

# Bayesian Statistics

## Converting OpenBUGS to RJAGS

**Greg Schreiter, M.S.**

*Instructional Associate*

School of Industrial and Systems Engineering

Introduction

# What is RJAGS?

RJAGS is an R package that allows an interface to the JAGS MCMC library.

Advantage: Models are specified nearly the same way as in OpenBUGS/WinBUGS, so it is easy to transfer between languages in most situations. Data may need to be changed to a list format.

Disadvantage: You can do some things in BUGS that you can't do in JAGS. ☹ Just need to be careful about this! Fortunately there are only a few such situations.

Documentation: <https://cran.r-project.org/web/packages/rjags/rjags.pdf>

JAGS User Manual: <https://sourceforge.net/projects/mcmc-jags/postdownload>

# Example Translation – Unit 1 Ex

## BUGS

### A Simple Regression

```
model{
  for (i in 1:N) {
    Y[i] ~ dnorm(mu[i],tau)
    mu[i] <- alpha + beta * (x[i] - x.bar)
  }
  x.bar <- mean(x[])
  alpha ~ dnorm(0, 0.0001)
  beta ~ dnorm(0, 0.0001)
  tau ~ dgamma(0.001, 0.001)
  sigma <- 1.0/sqrt(tau)
  beta0 <- alpha - beta * x.bar #intercept
}
#-----
```

### Data

```
list(N=5, x=c(1,2,3,4,5), Y=c(1,3,3,3,5))
```

```
#-----
```

### Inits

```
list(alpha = 0.1, beta = 0.6, tau = 1)
```

Notice that the  
model{} is the  
same for both!

## RJAGS

```
library(rjags)
library(coda)

#A Simple Regression

#Data
dat1=list(N=5,x=c(1,2,3,4,5),Y=c(1,3,3,3,5))

#Initial values for parameters
model.inits <- list(alpha = 0.1, beta = 0.6, tau = 1)

#Set iteration number and burn-in
iterations <- 10500
burnin <- 500
chains <- 1

model.sat.text<-"
model{
  for (i in 1:N) {
    Y[i] ~ dnorm(mu[i],tau)
    mu[i] <- alpha + beta * (x[i] - x.bar)
  }
  x.bar <- mean(x[])
  alpha ~ dnorm(0, 0.0001)
  beta ~ dnorm(0, 0.0001)
  tau ~ dgamma(0.001, 0.001)
  sigma <- 1.0/sqrt(tau)
  beta0 <- alpha - beta * x.bar #intercept
}"

model.sat.spec<-textConnection(model.sat.text)

#Run RJAGS Model

model.fit <- jags.model(model.sat.spec,
                        data=dat1,
                        inits=model.inits, n.chains = chains)

model.samples <- coda.samples(model.fit, c("alpha", "beta", "beta0",
                                           "tau", "sigma"), n.iter=iterations)

#View Results
summary(window(model.samples, start = burnin))
```

# BUGS commands that don't work in RJAGS

```
model{
  for(i in 1:5){
    n1[i] <- Tot1 #100
    n2[i] <- Tot2 #3
    y1[i] <- Positives1
    y2[i] <- Positives2
    y1[i] ~ dbin(p1[i],n1[i])
    y2[i] ~ dbin(p2[i],n2[i])
    diffps[i] <- p1[i]-p2[i] #100seller - 3seller
  }
}
```

Taken from Unit 4 Ebay example

Other files with this problem:

Unit6 Psoriasis

Unit6 zerothickjeremy

RJAGS gives an error message when you define a node multiple times (both deterministically and stochastically)! Fortunately, this is only an issue in a few of the example files.

