

OpenBugs

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We are trying to repeat the analysis by Dr. Johnson's for the ICBG evidency synthesis for ACE 151

OpenBugs Example

We followed the [Tutorial](#)

Repeating Dr. Johnson ICBG Analysis

```
rm(list=ls())

# Model with old data

model <- function() {

  #####
  # Blumenthal                                     #
  #####
  for(i in 0:3){
    logL[1,i+1] <- i*log(p[1,1]) +(18-i)*log(1-p[1,1]) - logfact(i) - logfact(18-i) + logfact(18)
    L[1,i+1] <- exp(logL[1,i+1])
    p1[i+1] <- L[1,i+1]/sum(L[1,1:4])
  }
  for(i in 16:18){
    logL[2,i-15] <- i*log(p[1,2]) + (18-i)*log(1-p[1,2]) - logfact(i) - logfact(18-i)+logfact(18)
    L[2,i-15] <- exp(logL[2,i-15])
    p2[i-15] <- L[2,i-15]/sum(L[2,1:3])
  }
  for(i in 1:2){
    d[i] <- 1
    d[i] ~ dbern(LogLike[i])
    LogLike[i] <- mean(L[i,1:(r[i])])
  }
  #####

  #####
  # Other Studies                                     #
  #####
  for(i in 1:3){
    for(j in 1:2){
      x[i,j] ~ dbin(p[i+1,j],N[i,j])
    }
  }
  #####
}
```

```
#####
# Priors #
#####
for(i in 1:4){
  for(j in 1:2){
    logit(p[i,j]) <- gamma[i,j]
  }
  gamma[i,1:2] ~ dmnorm(gamma[5,1:2],Tau[1:2,1:2])
  #gamma[i,1] ~ dnorm(gamma[5,1],
  or[i] <- exp(gamma[i,1]-gamma[i,2])
}
gamma[5,1] ~ dnorm(0,0.001)
gamma[5,2] ~ dnorm(0,0.001)
or[5] <- exp(gamma[5,1]-gamma[5,2])
logit(p[5,1]) <- gamma[5,1]
logit(p[5,2]) <- gamma[5,2]
nnt <- 1/(p[5,2] - p[5,1])
Sigma[1] ~ dt(0,3,1)#T(0,)
Sigma[2] ~ dt(0,3,1)#T(0,)
rho ~ dunif(-1,1)
Sigma[3] <- rho*sqrt(Sigma[1]*Sigma[2])
det <- Sigma[1]*Sigma[2] - Sigma[3] * Sigma[3]
Tau[1,1] <- Sigma[2]/det
Tau[2,2] <- Sigma[1]/det
Tau[1,2] <- -Sigma[3]/det
Tau[2,1] <- Tau[1,2]
}

# To transfer the model to OpenBUGS, we load the R2OpenBUGS extension
# and write the model to a temporary location using the method
# write.model. We denote the model file location by model.file.

library(R2OpenBUGS)
model.file <- file.path(tempdir(),
                         "model.txt")
write.model(model, model.file)

# We then identify data variables in a list called data.

data = list (r=c(4,3),
             N=structure(.Data=c(30,15,11,11,9,11),.Dim=c(3,2)),
             x=structure(.Data=c(2,5,2,6,0,7),.Dim=c(3,2)),
             Sigma=c(1,1,NA),rho=0)

# Gundes, Brull, Singh #

# And we identify the variable p to be monitored in a vector called
# params.

params <- c("or", "nnt", "p")

# Lastly, we may select some initial parameters for the simulation.
```

```
# A rule of thumb is to choose values as close to the expected result
# as possible. In this case, we initialize p to be 0.5. Notice how we
# wrap the initial values inside a list that is to be returned by a
# function.
```

```
#inits <- function() { list(p=0.5) }
```

```
# Then we invoke OpenBUGS with the namesake method bugs and save the
# result in a variable out. We select 10,000 iterations per simulation
# chain.
```

```
out <- bugs(data, inits = NULL, params, model.file, n.iter=10000)
out$summary
```

