

STAT 466 HW 10

Brody Anderson

2024-03-22

Question 1

```
age <- c(2.5, 7.5, 12.5, 17.5, 22.5, 27.5)
leaks <- c(2, 1, 4, 4, 2, 0)
t <- c(1052.0, 982.5, 756.9, 442.4, 230.9, 43.9)
n <- length(leaks)

#plot(leaks, age)
#plot(leaks, t)
#plot(leaks, age*t)

LeakModel <- "model {
  for(i in 1:n){
    leaks[i] ~ dpois(lambda[i]*t[i])
    log(lambda[i]) <- beta[1] + beta[2] * age[i]
  }
  beta[1] ~ dnorm(0,1/100)
  beta[2] ~ dnorm(0,1/100)
}
"
#beta[1] & beta[2] are independent priors

LeakModel.sim <- jags(
  data=c('age','leaks','t', 'n'),
  parameters.to.save=c('beta'),
  model.file=textConnection(LeakModel),
  n.iter=22000,
  n.burnin=2000,
  n.chains=5,
  n.thin=1
)
```

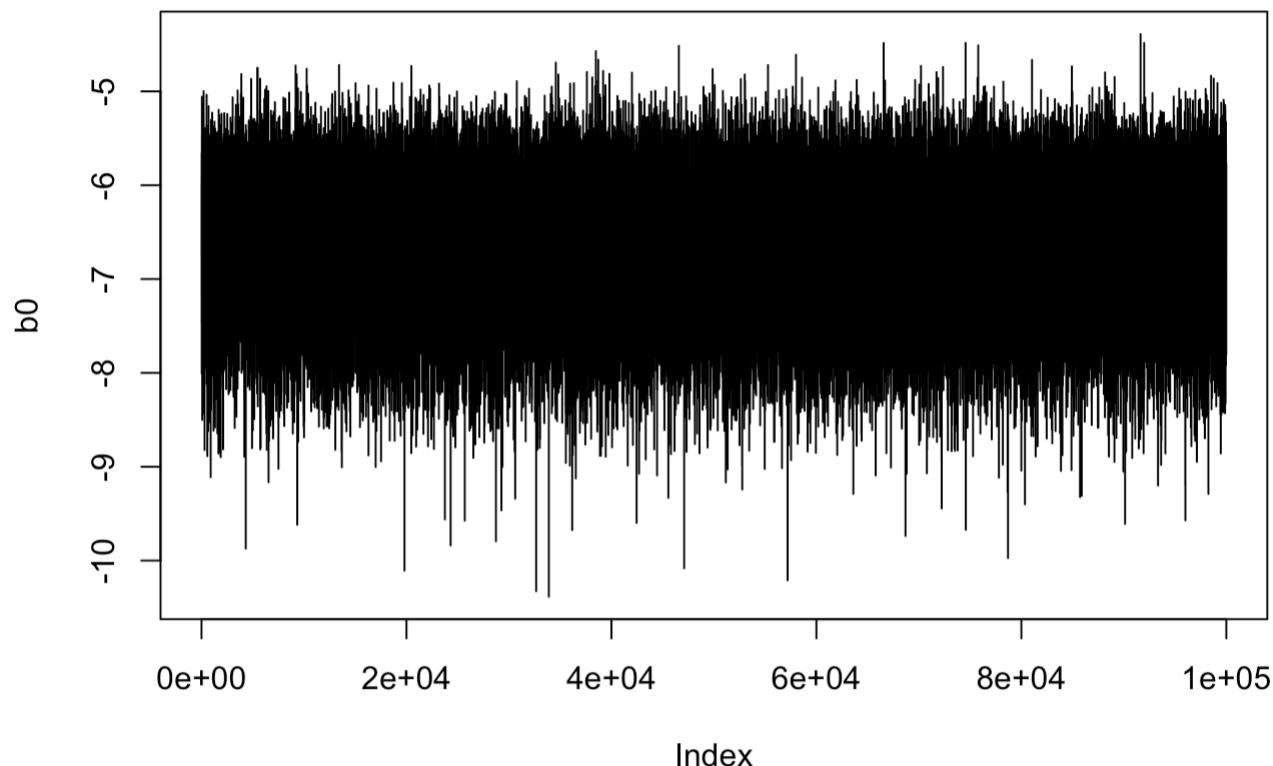
```
## Compiling model graph
## Resolving undeclared variables
## Allocating nodes
## Graph information:
##   Observed stochastic nodes: 6
##   Unobserved stochastic nodes: 2
##   Total graph size: 49
##
## Initializing model
```

```
# 100,000 MCMC samples obtained

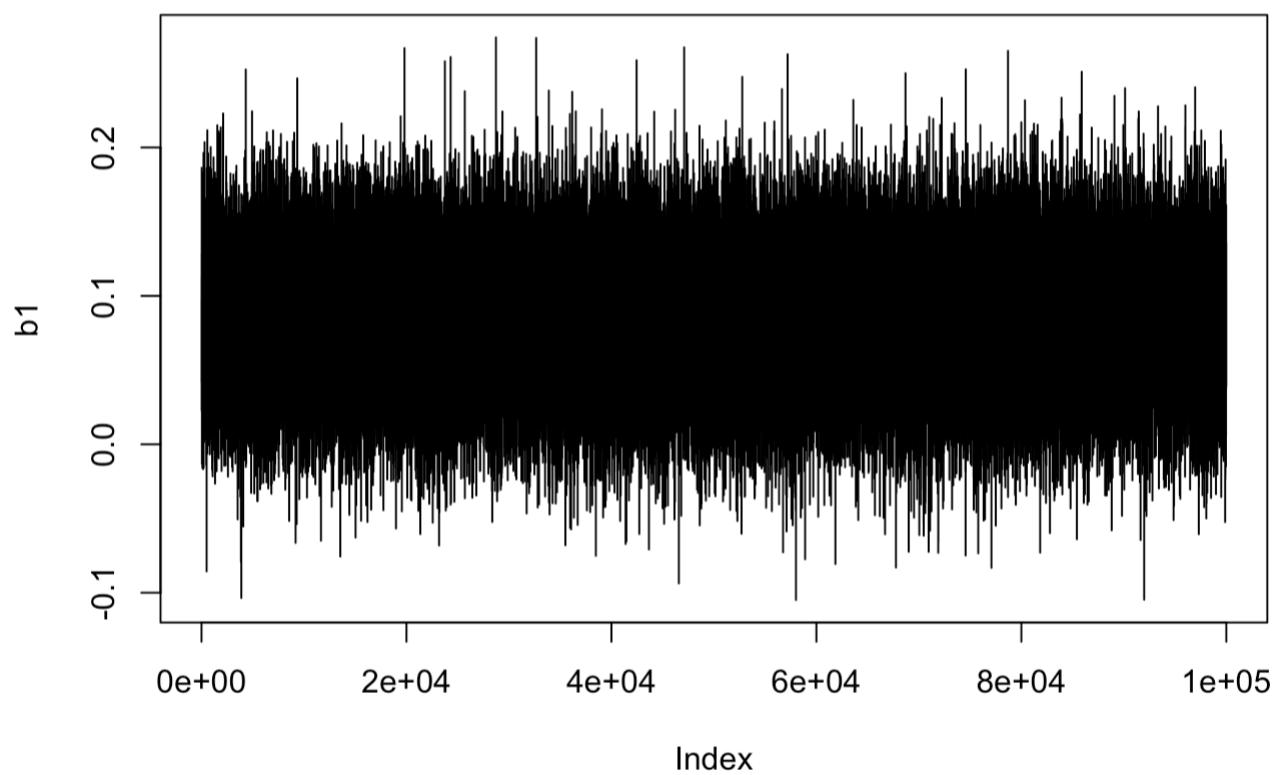
#head(LeakModel.sim$BUGSoutput$sims.matrix)

b0 <- LeakModel.sim$BUGSoutput$sims.matrix[,1]
b1 <- LeakModel.sim$BUGSoutput$sims.matrix[,2]

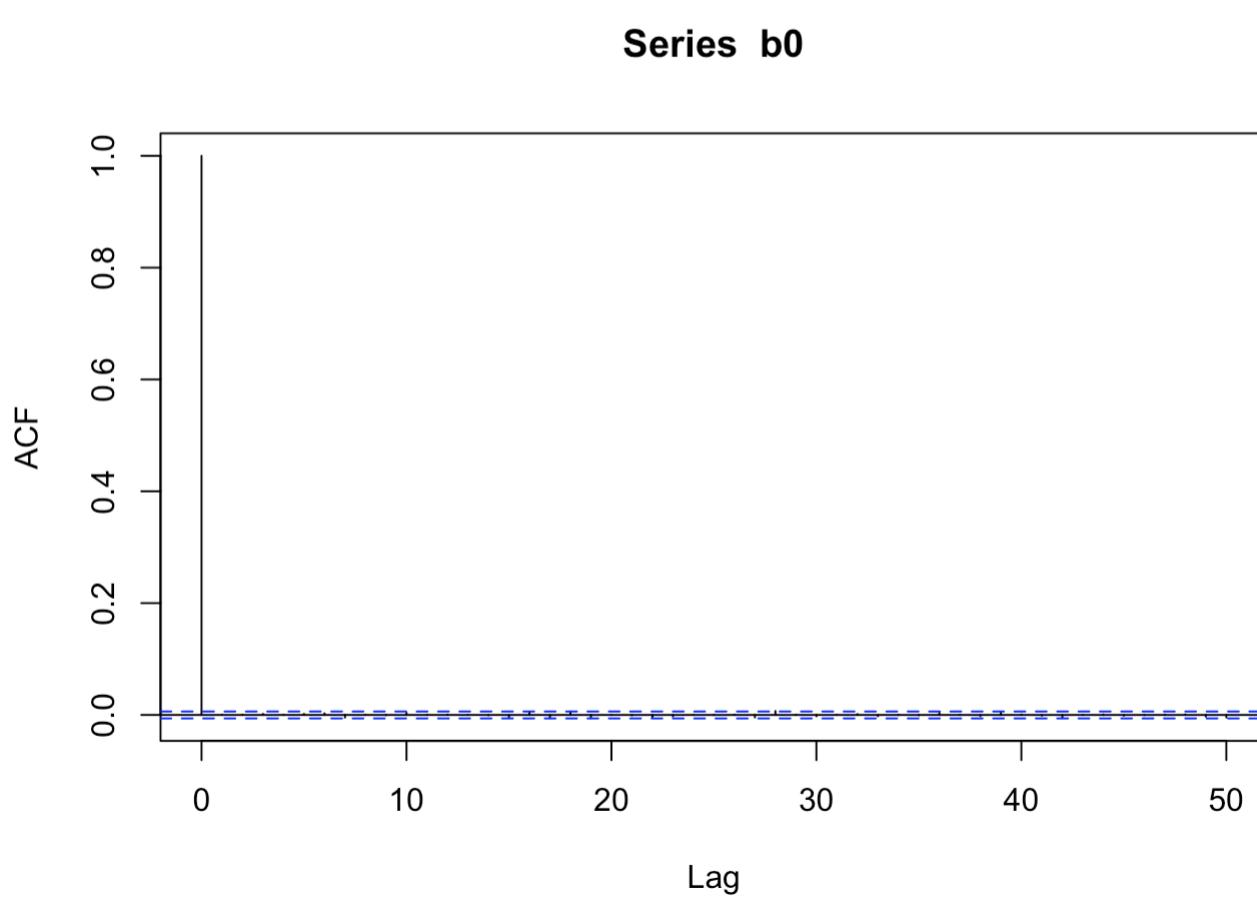
plot(b0,type="l")
```



