

Automating network meta-analysis

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Our research project aims at enabling quantitative benefit-risk decision analysis for medicines, based on the available clinical trials. We would argue that network meta-analysis is the most suitable evidence synthesis method to underpin such analyses. However, applying network meta-analysis entails a model specification problem that requires expert knowledge, beyond what is required in interpreting the results.

After a short discussion of this context, the talk will focus on how the manual model specification can be automated. To achieve this, the problem of specifying the structure of the Bayesian hierarchical model is formulated in a graph theoretic framework. Standard algorithms can then be applied to provide a solution. Heuristics are used to provide initial values and uninformative priors.

The methods have been implemented in (1) a stand-alone tool to generate BUGS/JAGS models, (2) an R-package that can generate and estimate a network meta-analysis without human intervention, and (3) the ADDIS software for storing and analysing clinical trials results.