A Likelihood Ratio Test For The Homogeneity of Between-Study Variance in Network Meta-Analysis

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Methodology

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Abstract

Background: Network meta-analysis (NMA) is a statistical method used to combine results from several clinical trials and simultaneously compare multiple treatments using direct and indirect evidence. Statistical heterogeneity is a characteristic describing the variability in the intervention effects being evaluated in the different studies in network meta-analysis. One approach to dealing with statistical heterogeneity is to perform a random effects network meta-analysis that incorporates a between-study variance into the statistical model. A common assumption in the random effects model for network meta-analysis is the homogeneity of between-study variance across all interventions. However, there are applications of NMA where the single between-study assumption is potentially incorrect and instead the model should incorporate more than one between-study variances.

Methods: In this paper, we develop an approach to testing the homogeneity of between-study variance assumption based on a likelihood ratio test. A simulation study was conducted to assess the type I error and power of the proposed test. This method is then applied to a network meta-analysis of antibiotic treatments for Bovine respiratory disease (BRD).

Results: The type I error rate was well controlled in the Monte Carlo simulation. The homogeneous between-study variance assumption is unrealistic both statistically and practically in the network meta-analysis BRD. The point estimate and conffdence interval of relative effect sizes are strongly inuenced by this assumption.

Conclusions: Since homogeneous between-study variance assumption is a strong assumption, it is crucial to test the validity of this assumption before conducting a network meta-analysis. Here we propose and validate a method for testing this single between-study variance assumption which is widely used for many NMA.

Full Text

This preprint is available for download as a PDF.

