

Automated generation of node-split models for the assessment of inconsistency in mixed treatment comparisons

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Abstract

Mixed Treatment Comparison (MTC) is an important family of meta-analytic methods that enable the simultaneous synthesis of a network of clinical trials comparing any number of treatments. The key assumption underlying MTC is that of consistency across treatment comparisons in the network. Several methods to detect inconsistency have been proposed, in particular ‘node-splitting’ which compares the estimate from direct evidence on a comparison with the estimate from the network of indirect evidence on that comparison. MTCs are usually implemented using general purpose Markov Chain Monte Carlo (MCMC) software such as BUGS or JAGS. This often means that a new model has to be written for each new analysis, or that the data have to be reorganized. This becomes tedious for node-splitting models, because a separate model has to be written for each potentially inconsistent comparison. In addition, one has to determine which comparisons are potentially inconsistent, which is difficult in the presence of multi-arm trials. Algorithms have been developed to automatically generate consistency models, but not node-splitting models. We present how node-splitting models can be generated automatically, including how to determine which nodes should be split. This also raises some interesting issues regarding the interpretation of inconsistency and heterogeneity, and how the node-split model relates to the consistency model when multi-arm trials are present.