Hint for Assignment 2

This file will contain structures that you can use as reference for your questions. Selective hard questions are given hints for:

Q3:

The right data interpretation will help in this question.

dataList = list (x= 15, n=20)

The model written in JAGS is given below:

```
modelString = "
model {
x ~ dbin( p, n )
p <- theta[pick]
pick ~ dcat(q[]) # categorical 1 produced prob q[1], etc
# pick is 2 if biased 1 unbiased
q[1]<-0.9
q[2]<-0.1
theta[1] <-0.5 # unbiased
theta[2] ~ dunif(0,1) # biased
biased <- pick - 1
}
" # close quote for modelString
```

Furthermore initialzation of chains can be as follows :

initsList = list(pick = 1)

Regardless the following skeleton can be used for better clarity

```
mypriormix = function(){
  # Load the functions used below:
  source("DBDA2E-utilities.R") # Must be in R's current working directory.
  require(rjags)               # Must have previously installed package rjags.

  # Struct the data:
  dataList = list(x=15, n=20)
  # Define the model:
  modelString = "
  model {
    x ~ dbin( p, n )
    p <- theta[pick]
    pick ~ dcat(q[]) # categorical 1 produced prob q[1], etc
    # pick is 2 if biased 1 unbiased
    q[1]<-0.9
    q[2]<-0.1
    theta[1] <-0.5 # unbiased
    theta[2] ~ dunif(0,1) # biased
    biased <- pick - 1
      }
```

```
      " # close quote for modelString
  writeLines( modelString , con="TEMPmodel.txt" )
  initsList = list( pick = 1)

      # Run the chains:
  jagsModel = jags.model( file="TEMPmodel.txt" , data=dataList , inits=initsList , n
.chains=3 , n.adapt=500 )
  update( jagsModel , n.iter=500 )
      codaSamples = coda.samples( jagsModel, variable.names=c("theta[2]","biased","t
heta[1]") ,                                  n.iter=3334)
  save( codaSamples , file=paste0(fileNameRoot,"Mcmc.Rdata") )

      # Examine the chains:
      # Convergence diagnostics: for parameter:theta[2]
  diagMCMC( codaObject=codaSamples , parName="theta[2]" )
  saveGraph( file=paste0(fileNameRoot,"Theta[2]Diag") , type="jpg" )
  # Posterior descriptives:
  openGraph(height=3,width=4)
  par( mar=c(3.5,0.5,2.5,0.5) , mgp=c(2.25,0.7,0) )
  plotPost( codaSamples[,"theta[2]"] , main="theta[2]" , xlab=bquote(theta[2]) )
   saveGraph( file=paste0(fileNameRoot,"Theta[2]Post") , type="jpg" )
  graphics.off() # this is done to prevent very last graph being displyed in RMD out
put
  list(su = summary(codaSamples), codaSamples = codaSamples)

    }

    #call function and show output
mypriormix() -> ans
```

Q4.

Q5:

a. Derive the formulae (eq. 6.7) given on pg. 131.

Given $\mu = \frac{a}{a+b}$, $\sigma^2 = \frac{\mu(1-\mu)}{a+b+1}$, $a = \mu\kappa$, $b = (1-\mu)\kappa$, and $\kappa = a + b$

In this question you must use your results from q4. Also the a hint for the model file can be as follows: model { x ~ dbin(p,n) p <- theta[pick]

#theta[1] represents fixed unbiased value theta[1] <-

equals(pick,1)*fixtheta1 + equals(pick,2)*fixtheta1 theta[2] <-

equals(pick,1)*pseudotheta2 + equals(pick,2)*theta2 pick ~

dcat(q[]) # categorical 1 produced prob q[1], etc

pick is 2 if biased 1 unbiased q[1]<-0.9

q[2]<-0.1 fixtheta1 <-0.5 # unbiased; fixed

probability theta2 ~ dunif(0,1) #true prior

of theta[2]

#shape parameters for pseudo prior will be part of dataList

pseudotheta2 ~ dbeta(alpha,beta)

biased <- pick - 1

}

Where alpha and beta are a and b,

a = mu*(mu*(1-mu)/(sd^2)-1) b =

(1-mu)*(mu*(1-mu)/(sd^2)-1)

Where mu = mean(pick2$`theta[2]`) and sd = sqrt(var(pick2$`theta[2]`)

……from the previous problem mcmc

Q. 5.e. i. A node is any **variable** that you are monitoring.

```
library(knitr)
  su = pseudo$su
  su2 = kable(pseudo$su[[1]])
```