Comparison of Bayesian Network Meta-Analyses in WinBUGS and SAS Frameworks for Binomial Models

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BACKGROUND

- Typically, network meta-analyses (NMAs) are conducted using the Bayesian software programs WinBUGS or Open BUGS.
- Introduced with SAS 9.2, the Monte-Carlo Markov-Chain (MCMC) procedure performs Bayesian analyses using the Metropolis-Hasting sampler.
- Despite being the primary statistical analysis package used in the pharmaceutical industry, SAS is rarely considered for performing NMAs.

OBJECTIVE

- The objective of this study was to perform Bayesian NMAs using WinBUGS and SAS and to investigate whether SAS represents a viable alternative to conduct NMAs for binomial models in a variety of treatment networks.

METHODS

- Literature was searched to identify articles containing datasets suitable for meta-analysis of binomial outcomes.
- Four networks of various complexity were built: head-to-head comparison,[1] closed-loop network,[2] star-shaped network,[3] and mixed-treatment comparison network[4] (Figure 1).
- WinBUGS meta-analyses were based on the code from Lu and Ades.[5] In each model run, there was a burn-in of 20,000 iterations, followed by 250,000 additional iterations. Thinning was set to 50 to reduce autocorrelations.
- SAS analyses used the MCMC procedure and were conducted in SAS v9.4. An initial 20,000 iterations were run as burn-in, completed by 2,000,000 simulations. (SAS requires more MCMC draws to achieve convergence.) Thinning was set to 100 to reduce autocorrelations.
- Comparison of results between the two software programs focused on the log-odds ratio (OR) of treatment versus control comparator (mean log-OR and 95% credible intervals [CrIs]).
- SAS computes two different CrIs by default: equal-tail and high posterior density (HPD). Equal-tail CrIs are reported. Significant differences with HPD are mentioned.

RESULTS

- Results showed strong consistency between SAS and WinBUGS estimates (Table 1, Figure 2, and Figure 3).
- Differences between mean log-OR estimates ranged from 0 to 0.074. Differences with the CrIs ranged from 0 to 0.217.
- Compared with the random-effect (RE) model, estimates from the fixed-effect (FE) model were more consistent between statistical packages.
- Discrepancies between the two softwares' results increase with the network's complexity and as the number of articles per comparison diminishes.
- For two comparisons, HPD intervals from SAS led to different conclusions than WinBUGS.
  - Star-shaped network: SAS HPD 95% CrI (–0.016 to 7.055) versus WinBUGS 95% CrI (0.372-7.391) (Figure 2, ETN)
  - Mixed-treatment comparison: SAS HPD 95% CrI (0.036-4.432) versus WinBUGS 95% CrI (–0.015 to 4.419) (Figure 3, MTX + SSZ + HCQ)

