

Network meta-analysis using integrated nested Laplace approximations

Burak Kursad Gunhan ^a

Meta-analysis provides a valuable tool for combining evidence from different trials. A broader type of meta-analysis, network meta-analysis (NMA), is gaining popularity for comparing multiple treatments in a single analysis. From different NMA models that are available, arm-based meta-analysis (a Bayesian hierarchical model) is commonly used. With this modelling framework, datasets with binomial, continuous or time-to-event (survival) endpoints can be modelled, covering a wide range of biomedical applications. Moreover, network meta-regression models can be used to incorporate trial-level covariates to the model. To perform inference within such NMA models, Bayesian inference is commonly used. The standard choice is Markov chain Monte Carlo, which is computationally expensive and requires convergence diagnostics. A deterministic approach to do fully Bayesian inference for latent Gaussian models (LGMs) are integrated nested Laplace approximations (INLA) which is a fast and accurate alternative to MCMC. In this talk, firstly, we show how these NMA models fit in the class of LGMs. Then, we show how NMA models are implemented using INLA and demonstrate that the estimates obtained by INLA are very close to the ones from MCMC. Specifically, we emphasize the design-by-treatment interaction model with random inconsistency parameters (Jackson model) and network meta-regression models. A publicly available R package, `nmainla`, is under development to automate the INLA implementation of models which are considered in this talk. Two applications illustrate the use of INLA for a NMA.

References

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^aDepartment of Medical Statistics, University Medical Center Goettingen, Goettingen, Germany