##	mean	sd	2.5%	25%	50%	75%
## or[1]	0.02898088	0.03609000	0.00135900	0.0079700	0.01708	0.036795
## or[2]	0.17943262	0.25244090	0.01922000	0.0675700	0.12385	0.215200
## or[3]	0.77981177	1.10537957	0.03368000	0.1955000	0.44330	0.922000
## or[4]	0.35703621	0.54743326	0.03722000	0.1276500	0.24390	0.424200
## or[5]	0.18438659	0.22373237	0.01642975	0.0621100	0.11935	0.226225
## nnt	1.79861033	80.35516247	1.27800000	1.7230000	2.17950	3.060000
## p[1,1]	0.12576713	0.08191095	0.01663000	0.0647075	0.10800	0.171000
## p[1,2]	0.85493579	0.08110129	0.66820000	0.8085000	0.86800	0.916000
## p[2,1]	0.16076467	0.05038020	0.08062000	0.1242000	0.15340	0.190200
## p[2,2]	0.59128411	0.16980111	0.24519750	0.4710000	0.60025	0.718200
## p[3,1]	0.23178505	0.08354132	0.09494000	0.1715000	0.22370	0.282900
## p[3,2]	0.42025329	0.21109977	0.09066872	0.2503000	0.39720	0.566900
## p[4,1]	0.31048797	0.08805502	0.16160000	0.2477000	0.30135	0.364100
## p[4,2]	0.63488947	0.16317124	0.29157997	0.5219000	0.64610	0.763825
## p[5,1]	0.19925542	0.09000219	0.06530950	0.1325750	0.18490	0.251725
## p[5,2]	0.64125676	0.15598838	0.31359750	0.5353000	0.65455	0.758500
## deviance	50.98876800	11.67956069	36.74000000	43.1700000	48.16000	55.830000
##	97.5%	Rhat	n.eff			
## or[1]	0.1375000	1.003711	4400			
## or[2]	0.6339025	1.001270	5400			
## or[3]	3.6120000	1.000967	15000			
## or[4]	1.2690250	1.001142	8200			
## or[5]	0.7362225	1.000973	15000			
## nnt	10.4212500	1.262702	8800			
## p[1,1]	0.3434000	1.002248	10000			
## p[1,2]	0.9710000	1.003973	1200			
## p[2,1]	0.2760000	1.001123	8900			
## p[2,2]	0.8880050	1.001455	4100			
## p[3,1]	0.4200150	1.000978	15000			
## p[3,2]	0.8672025	1.000919	15000			
## p[4,1]	0.5055075	1.001015	15000			
## p[4,2]	0.9025000	1.000956	15000			
## p[5,1]	0.4109000	1.001061	12000			
## p[5,2]	0.9020050	1.000914	15000			
## deviance	82.6204999	1.001458	3600			

```
# Better to invoke the CODA option to get mcmc.list as output.
```

```

out <- bugs(data, inits = NULL, params, model.file, codaPkg=TRUE,
            n.iter=10000)
out.coda <- read.bugs(out)

```

```

## Abstracting deviance ... 5000 valid values
## Abstracting nnt ... 5000 valid values
## Abstracting or[1] ... 5000 valid values
## Abstracting or[2] ... 5000 valid values
## Abstracting or[3] ... 5000 valid values
## Abstracting or[4] ... 5000 valid values
## Abstracting or[5] ... 5000 valid values
## Abstracting p[1,1] ... 5000 valid values
## Abstracting p[1,2] ... 5000 valid values
## Abstracting p[2,1] ... 5000 valid values
## Abstracting p[2,2] ... 5000 valid values
## Abstracting p[3,1] ... 5000 valid values
## Abstracting p[3,2] ... 5000 valid values
## Abstracting p[4,1] ... 5000 valid values
## Abstracting p[4,2] ... 5000 valid values
## Abstracting p[5,1] ... 5000 valid values
## Abstracting p[5,2] ... 5000 valid values
## Abstracting deviance ... 5000 valid values
## Abstracting nnt ... 5000 valid values
## Abstracting or[1] ... 5000 valid values
## Abstracting or[2] ... 5000 valid values
## Abstracting or[3] ... 5000 valid values
## Abstracting or[4] ... 5000 valid values
## Abstracting or[5] ... 5000 valid values
## Abstracting p[1,1] ... 5000 valid values
## Abstracting p[1,2] ... 5000 valid values
## Abstracting p[2,1] ... 5000 valid values
## Abstracting p[2,2] ... 5000 valid values
## Abstracting p[3,1] ... 5000 valid values
## Abstracting p[3,2] ... 5000 valid values
## Abstracting p[4,1] ... 5000 valid values
## Abstracting p[4,2] ... 5000 valid values
## Abstracting p[5,1] ... 5000 valid values
## Abstracting p[5,2] ... 5000 valid values
## Abstracting deviance ... 5000 valid values
## Abstracting nnt ... 5000 valid values
## Abstracting or[1] ... 5000 valid values
## Abstracting or[2] ... 5000 valid values
## Abstracting or[3] ... 5000 valid values
## Abstracting or[4] ... 5000 valid values
## Abstracting or[5] ... 5000 valid values
## Abstracting p[1,1] ... 5000 valid values
## Abstracting p[1,2] ... 5000 valid values
## Abstracting p[2,1] ... 5000 valid values
## Abstracting p[2,2] ... 5000 valid values
## Abstracting p[3,1] ... 5000 valid values
## Abstracting p[3,2] ... 5000 valid values
## Abstracting p[4,1] ... 5000 valid values
## Abstracting p[4,2] ... 5000 valid values

```

```
## Abstracting p[5,1] ... 5000 valid values
## Abstracting p[5,2] ... 5000 valid values
```

```
# Analyse using shinystan
```

```
library(shinystan)
```

```
library(coda)
```

```
# After verification that the object is now a mcmc.list  
# convert to shinstan object and call shinystan
```

```
is.mcmc.list(out.coda)
```

```
## [1] TRUE
```

```
out.shiny <- as.shinystan(out.coda)
```

```
# launch shinystan(out.shiny)
```