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MSR146

A Bayesian framework for network meta-analysis of individual patient data survival outcomes using flexible parametric survival models

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OBJECTIVES

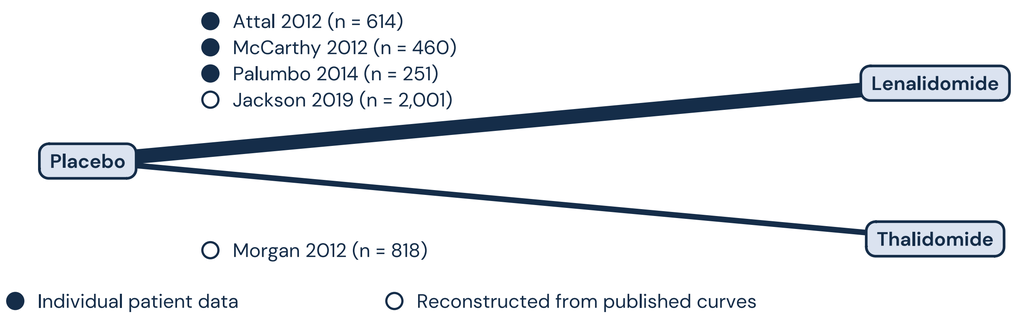
Network meta-analysis (NMA) of individual patient data (IPD) on survival compares several treatments at once, using direct and indirect evidence, with individual-level covariate adjustment and extrapolation beyond follow-up. We propose a Bayesian framework that models the baseline hazard with flexible parametric survival models, on the log cumulative hazard or log hazard scales.

One flexible framework: a Bayesian one-step IPD NMA, with the network entering through the baseline hazards and the treatment contrasts. Each trial has its own baseline level and shape; between-trial heterogeneity is captured by random treatment effects; non-proportional hazards by simple or complex functions of time. The No-U-Turn sampler (NUTS) carries full posterior uncertainty into standardised survival, restricted mean survival time and treatment rankings.

01 · THE NETWORK AND THE DATA

Five trials, three treatments

Maintenance after autologous transplant in newly diagnosed multiple myeloma: lenalidomide or thalidomide against placebo, progression-free survival. **The data are the published worked example, not the trials' original data:** simulated individual data for three trials (McCarthy 2012, Attal 2012, Palumbo 2014) and event times reconstructed from digitised published Kaplan-Meier curves for two (Morgan 2012, Jackson 2019). Thalidomide appears in one trial. No patient covariates are used, because two of the five trials have none at patient level.



4,144 patients and 2,523 events of progression or death in the five trials.

02 · COMPARING MODEL FIT

Building the model up, one term at a time

WHAT THE MODEL ALLOWS	DIC OF EACH FIT (SMALLER IS BETTER)
A level for each trial, constant treatment effects	M-spline **24,997** · Royston-Parmar **24,990**
and a shape for each trial (1 df)	Royston-Parmar **24,912**
and a shape for each trial (2 df)	log hazard **24,910** · Royston-Parmar **24,908**
and a treatment effect that changes over time	Royston-Parmar, the chosen model **24,892** · log hazard **24,892** · Royston-Parmar with random effects **24,892**

R · THE CHOSEN MODEL, AS RUN

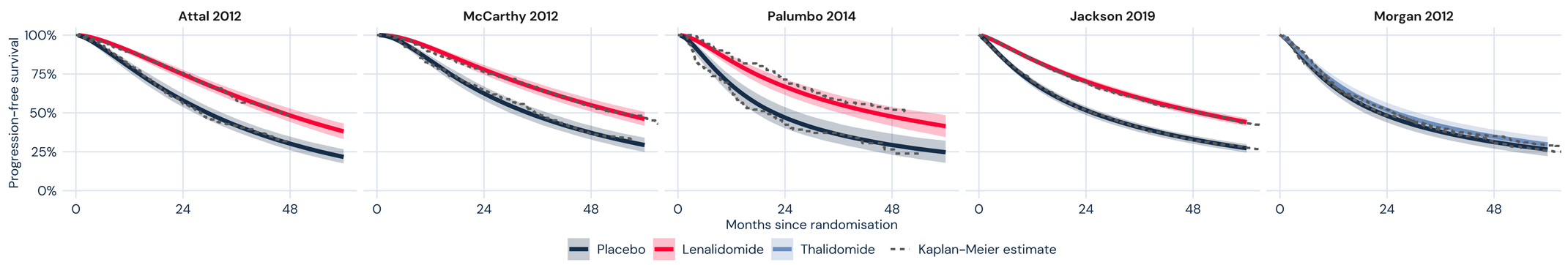
```
fit <- morgana(Surv(time, event) ~ len + thal + tr2 + tr3 + tr4 + tr5,
               data   = ndmm, family = "rp", df = 2,
               tde    = ~ tr2 + tr3 + tr4 + tr5 + len + thal,
               tde_df = c(tr2 = 2, tr3 = 2, tr4 = 2, tr5 = 2, len = 1, thal = 1),
               chains = 4, iter = 1000, warmup = 500, cores = 4, seed = 20261012)
```

The flexible parametric fits: Royston-Parmar, log hazard and M-spline. Each row adds one term to the row above, and every fit is the same command with different arguments. DIC: smaller is better, and a few units is not a meaningful difference. Chosen: the lowest Royston-Parmar DIC, unless another within 5 units has fewer parameters.

