The model was computed in R and JAGS. First the Cochrane dataset was stripped into 4 vectors a vector to represent $y0\_i$, $y1\_i$, $n0\_i$, and $n1\_i$.

The experiment was conducted in R and JAGS. I wrote a function for my chosen model in JAGS that accept 4 vector parameters. These 4 parameters are the treatment event, treatment total, and control event, and control total. This data was packaged into a list along with the common length of all 4 parameters and passed into JAGS. JAGS was set up to run 2 chains with 20000 iterations for each chain where 10000 were cast away as burn-ins. Resulting in a total of 20000 posterior samples for all parameters with 5 thinning. The first part of my experiment was to test for type1 errors. I wrote several loops. One for 1000, 2000 and 3000.

I also built a random number generator function that generated numbers for the treatment event and control event.