CONCLUSIONS

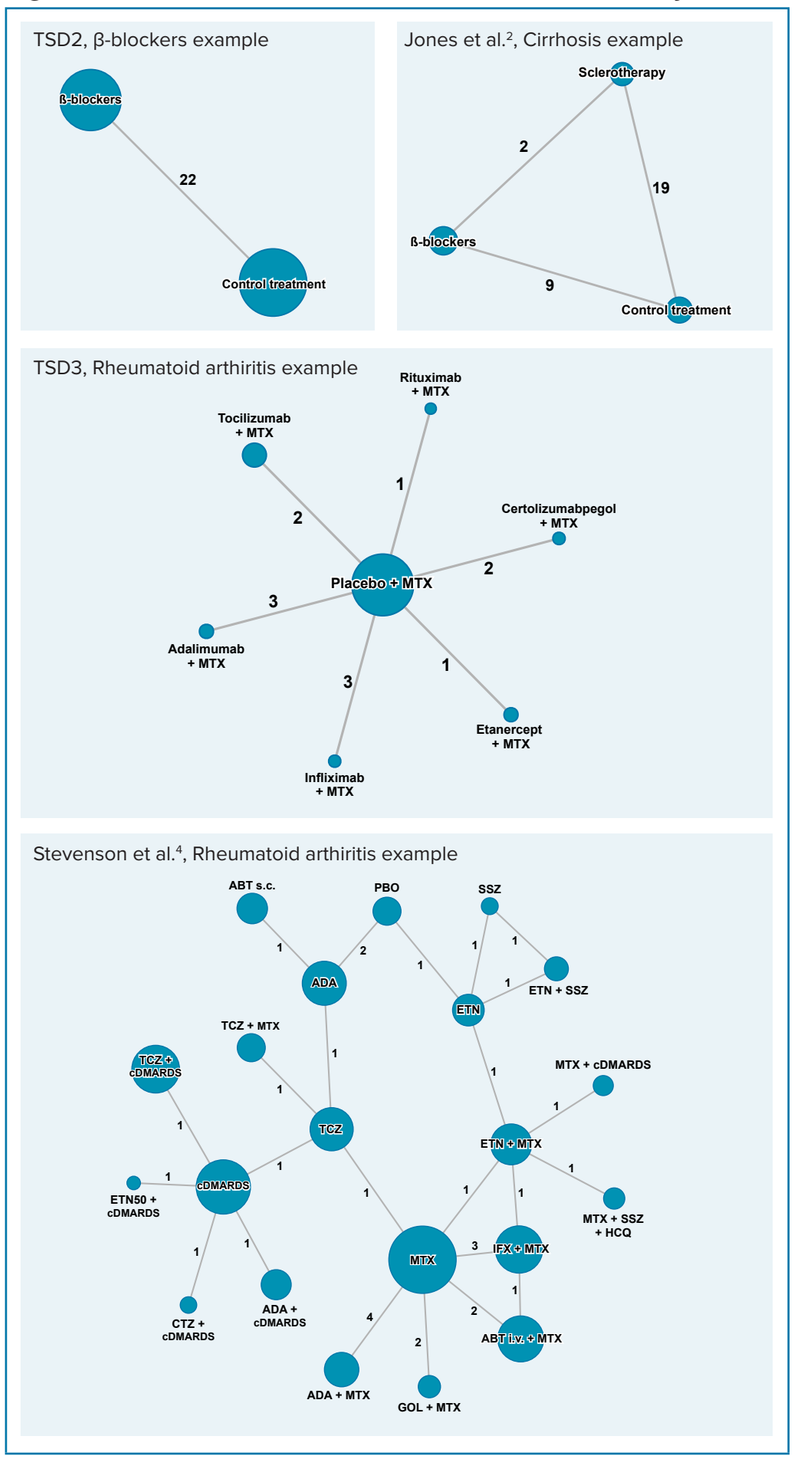
- Our results conducted on binomial outcomes show strong agreement between SAS and WinBUGS, despite the use of a different sampler. RE analyses produce larger discrepancies between the two software programs.
- When using SAS, attention needs to be given to which CrI to consider (equal-tail or HPD). With more sophisticated networks, HPD CrIs produced different conclusions than WinBUGS.
- Historical use of WinBUGS for NMAs has resulted in a preference for this software program by health technology assessment agencies. However, SAS is a valid alternative for certain types of NMAs and constitutes a potential means to validate WinBUGS results.

Table 1. Mean Log-OR and CrI Estimates for Head-to-Head and Closed-Loop Networks

		SAS—PROC MCMC		WinBUGS	
		Mean	CrI 95%[a]	Mean	CrI 95%
Head-to-head comparison					
FE model	Control vs. β-blockers	–0.261	–0.360 to –0.164	–0.262	–0.360 to –0.163
RE model	Control vs. β-blockers	–0.249	–0.374 to –0.117	–0.248	–0.374 to –0.116
Closed-loop model					
FE model	Control vs. sclerotherapy	–0.560	–0.784 to –0.340	–0.560	–0.783 to –0.339
	Control vs. β-blockers	–0.678	–0.997 to –0.364	–0.678	–0.998 to –0.366
	Sclerotherapy vs. β-blockers	–0.118	–0.494 to 0.259	–0.118	–0.490 to 0.254
RE model	Control vs. sclerotherapy	–0.601	–1.239 to 0.031	–0.626	–1.271 to 0.014
	Control vs. β-blockers	–0.792	–1.704 to 0.103	–0.728	–1.666 to 0.197
	Sclerotherapy vs. β-blockers	–0.174	–1.241 to 0.880	–0.101	–1.237 to 1.032

[a] Equal-tail CrI.

Figure 1. Networks of Evidence for the Conducted Analyses



ABT i.v. = intravenous abatacept; ABT s.c. = subcutaneous abatacept; ADA = adalimumab; cDMARDs = conventional disease-modifying anti-rheumatic drugs; CTZ = certolizumab; ETN = etanercept; ETN50 = etanercept 50 mg; GOL = golimumab; HCQ = hydroxichloroquine; IFX = infliximab; MTX = methotrexate; PBO = placebo; SSZ = sulfasalazine; TCZ = tocilizumab.

