Reviewer's report

Title: Network-meta analysis made easy: Detection of inconsistency using factorial analysis of variance models

Version: 2

Date: 12 March 2014

Reviewer: Guobing Lu

Reviewer's report:

This is an interesting paper, although I do not agree with the author that the paper provides an easier way for assessing inconsistency in network meta-analysis (NMA).

I am particularly interested in the innovative idea behind models (3) and (4): by introducing the new factors Dk to the modelling, the effect of design k can be detached from the effects of the rest designs, and thus the potential inconsistency can be located on single designs. I also like the concise writing style of the paper: by using the symbolic description of factorial models, the main ideas and methods are represented clearly and concisely with lots of unnecessary details omitted.

Minor Essential Revisions

1. P6, in the middle part of the first paragraph:
   “…… then designs 5 and 13 …..” should be “designs 6 and 13”?

Discretionary Revisions:

1. P4: Before model (2b), I would like to suggest adding formula G/S=G+G.S for a simple factorial model to help readers understand how the nesting operator “/” works.

2. P6, section “using influence diagnostics”:
   You found that the results based on PRESS residuals were in agreement with the tests in Table 5. This is, I think, a natural consequence, because in essence the Dk factor acts as a “deleting one” operation that separates the effect of the kth design from the rest, which is exactly the effect of PRESS residuals.

3. P8, section of Conclusion: “We think that the ANOVA approach has some practical advantages. Interpretation of results is facilitated by the focus on t treatment means rather than on t(t-1)/2 pairwise contrasts…….”

I do not think that the shift of focus on treatment arms is an advantage of the ANOVA approach over the methods based on treatment contrast. Firstly note that, in the Bayesian hierarchical modelling for NMA commonly used in practice today, the multiple treatment effects are actually described by (t-1) properly chosen basic contrast parameters (that form a spanning tree of the network),
rather than the total $t(t-1)/2$ pairwise contrasts, and the rest treatment contrasts are treated as the functional parameters that can be evaluated automatically from the estimation process.

Secondly, in many applications, one may be more interested in the pooled estimate of a relative effect of one treatment to another and the corresponding SD, rather than the “absolute” effect of a single treatment. But the ANOVA approach in this paper does not provide such estimates (particularly the estimated SD), which in this sense is a limitation of this method.

Therefore, to me, the ANOVA approach provides an alternative way for NMA, which may throw a new light on the NMA, and may be more appealing to those who are familiar with ANOVA but not so familiar with Bayesian software, e.g., WinBUGS.

**Level of interest:** An article of outstanding merit and interest in its field

**Quality of written English:** Acceptable

**Statistical review:** Yes, and I have assessed the statistics in my report.

**Declaration of competing interests:**

I declare that I have no competing interests