Untitled

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Due to the observation data, we got the following statistics:

Thus, the likelihood function will be:

Multiply the proposed joint prior distribution, we get the joint posterior distribution like:

where .

We do a logit transformation on to by , and the corresponding Jacobian is .

Thus, we could rewrite the joint posterior distribution like:

Adapted from the posterior distribution, the log target distribution is like:

Accordingly, those conditional distirbution for parameters and hyperparameters are:

and it does not look like any commonly seen classic distribution.

*Note: denotes conditional on all other parameters and data.*

Now, the implementation of this hybrid Gibbs sampler works like:

Step 1: Sample from ~ Unif(0,1), and let ;

Set ;

Set all hyperparameters with the reasonable values suggested by physicians, .

Step 2: Given ,

Sample from ;

Sample under M-H algorithm with a ~ N(0, 0.52) random walk proposal distribution because the conditional distribution follows does not have a closed form.

Transfer back to by

The r code to implement this hybrid Gibbs sampler is as follows:

niter = 100000 # number of iterations  
theta = rep(0,niter) # define (hyper)parameters  
tau = rep(0,niter)  
a = rep(0,niter)  
b = rep(0,niter)   
c = rep(0,niter)  
d = rep(0,niter)   
  
# Gibbs Sampler Implementation  
set.seed(1) # set random seed  
  
theta[1] = runif(1, min = 0, max = 1) # Initialization of (hyper)parameters  
tau[1] = runif(1, min = 0, max = 1)  
a[1] = 3  
b[1] = 1  
c[1] = 60  
d[1] = 120  
  
for (i in 2:niter) { # for-loop for Gibbs sampler  
 # update d  
 d[i]<-rexp(1, rate = tau[i-1]\*theta[i-1])  
 # update c  
 c[i]<-rexp(1, rate = theta[i-1])  
 # update b  
 b[i]<-rexp(1, rate = -log(tau[i-1]))  
 # update a  
 a[i]<-rexp(1, rate = -log(theta[i-1]))  
 # update tau in (0,1)  
 temp <- rgamma(1,shape = 16+b[i], rate = theta[i-1]\*(1526+d[i]))  
 tau[i] <- exp(temp)/(exp(temp)+1)  
 # update theta in (0,1)  
 temp <- rgamma(1,shape = 26+a[i], rate = tau[i]\*(1526+d[i])+1233+c[i])  
 theta[i] <- exp(temp)/(exp(temp)+1)  
}

Appendix:

# H treatment group  
data1=c(2,1,4,1,6,1,9,1,9,1,9,1,13,1,14,1,18,1,23,1,31,1,32,1,33,1,34,1,43,1,10,0,14,0,14,0,16,0,17,0,18,0,18,0,19,0,20,0,20,0,21,0,21,0,23,0,24,0,29,0,29,0,30,0,30,0,31,0,31,0,31,0,33,0,35,0,37,0,40,0,41,0,42,0,42,0,44,0,46,0,48,0,49,0,51,0,53,0,54,0,54,0,55,0,56,0)  
yh=matrix(data = data1,53,2,byrow = T)  
# Control group  
data2=c(1,1,4,1,6,1,7,1,13,1,24,1,25,1,35,1,35,1,39,1,1,0,1,0,3,0,4,0,5,0,8,0,10,0,11,0,13,0,14,0,14,0,15,0,17,0,19,0,20,0,22,0,24,0,24,0,24,0,25,0,26,0,26,0,26,0,28,0,29,0,29,0,32,0,35,0,38,0,39,0,40,0,41,0,44,0,45,0,47,0,47,0,47,0,50,0,50,0,51,0)  
yc=matrix(data = data2, ncol=2,byrow = T)  
  
# summary stats  
n.h.r=sum(yh[,2])  
n.c.r=sum(yc[,2])  
t.h= sum(yh[,1])  
t.c= sum(yc[,1])