Figure 2. Forest Plots for SAS and WinBUGS Results for Star-Shaped Network—TSD3, Rheumatoid Arthritis Example

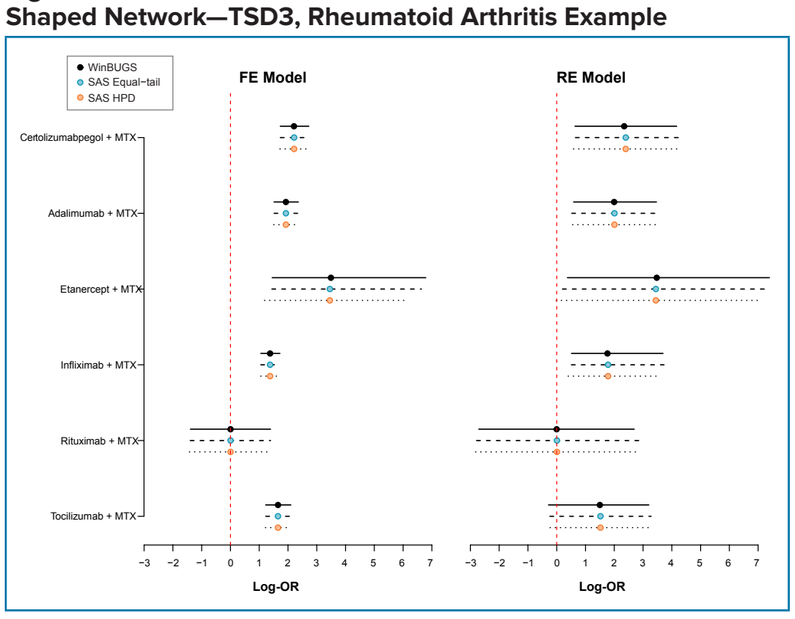
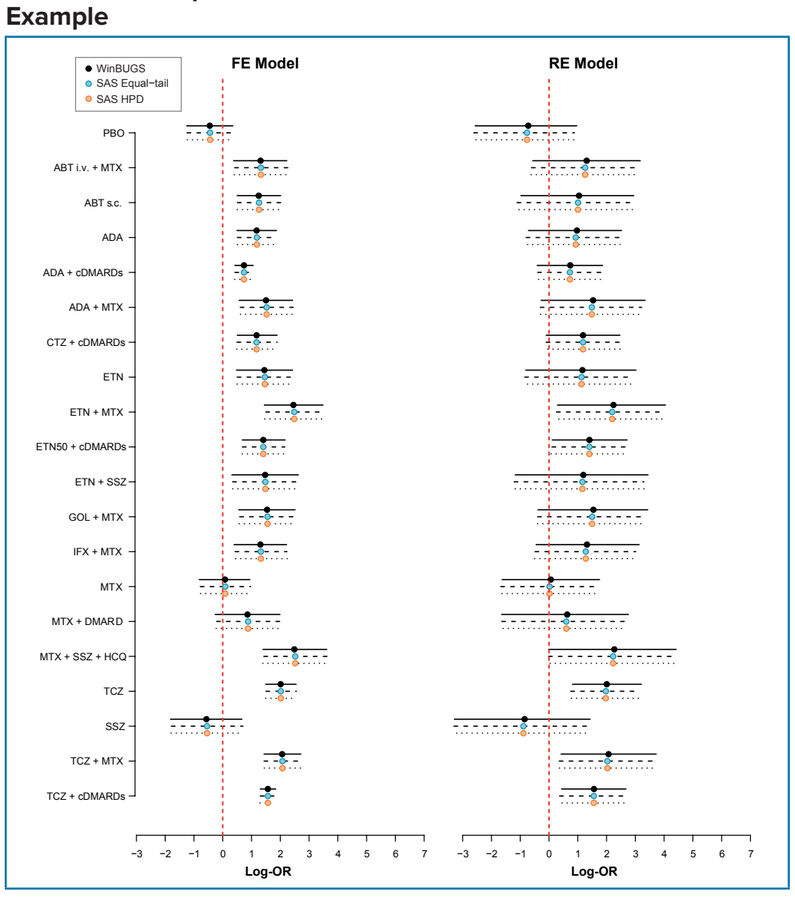


Figure 3. Forest Plots for SAS and WinBUGS Results for Mixed-Treatment Comparison—Stevenson et al.[4], Rheumatoid Arthritis Example



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