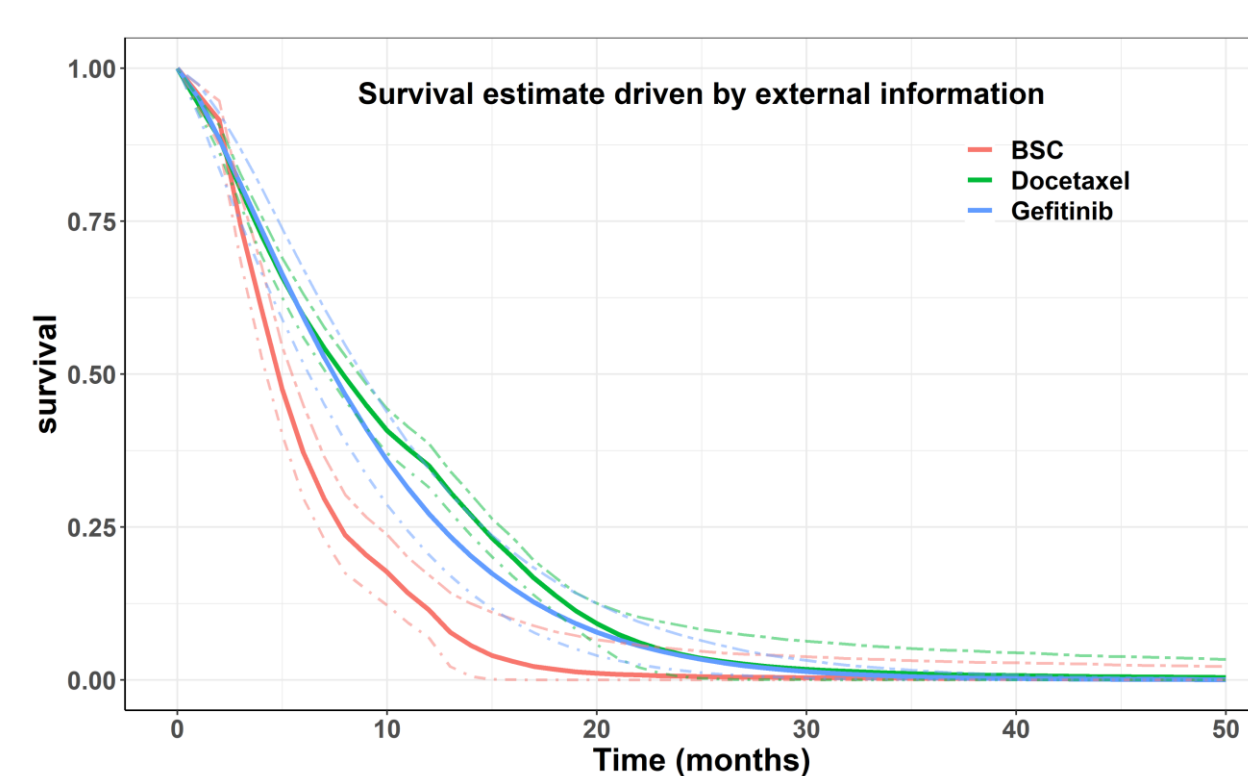
### Observed period: Best fit to the network

There is no restriction to the models used in the NMA, but in this example, the Weibull distribution provides the best fit according to goodness-of-fit criteria.



