

Hamra et al. eSupplement: R code

```
rm(list=ls())
```

```
#####
```

```
#### Asbestos Analysis using hierarchical regression w/ JAGS
```

```
#### code to replicate analyses
```

```
#### dataset title: aag0906_dl_160609_l10.dta
```

```
#####
```

```
## load necessary libraries
```

```
library(R2jags)
```

```
library(foreign)
```

```
library(Epi)
```

```
library(coda)
```

```
##set working directory and read in data
```

```
setwd()
```

```
load(DATA)
```

```
asb <- DATA
```

```
str(asb)
```

```
##Calculate exposure as per 100 fiber-year/mL
```

```
asb$x1 <- asb$ce1lag0/100
```

```
asb$x2 <- asb$CE2LAG0/100
```

```
asb$x3 <- asb$CE3LAG0/100
```

```
asb$x4 <- asb$CE4LAG0/100
```

```
asb$x5 <- asb$CE5LAG0/100
```

```
asb$x6 <- asb$CE6LAG0/100
```

```
asb$x7 <- asb$CE7LAG0/100
```

```
asb$x8 <- asb$CE8LAG0/100
```

```
asb$x9 <- asb$CE9LAG0/100
```

```
asb$x10 <- asb$CE10LAG0/100
```

```
asb$x11 <- asb$CE11LAG0/100
```

```

asb$x12 <- asb$CE12LAG0/100
asb$x14 <- asb$CE14LAG0/100
asb$x15 <- asb$CE15LAG0/100
asb$x16 <- asb$CE16LAG0/100
asb$x17 <- asb$CE17LAG0/100
asb$x18 <- asb$CE18LAG0/100
asb$x21 <- asb$CE21LAG0/100
asb$x22 <- asb$CE22LAG0/100
asb$x23 <- asb$CE23LAG0/100
asb$x24 <- asb$CE24LAG0/100
asb$year_c <- as.numeric(cut(as.numeric(asb$calyear),
c(1950,1960,1970,1980,1990,2000,2005), right=F, include.lowest=T))-1
#asb$state_n <- ifelse(asb$state=='SC',1,0)

#### create nested CC dataset to simplify computational time, match on age

asb$year <- as.numeric(asb$calyear)
asb$by <- (asb$year) - asb$agenow

set.seed(20011402)
nested_asb <- ccwc(entry=by, exit=year, fail=lung_ca,
  control=10,
  match=agenow,
  include=list(agenow, lung_ca,
    year_c, race2, gender,
    x1,x2,x3,x4,x5,x6,x7,
    x8,x9,x10,x11,x12,x14,x15,x16,x17,
    x18,x21,x22,x23,x24),
  data=asb)

####NOTE: Disregard warning

## Define vector of variables and exclude missings (NAs)

keep <- c('lung_ca','agenow','year_c','race2','gender',
  'x1','x2','x3','x4','x5','x6','x7',
  'x8','x9','x10','x11','x12','x14','x15','x16','x17',
  'x18','x21','x22','x23','x24')

asb.bayes <- na.omit(nested_asb[keep])

cc <- asb.bayes$lung_ca
age <- asb.bayes$agenow

```

```

year <- asb.bayes$year_c
sex <- asb.bayes$gender
race <- asb.bayes$race2
N <- length(asb.bayes$lung_ca)
x1 <- asb.bayes$x1
x2 <- asb.bayes$x2
x3 <- asb.bayes$x3
x4 <- asb.bayes$x4
x5 <- asb.bayes$x5
x6 <- asb.bayes$x6
x7 <- asb.bayes$x7
x8 <- asb.bayes$x8
x9 <- asb.bayes$x9
x10 <- asb.bayes$x10
x11 <- asb.bayes$x11
x12 <- asb.bayes$x12
x14 <- asb.bayes$x14
x15 <- asb.bayes$x15
x16 <- asb.bayes$x16
x17 <- asb.bayes$x17
x18 <- asb.bayes$x18
x21 <- asb.bayes$x21
x22 <- asb.bayes$x22
x23 <- asb.bayes$x23
x24 <- asb.bayes$x24

```

```
str(asb.bayes)
```

```

correlations <- cor(asb.bayes)
write.csv(correlations,'correlations.csv')

```

```
#####
```

```
## create the hierarchical model
```

```
#####
```

```

model.jags <- function() {
  for (n in 1:N){

    cc[n] ~ dbern(mu[n])
    p[n] <- alpha + phi1*age[n] + phi2*year[n] + phi3*race[n] + phi4*sex[n]

```

```

+ beta[1]*x1[n]
+ beta[2]*x2[n]
+ beta[3]*x3[n]
+ beta[4]*x4[n]
+ beta[5]*x5[n]
+ beta[6]*x6[n]
+ beta[7]*x7[n]
+ beta[8]*x8[n]
+ beta[9]*x9[n]
+ beta[10]*x10[n]
+ beta[11]*x11[n]
+ beta[12]*x12[n]
+ beta[13]*x14[n]
+ beta[14]*x15[n]
+ beta[15]*x16[n]
+ beta[16]*x17[n]
+ beta[17]*x18[n]
+ beta[18]*x21[n]
+ beta[19]*x22[n]
+ beta[20]*x23[n]
+ beta[21]*x24[n]
mu[n] <- 1/(1 + exp(-p[n]))
}

