

Ottawa Hospital Research Institute Institut de recherche de l'Hôpital d'Ottawa

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Dear Editor

Brian Hutton, MSc, PhD

Assistant Professor, Ottawa University Dept. of Epidemiology and Community Medicine

Associate Scientist Knowledge Synthesis Group Clinical Epidemiology Program

☎ 613- 737- 8899
(73842)
№ 613- 739- 6938
≦ bhutton@ohri.ca

Dr. Niloy Datta has recently approached me in relation to his submitted manuscript '*Hyperthermia and radiotherapy with or without chemotherapy in locally advanced cervical cancer: A systematic review with conventional and network metaanalyses*', which has been submitted to your journal. He indicated that it would be of help to the article's consideration for publication to receive a letter of support from me regarding the use of NMA in this report because the journal is not familiar with this technique. I am happy to provide such a letter.

Since 2008, the use of network meta-analysis as an analytic framework has increased dramatically in he context of systematic reviews because of the common need to draw comparisons between not just two interventions, but multiple interventions and with the use of both direct and indirect information from randomized trials. Dr. Datta approached me via email in 2015 for additional clarity on the aspects of using a software tool which I helped to create in 2014 called NetMetaXL. This is an excel-based tool that can be used in the process of conucting Bayesian network meta-analyses; while WinBugs software is commonly used for this purpose, its interface is imposing or non-expert users. NetMetaXL was created to make bayesian NMA more accessible for researchers, and is a freely available tool which was described and published in an aopen access journal which can be found at the following link: (http://systematicreviewsjournal.biomedcentral.com/articles/10.1186/2046-4053-3-110).

I am happy to confirm that NetMetaXL employs the same model for binary endpoints which is described the National Institute Clinical Excellence's Technical Support by or Document (http://www.nicedsu.org.uk/evidence-synthesis-tsd-series(2391675).htm), and thus can be considered robust. We had one of the experts involved in the preparation of that documentation peer review our tool as well to ensure its statistical content matched well. NetMetaXL also auotmates preparation of figures from NMAs including network diagrams, league tables and rankograms, making it relatively simple to include accurate summaries rom analyses. Dr. Datta and colleagues also appear to have reported model fit statistics, a key feature for bayesian NMAs, and model fit appears reasonable in their analyses based on the available findings.

I hope this letter helps to shed insight and provide clarity regarding network meta-analysis and the methods used for Dr. Datta's paper. Regarding peer review, aside from the statistics, the points which reviewers would usually be asked to watch for are aspects of clinical and methodologic heterogeneity, watching to ensure that it is sensible and appropriate for the available studies to be combined statistically (i.e. ensuring no outliers present and that study populations and study methods are comparable across included trials). This is analogous to what reviewers should always look for in a 'traditional' (i.e. comparing 2 treatments) meta-analysis, and thus should be more familiar to reviewers than the statistical aspect. As I am not a clinician and do not know the trials in this review, I cannot comment on this aspect of Dr. Datta's review, and I leave to the journal's expert reviewers to assess in their rounds of assessment of the manuscript.

Best wishes,

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Dr. Brian Hutton, MSc, PhD

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