MTH422A Assignment5

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 $\mathbf{2}$

3

for(i in 1:n){

```
### que3
library(rjags)
## Warning: package 'rjags' was built under R version 4.3.3
## Loading required package: coda
## Warning: package 'coda' was built under R version 4.3.3
## Linked to JAGS 4.3.1
## Loaded modules: basemod, bugs
Y \leftarrow c(563,10)
N_s \leftarrow c(2820, 27)
c <- 1
n <- 2
# Baye factor
((Y[1] + Y[2] + 1) * log(N_s[1] + N_s[2]) + lgamma(Y[1] + 1) + lgamma(Y[2] + 1))
# Calculate the exponential of lgconst
result <- exp(lgconst)</pre>
bf21_c1 <- result*c*pgamma(c,shape = Y[1]+Y[2]+1, rate = N_s[1] + N_s[2])/(pgamma(c,Y[1] + 1,N_s[1])*pg
data <- list(Y = Y, n = length(Y), N_s = N_s,c= c)</pre>
model_string <- textConnection("model{</pre>
# Likelihood
```

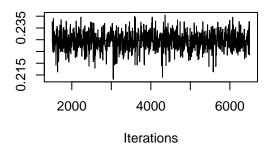
```
Y[i] ~ dpois(N_s[i]*lambda[i])
like[i] <- dpois(Y[i],N_s[i]*lambda[i])</pre>
#prior
for(i in 1:n){
  lambda[i] ~ dunif(0,c)
}")
model <- jags.model(model_string, data = data, n.chains = 2,quiet = TRUE)</pre>
update(model,10000,progress.bar = "none")
samples <- coda.samples(model, variable.names = c("like"),</pre>
                                                                   n.iter = 50000,progress.bar = "none")
## dic
DIC1 <- dic.samples(model,n.iter = 50000 ,progress.bar = "none")
DIC1
## Mean deviance: 14.34
## penalty 1.986
## Penalized deviance: 16.32
# Compute WAIC
like <- rbind(samples[[1]],samples[[2]]) # Combine the two chains
fbar <- colMeans(like)</pre>
Pw <- sum(apply(log(like),2,var))
WAIC1 \leftarrow -2*sum(log(fbar)) + 2*Pw
WAIC1
## [1] 15.74768
### c=10
c <- 10
# Baye factor
lgconst \leftarrow lgamma(Y[1] + Y[2] + 1) + (Y[1] + 1) * log(N_s[1]) + (Y[2] + 1) * log(N_s[2]) - (Y[1] + 1) * log(N_s[2]) + (Y[2] + 1)
      ((Y[1] + Y[2] + 1) * log(N_s[1] + N_s[2]) + lgamma(Y[1] + 1) + lgamma(Y[2] + 1))
# Calculate the exponential of lgconst
result <- exp(lgconst)</pre>
bf21_c10 <- result * c * pgamma(c,shape = Y[1]+Y[2]+1, rate = N_s[1] + N_s[2])/(pgamma(c,Y[1] + 1,N_s[1]
data \leftarrow list(Y = Y, n = length(Y), N_s = N_s,c= c)
model_string <- textConnection("model{</pre>
```

```
# Likelihood
for(i in 1:n){
Y[i] ~ dpois(N_s[i]*lambda[i])
like[i] <- dpois(Y[i],N_s[i]*lambda[i])</pre>
#prior
for(i in 1:n){
 lambda[i] ~ dunif(0,c)
}
}")
model <- jags.model(model_string, data = data, n.chains = 2,quiet = TRUE)</pre>
update(model,10000,progress.bar = "none")
samples_10 <- coda.samples(model, variable.names = c("like"),</pre>
                             n.iter = 50000,progress.bar = "none")
## dic
DIC_10 <- dic.samples(model,n.iter = 50000 ,progress.bar = "none")
DIC_10
## Mean deviance: 14.33
## penalty 1.986
## Penalized deviance: 16.32
# Compute WAIC
like <- rbind(samples_10[[1]],samples_10[[2]]) # Combine the two chains
fbar <- colMeans(like)</pre>
Pw <- sum(apply(log(like),2,var))</pre>
WAIC_10 \leftarrow -2*sum(log(fbar)) + 2*Pw
WAIC_10
## [1] 15.74132
BF21 <- c(bf21_c1,bf21_c10)
C \leftarrow c(1,10)
DIC \leftarrow c(14.35,14.35)
Waic <- c(WAIC1,WAIC_10)</pre>
tab <- data.frame(C,BF21,DIC,Waic)</pre>
print(tab)
##
      C
              BF21 DIC
                              Waic
## 1 1 0.7155665 14.35 15.74768
## 2 10 7.1544884 14.35 15.74132
```

