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Introduction

The data consist of randomized trials before 1980 of corticosteroid therapy in premature labor and its effects on neonatal death. This experiment was done at 7 different locations or clinics(trials). Each trial consists of a treatment group and control group. Within each group the total count of patients was recorded along with the corresponding mortality for each group(events). The goal of my experiment is to first consult an authoritative source for an appropriate Bayesian meta-analysis method to model this data. Defend the use of this method. Simulate type 1 errors based on the chosen method. Finally, apply chosen method to the data and summarize findings.

Methods

The therapy effects would vary across the 7 trials. If we assume that that each trial was carried out in different medical centers within different locations. The researchers might want to deploy their study on females of different child bearing ages within different environmental conditions, either rural or urban. Where some trails might have a higher population of one group over the other group. For example,Block trial might be conducted in a location where most of the females might be in their early 20-30 group while in another location like Auckland, females might be in their 35 -45 age group.

Based on my assumptions the data for each trial is independent of the order in which they were carried out over the population of interest and can be considered exchangeable. This exchangeability points to the effects of the therapy from each trial coming from a common distribution. As a result of this reasoning I preferred a Bayesian meta- analysis random effects model. Let $i = 1, \ldots, 7$ be the number of trials. Then the choosen Bayesian meta- analysis random effects model is:

$$y0_i \sim bin(c_i, n0_i)$$
$$y1_i \sim bin(t_i, n1_i)$$
$$logit(c_i) = \mu_i$$
$$logit(t_i) = \mu_i + \delta_i$$
$$\mu_i \sim norm(0, .0001), \delta_i \sim norm(d, \tau), d \sim norm(0, .0001), \tau = \sigma^{-2}, \sigma \sim uni(0, 2), or = exp(d)$$

In the model's data layer there are two likelihoods, one likelihood for the control group($y0_i$) and the other for the treatment group($y1_i$).Within each group we have the total number of patients and the corresponding events, so binominal likelihoods were used. Where the total number of patients for the control group is $n0_i$ and for the treatment group $n1_i$. c_i and t_i are the probabilities in the two likelihoods. In the process layer we use logit function c_i and t_i so the probabilities of success are modelled on a logit scale.

μ_i are trial specific baselines representing the log odds of the outcome in the control group. While δ_i are the trial specific log odds ratio in the control group compared with the treatment group. Where μ_i , d the prior for therapy effects and σ prior for between trials standard deviations are vague or uninformative because of focus on the data.