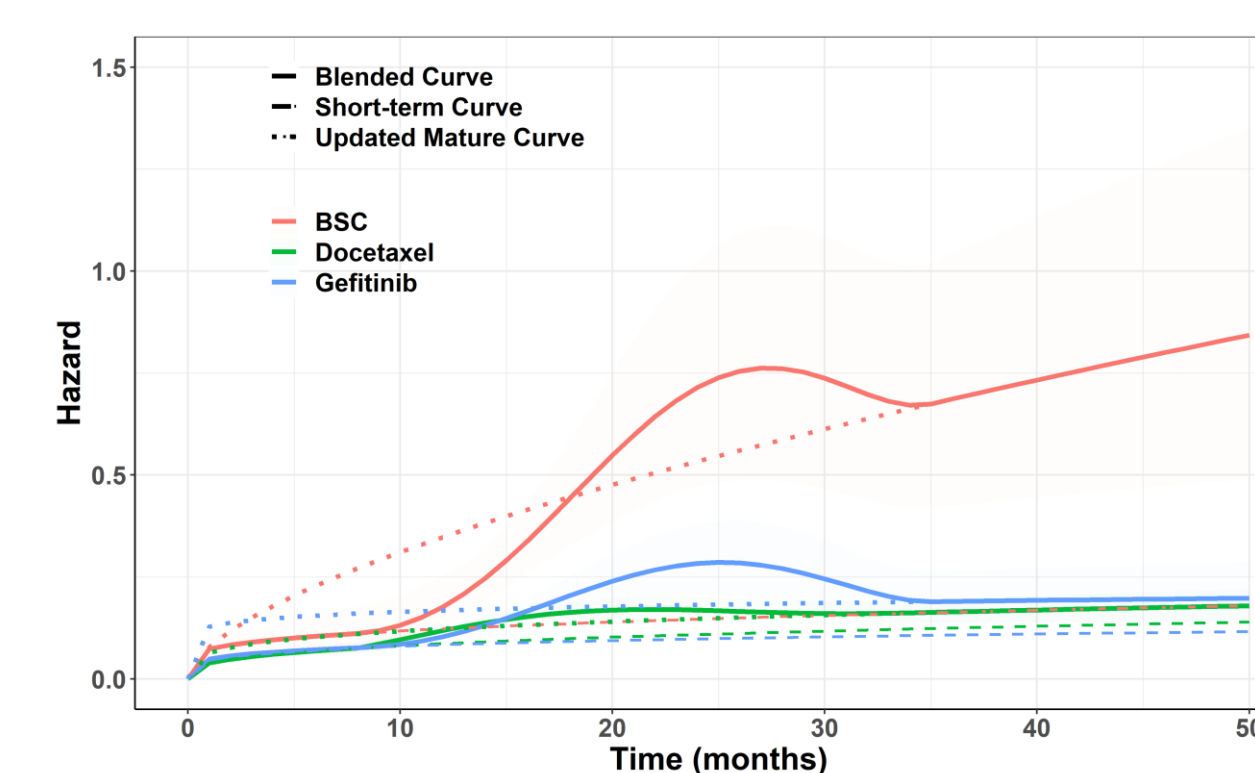
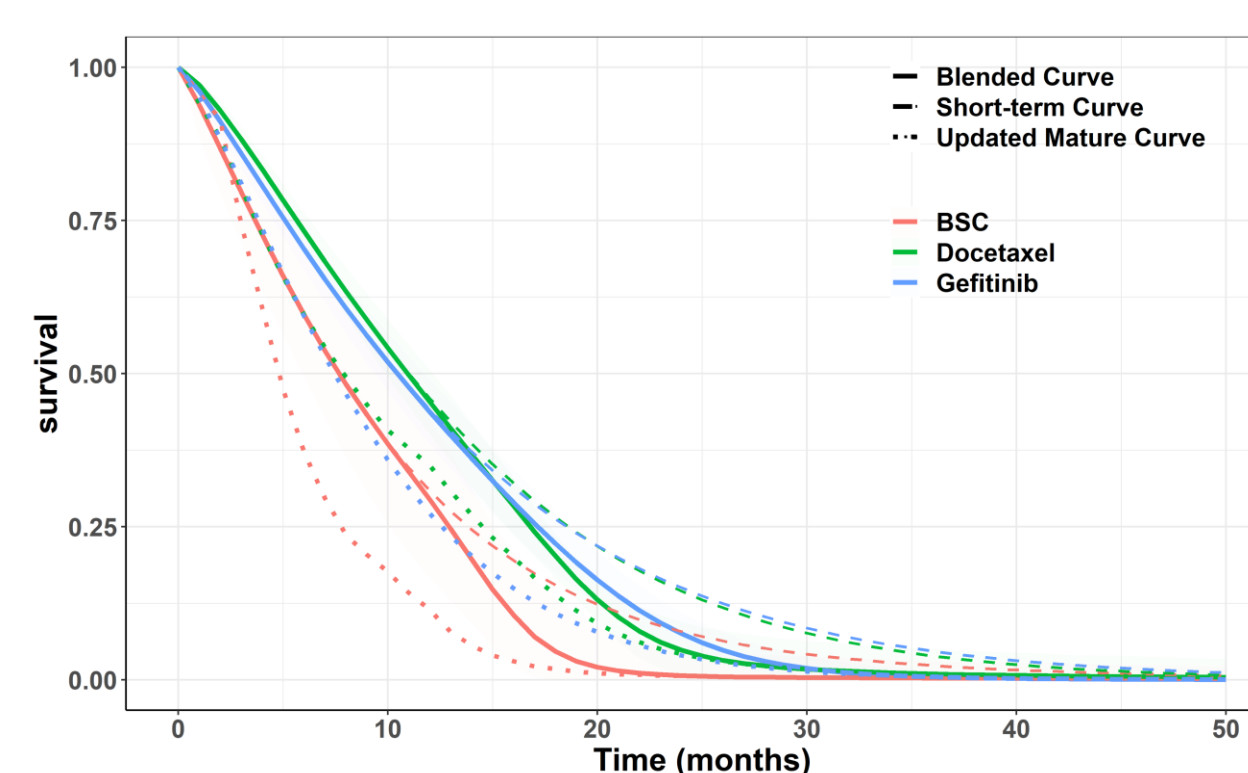
### Extrapolated period: using external evidence

For the arm docetaxel and BSC, a piecewise constant hazard model is fitted to the external reconstructed patient-level data. In terms of gefitinib, we translate the clinical constraints into appropriate estimate of survival.



### Blended curves

The short-term and long-term estimates are blended over time interval ( $a = 8, b = 30$ ) based on the weight function with  $\alpha = \beta = 3$ .



## CONCLUSION

The blended NMA method provides flexibility and allows the extrapolation taking advantage of external knowledge that manufacturers might have in form of hard data or elicited belief. A range of assumptions for treatment effect can be carefully considered.

## REFERENCES

- Che Z, Green N, Baio G. Blended Survival Curves: A New Approach to Extrapolation for Time-to-Event Outcomes from Clinical Trials in Health Technology Assessment. *Medical Decision Making*. 2023; 43(3): 299-310. doi:10.1177/0272989X221134545
- Jansen, J.P. Network meta-analysis of survival data with fractional polynomials. *BMC Med Res Methodol* 11,61(2011). https://doi.org/10.1186/1471-2288-11-61