Figures

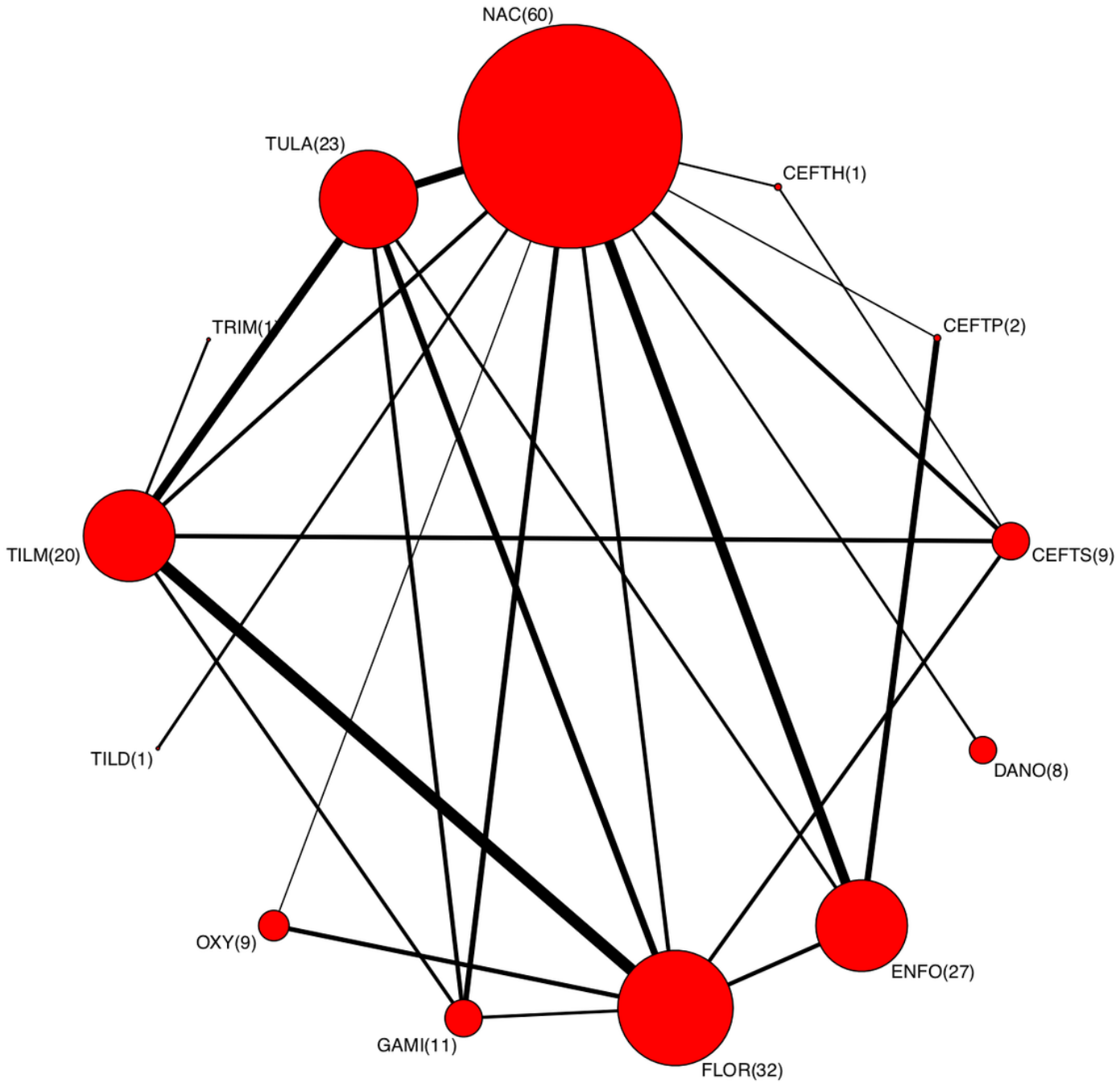

Figure 1

The network plot is shown in Figure 1. The size of the node is proportional to the number of arms and the thickness of the edges represents the total size of direct comparisons between each treatment pair. The number in the parentheses after a treatment abbreviation is the number of studies containing that treatment. The absence of a line means that there is no direct comparison in the evidence network.

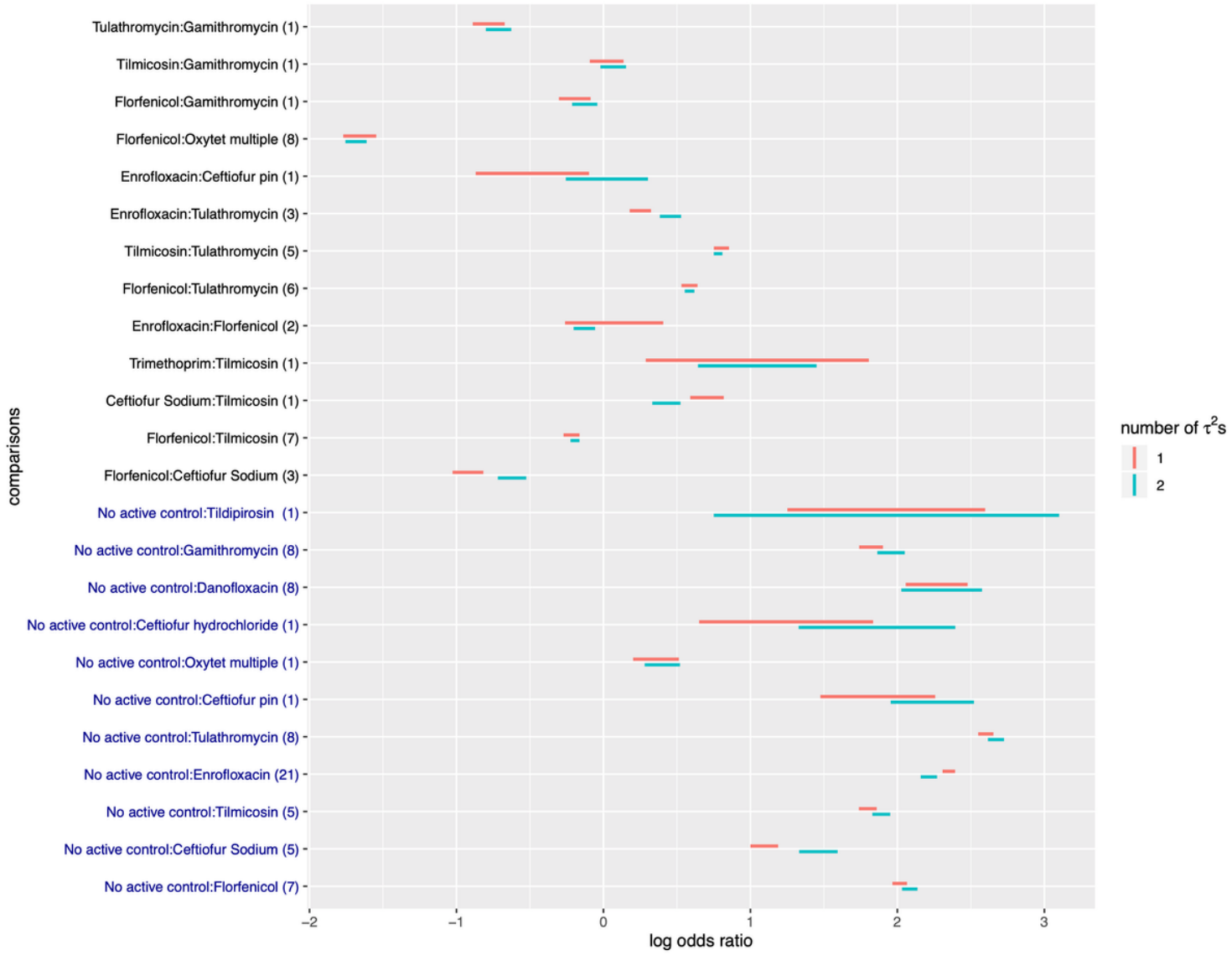

Figure 2

The effect of models with different heterogeneity parameters on the point estimates and confidence intervals of the relative effect sizes, are presented in Figure 2.