A Bayesian model for heterogeneous treatment effects on the additive risk scale in meta-analysis

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Abstract:

Faced with a newly diagnosed patient, clinicians consider which of the available treatments will provide the largest absolute risk reduction. To answer this question requires statistical methods that quantify heterogeneous 'personalized' treatment effects on the clinically relevant scale.

We propose a Bayesian (meta-)regression model for binary outcomes on the additive risk scale. The model was applied in single trial analysis, meta-analysis and network meta-analysis of 20 hepatitis C trials. We compared our model to two other approaches: an alternative additive risk model (Warn et al. (2002)) and a logistic model that transforms predictions back to the natural scale after regression (Chalkou et al. (2020)).

Some trials had cure rates close to 100%, illuminating the main differences. Our model is very sensitive at the boundaries of the risk parameter support [0,1], whereas patients with predicted risks close to 0 or 1 contribute little to posterior precision in the model by Warn et al. In such cases, the logistic model sometimes produced extreme effect estimates, leading to instability in the network setting.

Their respective characteristics make the compared models suitable for different analysis settings. Our proposed model contributes to the statistical methods to model heterogeneous treatment effects on the additive risk scale.

Key words: treatment effect, heterogeneity, trial, risk difference, meta-analysis, Bayesian methods, personalized medicine

References

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