Implementation of Contrast-Based and Shared Parameter Models in BUGSnet, an R Package for Conducting Bayesian Network Meta-Analysis

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COVALENCE RESEARCH

OBJECTIVES

BUGSnet is a published, open-source R package to facilitate the execution of network meta-analyses (NMAs) and generation of outputs that satisfy the statistical elements of prominent best-practice NMA guidelines and checklists, including the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) checklist, the ISPOR-AMCP-NPC guidelines, and National Institute for Health and Care Excellence (NICE) Decision Support Unit (DSU) Technical Support Document (TSD) 2.[1,2,3,4]

The first version of BUGSnet lacked support for contrast-based or shared parameter models (i.e. models including both contrast and arm-based data). The aim of the present project was to implement support for such models.

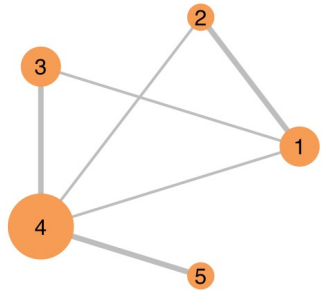
METHODS

BUGSnet was expanded to support contrast-based and shared parameter models by adding two new functions to the R package, `nma.model.contrast` and `nma.model.shared`, with each function generating the corresponding Just Another Gibbs Sampler (JAGS) code to run the analyses. The original `nma.model` function was retained for backwards compatibility with existing BUGSnet scripts.

Contrast-based analyses are specified using "NA" for the first or "reference" arm of each trial and odds or hazard ratios or mean differences for all other arms. Results from contrast-based and shared parameter analyses were validated against previous analyses of interventions for Parkinson's disease conducted by the NICE DSU.

The Parkinson's disease analysis captures differences in "off-time" reduction (where off-time is when motor and/or non-motor symptoms of Parkinson's occur between medication doses). The analysis relies on these differences between the intervention and control arms for each trial and their standard errors,

Figure 1 Evidence network rendered using the BUGSnet `net.plot` function and source data for the Parkinson's analysis



study	treatment	differences	se.diffs	var.arm1
1	1	NA	NA	NA
1	3	-0.31	0.6681	NA
2	1	NA	NA	NA
2	2	-1.70	0.3826	NA
3	1	NA	NA	0.2547
3	2	-2.30	0.7177	NA
3	4	-0.90	0.6950	NA
4	3	NA	NA	NA
4	4	-0.35	0.4419	NA
5	3	NA	NA	NA
5	4	0.55	0.5551	NA
6	4	NA	NA	NA
6	5	-0.30	0.2742	NA
7	4	NA	NA	NA
7	5	-0.30	0.3201	NA

The Parkinson's disease analysis includes a three-arm trial, which requires an additional data column to specify the variance of the response in arm 1; this column has the variance in the row corresponding to the first arm and "NAs" elsewhere (Figure 1).

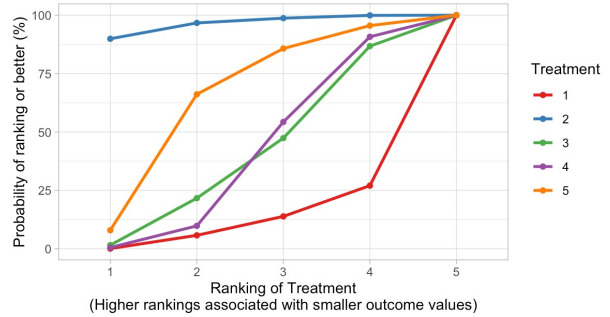
When contrast-based summary data are used, the Normal distribution is used with the identity link for all types of contrast data. BUGSnet supports the use of the following contrast-based measures: log odds ratios, mean differences, log hazard ratios, and risk differences. In the Parkinson's disease dataset, the data are expressed as mean differences.

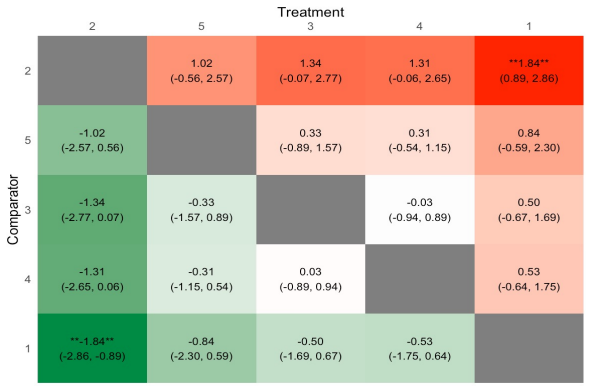
The `nma.model.contrast` function creates BUGS code for contrast-based data that is subsequently input into `nma.run()` and analysed using JAGS. A reference parameter indicates the name or identifier of the treatment that will be seen as the "referent" comparator (commonly placebo) and corresponds to the treatment labelled as 1. The `scale` parameter is used to specify what the scale of the contrasts is, for example, `Log-odds ratio` or `Mean difference`. The parameter is used to label outputs in the subsequent plotting functions such as `nma.forest`.

RESULTS

BUGSnet version 1.1.0 now includes support for conducting contrast-based and shared parameter NMAs. The results of analyses conducted using the new contrast-based and shared parameter models closely matched those conducted by the NICE DSU in TSD 2 (Figure 2).

Figure 2 Surface under the cumulative ranking curve (SUCRA) plot and league heat plot from the Parkinson's disease network meta-analysis using contrast data from 2- and 3-arm trials





DISCUSSION

The present project addressed one of the most notable limitations of the first version of BUGSnet, thereby broadening the range of applications to include synthesizing evidence from trials reporting contrast and/or arm-based data.

Additional work on BUGSnet is ongoing, including expanding the unit test coverage of the codebase, improving JAGS error reporting, and transitioning the generation of plots still using base R graphics to use the ggplot2 data visualization package.

The alignment of BUGSnet outputs with the requirements of best-practice NMA guidelines from multiple prominent healthcare stakeholders makes the package a compelling tool for conducting NMAs suitable for inclusion in peer-reviewed publications or health technology appraisal processes.

REFERENCES

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