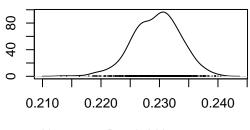
So, We can conclude that M1 is best model

```
### Assign-5 que-4
library(geoR)
## Warning: package 'geoR' was built under R version 4.3.3
## Analysis of Geostatistical Data
## For an Introduction to geoR go to http://www.leg.ufpr.br/geoR
## geoR version 1.9-4 (built on 2024-02-14) is now loaded
library(rjags)
Y <- gambia$pos
X <- gambia[,4:8]</pre>
X <- scale(X)</pre>
data <- list(Y=Y,X=X,n=length(Y))</pre>
# Fit logistic model
model_string <- textConnection("model{</pre>
for(i in 1:n){
 Y[i] ~ dbern(pi[i])
 logit(pi[i]) <- beta[1] + X[i,1]*beta[2] +
                   X[i,2]*beta[3] + X[i,3]*beta[4] +
                   X[i,4]*beta[5] + X[i,5]*beta[6]
 }
 #priors
 for(j in 1:6){
 beta[j] ~ dnorm(0,0.01)
# Posterior preditive checks
for(i in 1:n){
Y1[i] ~ dbern(pi[i])
D[1] \leftarrow mean(Y1[]^2) - mean(Y1[])^2
D[2] \leftarrow mean(Y1[])
}")
model <- jags.model(model_string,data = data, n.chains=1,quiet=TRUE)</pre>
```

Trace of D[1]

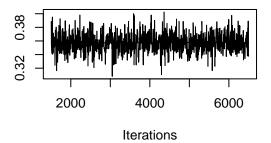


Density of D[1]

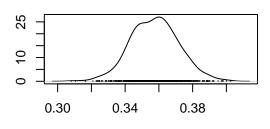


N = 1000 Bandwidth = 0.001075

Trace of D[2]



Density of D[2]



N = 1000 Bandwidth = 0.003773

```
D.m <- samples[[1]]

##Compute the Bayesian p-values
D0 <- c(var(Y), mean(Y))
Dnames <- c("Var Y", "Mean Y")

# Compute the test stats for the models
pval1 <- rep(NA, 2)
names(pval1) <- c("Var Y", "Mean Y")

for(j in 1:2){
   pval1[j] <- mean(D.m[ , j] > D0[j])
}
```

```
## Var Y Mean Y
## 0.506 0.506
5
### assign5 ques5
Y <- WWWusage
Y <- as.numeric(Y)
data1 <- list( Y = Y )</pre>
## ar1
Ar1_model <- textConnection("model{</pre>
for(t in 2:100){
Y[t] ~ dnorm(mu[t],tau)
mu[t] \leftarrow beta[1] + beta[2]*Y[t-1]
like[t] <- dnorm(Y[t],mu[t],tau)</pre>
## priors
## priors
for(j in 1:2){
beta[j] ~ dnorm(0,0.01)
tau ~ dgamma(0.1,0.1)
}")
model <- jags.model(Ar1_model,data = data1, n.chains=2,quiet=TRUE)</pre>
update(model, 10000, progress.bar = "none")
dic1 <- dic.samples(model,n.iter = 50000)</pre>
print(dic1)
## Mean deviance: 626.5
## penalty 3.012
## Penalized deviance: 629.5
samps1 <- coda.samples(model, variable.names = c("like"),</pre>
                         n.iter = 50000, thin = 5, progress.bar = "none")
```

