Objectives

- Network meta-analysis (NMA) of clinical trial outcomes is usually based on Bayesian statistics and hence requires software for Monte Carlo Markov chain (MCMC) sampling.
- The most common choice of software for NMA is currently WinBUGS, in part because there is a large body of WinBUGS code for NMA in the literature.
- However, WinBUGS can be slow and difficult to use – the error messages are often unclear and the language does not allow for vector operations or if/then statements.
- This project aimed to identify and evaluate alternatives to WinBUGS for use in Bayesian network meta-analysis.
- Specifically we were interested in software that was suitable for applied statistical analysis in the setting of a clinical consultancy.

Methods

- We identified candidate alternatives for evaluation via journal articles and websites.
- We performed an evaluation of the candidates against a set of criteria:
  - ease of use,
  - flexibility,
  - speed,
  - ability to handle large datasets,
  - availability of documentation,
  - publication quality graphics (in the system or ease of linking with an external program such as R)
  - cost and
  - compatibility with Windows.
- We performed a validation of the top-ranked choice by replicating a set of WinBUGS examples found in the NICE Decision Support Unit Technical Support Documents [1].

Results: Software evaluation

- Nine candidate software packages were found.
- JAGS, PyMC and Stan were identified as potential alternatives to WinBUGS.
- Of these three options we felt that Stan was the best alternative for us because:
  - It uses the latest available MCMC methodology: Hamiltonian Monte Carlo (HMC) and no-U-Turn samplers.
  - It has a flexible modelling language, including individual arm data, random effects.
  - It provides useful error messages.
  - It is being actively developed and updated.
  - It is clearly documented with a 500+ page manual.
  - It integrates with R for producing publication quality graphics.

- We carried out the validation by replicating a set of WinBUGS examples found in the NICE Decision Support Unit Technical Support Documents [1].

Conclusions

- The use of NMA has grown rapidly in recent years, and more complex models are becoming increasingly common.
- WinBUGS is currently the most common choice of software for Bayesian NMA models, and whilst it is satisfactory, it can be difficult to use.
- We found Stan, an open source program for MCMC sampling, to be the best alternative to WinBUGS for our NMA work.
- Stan provides an excellent balance of model flexibility, allowing for manual user specification, and is easily integrated with R for producing publication quality graphics.
- We found it straightforward to learn because it is accompanied by an extensive user manual and provides helpful error messages.
- We recommend that NMA practitioners should consider Stan as an alternative to WinBUGS.

Future work

- We plan to extend the validation exercise to cover more of the examples from the NICE Decision Support Unit Technical Support Documents [1].
- We also plan to investigate the comparative performance of WinBUGS and Stan on some NMA models that are known to have poor convergence.

Acknowledgements

This research project was funded by Quantics.

References


About the authors

Quantics provides expert statistical support for health technology assessment. Our areas of expertise include meta-analysis, network meta-analysis and survival analysis.

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Quantics has a strategic partnership with the Department of Mathematics and Statistics at the University of Guelph. This partnership helps us to fulfill our research and development goals and provides students with the opportunity to work with a leading statistical consultancy. Matthew is currently studying for his Ph.D. in statistics. www.uguelph.ca