MORGANA FOR R · MERLIN FOR R 2.0.0 · DEVELOPMENT VERSIONS

03 · SURVIVAL AT EVERY NODE OF THE NETWORK

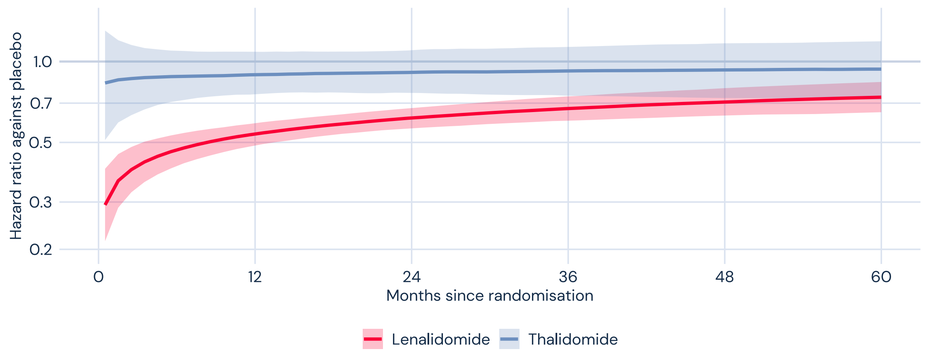
The model over the Kaplan-Meier estimate, by trial and arm



Posterior median and 95% credible band per arm, over the Kaplan-Meier estimate. NUTS, 4 chains of 1,000 iterations (500 warm-up); no divergent transitions; largest R-hat 1.006. MORGANA FOR R · DEVELOPMENT VERSION

04 · TREATMENT EFFECTS

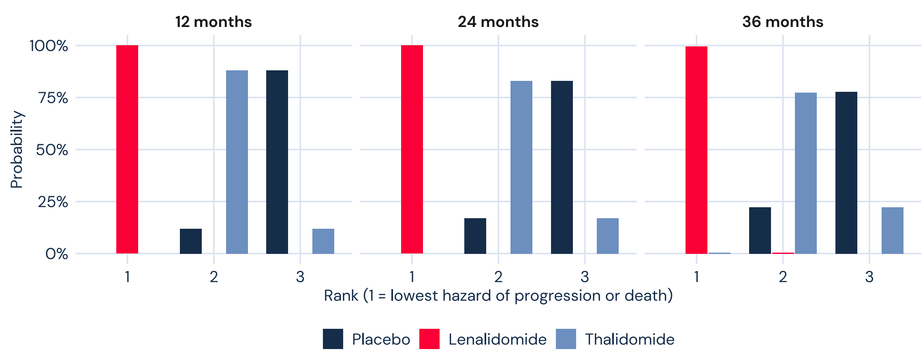
Against placebo, over time



Lenalidomide: hazard ratio 0.53 (0.48 to 0.59) at 12 months, 0.71 (0.63 to 0.80) at 48; 7.21 more progression-free months over 48 (6.14 to 8.29). **Thalidomide**, one trial: 0.89 (0.75 to 1.09) at 12 months. Medians, 95% credible intervals.

05 · RANKINGS

Which treatment is best, and how sure



Rank 1 is the lowest hazard of progression or death at that time, from 1,000 posterior draws. Lenalidomide ranks first in all 1,000 draws at 12 months, and with probability 0.996 at 36; placebo ranks last with 0.881 and 0.778. With three treatments the ranks restate the hazard ratios in 04, so read the two together.

RESULTS AND CONCLUSIONS

- **One flexible framework:** a baseline level and shape for each trial, the treatment contrasts, random treatment effects and effects that change over time all go into one morgana call, on the log cumulative hazard or the log hazard scale.
- **One set of posterior draws:** morgana_standardise() returns standardised survival at every node of the network, hazard ratios over time and restricted mean survival, and the rankings come from the same draws, each with full posterior uncertainty.
- Non-proportional hazards are modelled, not assumed away: lenalidomide's hazard ratio against placebo rises from 0.53 at 12 months to 0.71 at 48. The Royston-Parmar and log hazard models agree closely.
- **The approach gives simultaneous treatment comparison, coherent propagation of uncertainty and clinically interpretable survival predictions. Next steps will include incorporating study-level covariate data.**

SOFTWARE, NOVEMBER 2026

What you can install

COMMAND	STATA	R
merlin	v2.5.0 released · install from reddooranalytics.se/software/merlin/stata · v3.0.0 coming at the end of November	v2.0 development version · built and tested · install from reddooranalytics.se/software/merlin/r
morgana	v1.0.2 released · install from reddooranalytics.se/software/morgana	in development, not yet public

Every result on this poster was run on development versions of morgana and merlin for R. **Try them on your own data:** merlin and morgana for Stata are ready to install, and so is the development version of merlin for R; morgana for R, which fitted this network, is in development. Install lines and what is coming next: reddooranalytics.se/software

Data. The worked example of the R package multinma, version 0.9.1 (Phillippo DM), constructed to resemble the data of Leahy J, Walsh C. Res Synth Methods 2019;10(4):546-568. Trials: Attal M et al. N Engl J Med 2012;366:1782–91. McCarthy PL et al. N Engl J Med 2012;366:1770–81. Palumbo A et al. N Engl J Med 2014;371:895–905. Jackson GH et al. Lancet Oncol 2019;20:57–73. Morgan GJ et al. Blood 2012;119:7–15. M-splines: Phillippo DM, Dias S, Ades AE, Welton NJ. J R Stat Soc A 2026;189:1856–75.



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