# Other problems in RJAGS

One must be more careful defining bounds for a loop in RJAGS than in BUGS. To illustrate, the following model specification generated an error:

```
model{
  for (i in 1:ntotal){
    times[i] ~ dnorm( mu[i], tau )
    mu[i] <- mu0 + alpha[diets[i]]
  }
  #alpha[1] <- 0.0;      #CR constraints
  alpha[1] <- -sum( alpha[2:a] ); #STZ Constraint

  mu0 ~ dnorm(0, 0.0001)
  alpha[2] ~ dnorm(0, 0.0001)
  alpha[3] ~ dnorm(0, 0.0001)
  alpha[4] ~ dnorm(0, 0.0001)
  tau ~ dgamma(0.001, 0.001)
  sigma <- sqrt(1/tau)
  #pairwise
  for(i in 1:3){
    for(j in i+1:4){
      adiff[i,j] <- alpha[i]-alpha[j]
    }
  }
}
```

From Unit 7 anovacoagulation example

# Other problems in RJAGS

This was fixed by adding parentheses around the lower bound:

```
#Model Specification
model.sat.text<-"model{
  for (i in 1:ntotal){
    times[i] ~ dnorm( mu[i], tau )
    mu[i] <- mu0 + alpha[diets[i]]
  }
  #alpha[1] <- 0.0;      #CR constraints
  alpha[1] <- -sum( alpha[2:a] ); #STZ Constraint

  mu0 ~ dnorm(0, 0.0001)
  alpha[2] ~ dnorm(0, 0.0001)
  alpha[3] ~ dnorm(0, 0.0001)
  alpha[4] ~ dnorm(0, 0.0001)
  tau ~ dgamma(0.001, 0.001)
  sigma <- sqrt(1/tau)
  #pairwise
  for(i in 1:3){
    for(j in (i+1):4){
      adiff[i,j] <- alpha[i]-alpha[j]
    }
  }
}
```

# Problems with data specification

When the data is specified as a data matrix and not a list, R cannot read it!

Unit7fat2ddata - Notepad

File	Edit	Format	View	Help					
Y[ , ]	X[,2]	X[,3]	X[,4]	X[,5]	X[,6]	X[,7]	X[,8]	X[,9]	
12.6	23	154.25	67.75	23.7	36.2	93.1	85.2	94.5	59.0
6.9	22	173.25	72.25	23.4	38.5	93.6	83.0	98.7	58.7
24.6	22	154.00	66.25	24.7	34.0	95.8	87.9	99.2	59.6
10.9	26	184.75	72.25	24.9	37.4	101.8	86.4	101.2	60.1
27.8	24	184.25	71.25	25.6	34.4	97.3	100.0	101.9	63.2
20.6	24	210.25	74.75	26.5	39.0	104.5	94.4	107.8	66.0
19.0	26	181.00	69.75	26.2	36.4	105.1	90.7	100.3	58.4
12.8	25	176.00	72.50	23.6	37.8	99.6	88.5	97.1	60.0
5.1	25	191.00	74.00	24.6	38.1	100.9	82.5	99.9	62.9
12.0	23	198.25	73.50	25.8	42.1	99.6	88.6	104.1	63.1
7.5	26	186.25	74.50	23.6	38.5	101.5	83.6	98.2	59.7
8.5	27	216.00	76.00	26.3	39.4	103.6	90.9	107.7	66.2
20.5	32	180.50	69.50	26.3	38.4	102.0	91.6	103.9	63.4
20.8	30	205.25	71.25	28.5	39.4	104.1	101.8	108.6	66.0
21.7	35	197.75	69.50	27.4	40.5	101.3	95.4	100.1	60.0

Affected files from Unit7:  
fat2d  
fatmulti  
NHANESmulti

# Other problems – Censored Data

RJAGS has no equivalent to OpenBUGS C() censoring function, so models with censored data do not work reliably! The indicator function I() is also problematic with non-fixed parameters.

This affects the Unit 8 material.  
Recommend some other program for this!



# Summary

OpenBUGS and MATLAB are still the way to go for the course, but perhaps this will make it easier for MAC users to use R with the course. There are also other R implementations of MCMC algorithms that may have functionality this package does not. Please read the RJAGS documentation to see if it is right for you!

As a reminder, the links to the documentation and user guide are

Documentation: <https://cran.r-project.org/web/packages/rjags/rjags.pdf>

JAGS User Manual: <https://sourceforge.net/projects/mcmc-jags/postdownload>