```

```

# hyperprior for the betas

```

```

for (j in 1:21) {
  beta[j] ~ dnorm(beta.m,beta.tau)
}

```

```

# Priors for other variables
alpha ~ dnorm(0,0.0001)
phi1 ~ dnorm(0,0.0001)
phi2 ~ dnorm(0,0.0001)
phi3 ~ dnorm(0,0.0001)
phi4 ~ dnorm(0,0.0001)
sigma.beta ~ dunif(0,100)
beta.tau <- 1/(pow(sigma.beta,2))
beta.m ~ dnorm(0,0.0001)
}

```

```

## TELL JAGS what variables to monitor

```

```
asb.parms <- c('alpha', 'beta[1:21]', 'phi1', 'phi2', 'phi3', 'phi4',  
              'beta.m', 'beta.tau')
```

```
## Read the data as a list for JAGS and STAN
```

```
asb.data <- list('cc','race','age','year', 'sex','N',  
                'x1','x2','x3','x4','x5','x6','x7',  
                'x8','x9','x10','x11','x12','x14','x15','x16','x17',  
                'x18','x21','x22','x23','x24')
```

```
## Run JAGS model
```

```
set.seed(20011401)  
asb.jags <- jags(data=asb.data,parameters.to.save= asb.parms,  
                n.chains=3, n.iter=100000, n.burnin=10000,n.thin=2,  
                model.file=model.jags)
```

```
## create an excel table of results
```

```
JAGS.results <- asb.jags$BUGSoutput$summary  
write.table(x=JAGS.results, file='RESULTS_sharedmean.csv', sep=",")
```

```
#####
```

```
## Order constraint model
```

```
#####
```

```
model.jags <- function() {  
  for (n in 1:N){  
  
    cc[n] ~ dbern(mu[n])  
    p[n] <- alpha + phi1*age[n] + phi2*year[n] + phi3*race[n] + phi4*sex[n]  
    + beta[1,1]*x1[n]  
    + beta[1,2]*x2[n]  
    + beta[1,3]*x3[n]  
    + beta[1,4]*x4[n]  
    + beta[1,5]*x5[n]  
    + beta[1,6]*x6[n]  
    + beta[2,1]*x7[n]  
    + beta[2,2]*x8[n]  
    + beta[2,3]*x9[n]
```

```

+ beta[2,4]*x10[n]
+ beta[2,5]*x11[n]
+ beta[2,6]*x12[n]
+ beta[3,2]*x14[n]
+ beta[3,3]*x15[n]
+ beta[3,4]*x16[n]
+ beta[3,5]*x17[n]
+ beta[3,6]*x18[n]
+ beta[4,3]*x21[n]
+ beta[4,4]*x22[n]
+ beta[4,5]*x23[n]
+ beta[4,6]*x24[n]
mu[n] <- 1/(1 + exp(-p[n]))
}

```

hyperprior for the psis: 4 width groups

```

psi[1] ~ dnorm(0,10)
psi[2] ~ dnorm(0,10);T(,psi[1])
psi[3] ~ dnorm(0,10);T(,psi[2])
psi[4] ~ dnorm(0,10);T(,psi[3])

```

hyperprior for the betas: 4 width groups, 6 length groups

```

for (i in 1:4) {

  beta[i,1] ~ dnorm(psi[i],10);T(0,)
  beta[i,2] ~ dnorm(psi[i],10);T(beta[i,1],)
  beta[i,3] ~ dnorm(psi[i],10);T(beta[i,2],)
  beta[i,4] ~ dnorm(psi[i],10);T(beta[i,3],)
  beta[i,5] ~ dnorm(psi[i],10);T(beta[i,4],)
  beta[i,6] ~ dnorm(psi[i],10);T(beta[i,5],)

}

```

Priors for other variables

```

alpha ~ dnorm(0,0.0001)
phi1 ~ dnorm(0,0.0001)
phi2 ~ dnorm(0,0.0001)
phi3 ~ dnorm(0,0.0001)
phi4 ~ dnorm(0,0.0001)

```

```

}

```

```
## Read the data as a list for JAGS and STAN
```

```
asb.data <- list('cc','race','age','year', 'sex','N',  
  'x1','x2','x3','x4','x5','x6','x7',  
  'x8','x9','x10','x11','x12','x14','x15','x16','x17',  
  'x18','x21','x22','x23','x24')
```

```
## Tell JAGS what variables to monitor
```

```
asb.parms <- c('alpha', 'beta[1,1]', 'beta[1,2]', 'beta[1,3]', 'beta[1,4]',  
  'beta[1,5]', 'beta[1,6]', 'beta[2,1]', 'beta[2,2]',  
  'beta[2,3]', 'beta[2,4]', 'beta[2,5]', 'beta[2,6]',  
  'beta[3,2]', 'beta[3,3]', 'beta[3,4]', 'beta[3,5]',  
  'beta[3,6]', 'beta[4,3]', 'beta[4,4]', 'beta[4,5]',  
  'beta[4,6]', 'phi1', 'phi2', 'phi3', 'phi4', 'beta.m', 'beta.tau')
```

```
## Run JAGS model
```

```
asb.jags <- jags(data=asb.data, parameters.to.save=asb.parms,  
  n.chains=2, n.iter=100000, n.burnin=10000, n.thin=3,  
  jags.seed=04142015,  
  model.file=model.jags)
```

```
## create an excel table of results
```

```
JAGS.results <- asb.jags$BUGSoutput$summary  
write.table(x=JAGS.results, file='RESULTS_constraint.csv', sep=",")
```