print(pval1)

```
# Compute WAIC
like <- rbind(samps1[[1]],samps1[[2]]) # Combine the two chains
fbar <- colMeans(like)</pre>
Pw <- sum(apply(log(like),2,var))
WAIC1 \leftarrow -2*sum(log(fbar)) + 2*Pw
WAIC1
## [1] 629.1302
## ar2
Ar2 model <- textConnection("model{</pre>
for(t in 3:100){
Y[t] ~ dnorm(mu[t],tau)
mu[t] \leftarrow beta[1] + beta[2]*Y[t-1] + beta[3]*Y[t-2]
like[t] <- dnorm(Y[t],mu[t],tau)</pre>
}
## priors
for(j in 1:3){
 beta[j] ~ dnorm(0,0.01)
tau ~ dgamma(0.1,0.1)
}")
model <- jags.model(Ar2_model,data = data1, n.chains=2,quiet=TRUE)</pre>
update(model, 10000, progress.bar = "none")
## dic
dic2 <- dic.samples(model,n.iter = 50000)</pre>
print(dic2)
## Mean deviance: 517.7
## penalty 4.025
## Penalized deviance: 521.8
# Compute WAIC
samps2 <- coda.samples(model, variable.names = c("like"),</pre>
                        n.iter = 50000, thin = 5, progress.bar = "none")
like <- rbind(samps2[[1]],samps2[[2]]) # Combine the two chains
fbar <- colMeans(like)</pre>
Pw <- sum(apply(log(like),2,var))
WAIC2 \leftarrow -2*sum(log(fbar)) + 2*Pw
WAIC2
```

[1] 521.3996

```
## ar3
Ar3_model <- textConnection("model{</pre>
for(t in 4:100){
Y[t] ~ dnorm(mu[t],tau)
mu[t] \leftarrow beta[1] + beta[2]*Y[t-1] + beta[3]*Y[t-2] + beta[4]*Y[t-3]
like[t] <- dnorm(Y[t],mu[t],tau)</pre>
}
 ## priors
for(j in 1:4){
 beta[j] ~ dnorm(0,0.01)
tau ~ dgamma(0.1,0.1)
}")
model <- jags.model(Ar3_model,data = data1, n.chains=2,quiet=TRUE)</pre>
update(model, 10000, progress.bar = "none")
dic3 <- dic.samples(model,n.iter = 50000)</pre>
print(dic3)
## Mean deviance: 507.4
## penalty 5.503
## Penalized deviance: 512.9
# Compute WAIC
samps3 <- coda.samples(model, variable.names = c("like"),</pre>
                         n.iter = 50000, thin = 5, progress.bar = "none")
like <- rbind(samps3[[1]],samps3[[2]]) # Combine the two chains
fbar <- colMeans(like)</pre>
Pw <- sum(apply(log(like),2,var))</pre>
WAIC3 \leftarrow -2*sum(log(fbar)) + 2*Pw
WAIC3
## [1] 511.6005
## ar4
Ar4_model <- textConnection("model{</pre>
for(t in 5:100){
Y[t] ~ dnorm(mu[t],tau)
mu[t] \leftarrow beta[1] + beta[2]*Y[t-1] + beta[3]*Y[t-2] + beta[4]*Y[t-3] + beta[5]*Y[t-4]
like[t] <- dnorm(Y[t],mu[t],tau)</pre>
}
 ## priors
 for(j in 1:5){
 beta[j] ~ dnorm(0,0.01)
```

```
tau ~ dgamma(0.1,0.1)
}")
model <- jags.model(Ar4_model,data = data1, n.chains=2,quiet=TRUE)</pre>
update(model, 10000, progress.bar = "none")
## dic
dic4 <- dic.samples(model,n.iter = 50000)</pre>
print(dic4)
## Mean deviance: 489.6
## penalty 5.65
## Penalized deviance: 495.2
# Compute WAIC
samps4 <- coda.samples(model, variable.names = c("like"),</pre>
                        n.iter = 50000, thin = 5, progress.bar = "none")
like <- rbind(samps4[[1]],samps4[[2]]) # Combine the two chains
fbar <- colMeans(like)</pre>
Pw <- sum(apply(log(like),2,var))</pre>
WAIC4 \leftarrow -2*sum(log(fbar)) + 2*Pw
WAIC4
## [1] 493.1161
### table for comparision
L \leftarrow c(1:4)
DIC < c(626.5,517.9,506.9,487.8)
WAIC <- c(WAIC1, WAIC2, WAIC3, WAIC4)
model_compar <- data.frame(L,DIC,WAIC)</pre>
print(model_compar)
   L DIC
                  WAIC
## 1 1 626.5 629.1302
## 2 2 517.9 521.3996
## 3 3 506.9 511.6005
## 4 4 487.8 493.1161
```

From above information L=4 best