London School of Hygiene & Tropical Medicine

ASSESSMENT FEEDBACK
2017 - 2018

<u>1st Marker only</u>: Please put your comments on this sheet which will be returned to the student together with their assessment grade.
Please do not write the grade on this sheet.

LSHTM Candidate No	**109963**	**Module Code**	**2463**

Summary of the main characteristics of the work *(strengths and weaknesses) plus* ***specific comments*** *(illustrated with reference to the student's work; comments may refer to the work's content, structure, use of literature, understanding, rigour of argument, presentation etc). Be sure to include an* ***Explanation of the grade given*** *(refer to grade criteria, explain why it is not better) and* ***how the work might have been improved***

Congratulations on producing an exceptional report, with well chosen tables and plots, and attention to detail. You have obviously put much thought and effort into this assignment, and demonstrate excellent understanding of the principles of Bayesian analysis. The DMC is fortunate to have an exceedingly competent Bayesian statistician assigned to this trial, and pass on their thanks for such a comprehensive and clear report!

In particular, I appreciated the concise description and interpretation of the results, that avoided repetition of the tabulated numbers. Figure 2 is a helpful addition – a more sophisticated version of this plot can be created using 'density strips', which are implemented in OpenBUGS and an R package (google Chris Jackson, density strips for more information if you are interested).

The main omission is an explanation of why the ORs calculated in the first three models can be considered equivalent and therefore used for linking sub-models directly or through informative priors.

A few other minor quibbles as follow:

- You mention missing values in your introduction, but your data is complete (unless you count the lack of covariates, details of adverse events …).
- Strictly speaking, each trial does not give equal weighting to the results – patients from each trial are given equal weighting, so each trial is weighted by size.
- In your methods section, you could mention that no adjustment is made for covariates – although you picked up on this in your discussion.
- Your models are very precisely defined in the technical appendix, but for completeness you should say that you are parameterising the normal distribution in terms of the mean and variance throughout.
- In Appendix A2, bullet point on assessment of convergence – reaching stability does not mean 'the Markov chain contains sufficient information for reliable inferences', rather subsequent iterations can be used for valid inference. Whether these have sufficient information to be reliable depends on the number of iterations and the level of autocorrelation.