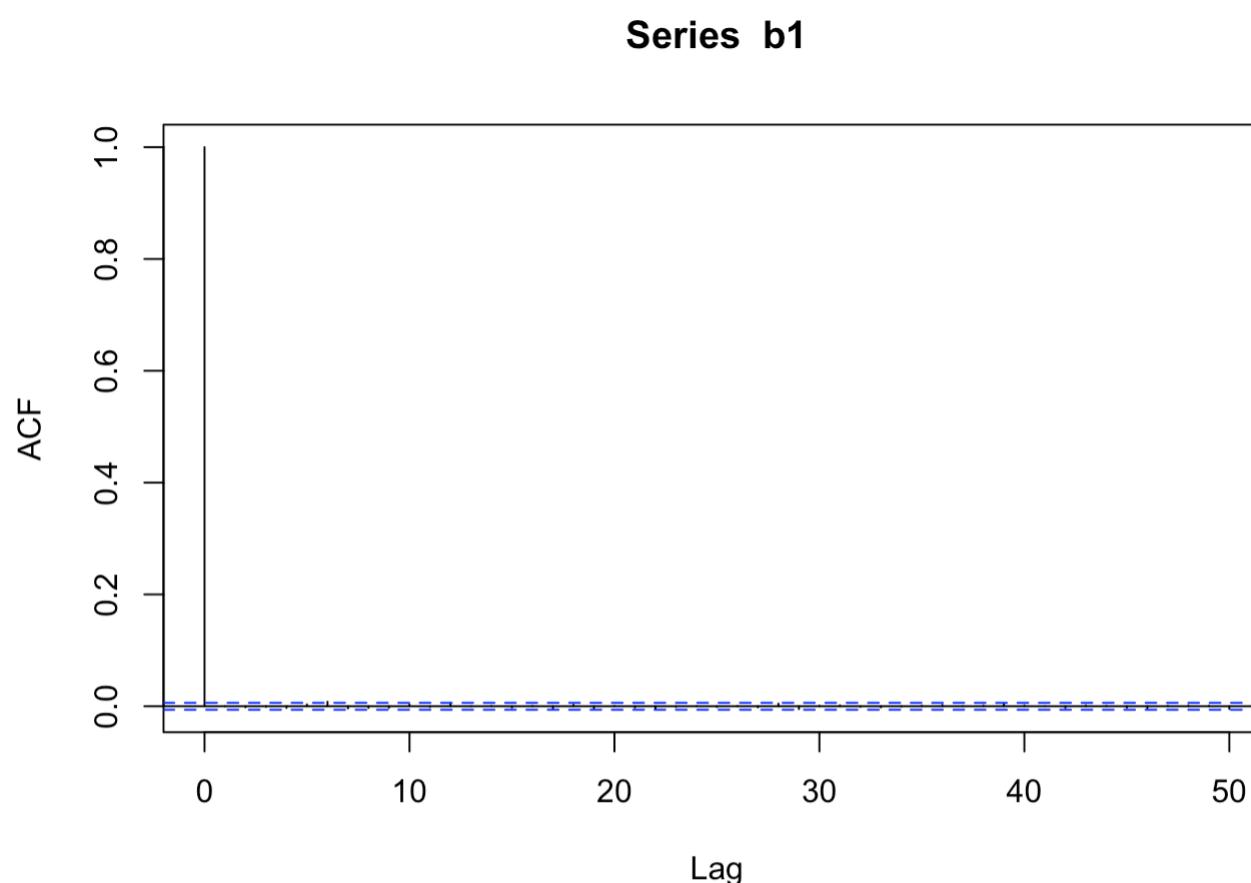
```
plot(b1,type="l")
```



```
acf(b0)
```



```
acf(b1)
```



```
gelman.diag(LeakModel.sim$BUGSoutput)
```

```
## Potential scale reduction factors:  
##  
##          Point est. Upper C.I.  
## beta[1]      1      1  
## beta[2]      1      1  
## deviance    1      1  
##  
## Multivariate psrf  
##  
## 1
```

```
effectiveSize(LeakModel.sim)
```

```
##   beta[1]   beta[2]  deviance  
## 7417.693 7593.643 16466.997
```

```
LeakModel.sim$BUGSoutput$DIC
```

```
## [1] 21.18689
```

```

#####
# Check Model Fit w/ the GoF Test
y <- leaks

# Calculating the fitted quantiles for each posterior model
# and adjusting for a discrete model
GoF <- matrix(NA, ncol=length(age), nrow=length(b0))
for (i in 1:length(b0)) {
  for (j in 1:length(age)) {
    vals <- ppois(c(y[j]-1,y[j]),exp(b0[i]+b1[i]*(age[j])))
    GoF[i,j] <- runif(1,vals[1],vals[2])
  }
}

# Function requires fitted quantiles and returns a p-value
GoF_Test <- function(fitted_quantiles) {
  n <- length(fitted_quantiles)
  K <- round((n)^0.4)
  mK <- table(cut(fitted_quantiles,(0:K)/K))
  np <- n/K
  RB <- sum(((mK-np)^2)/np)
  return(1-pchisq(RB,K-1))
}

# Calculating the p-values for each posterior model
GoF_Summary <- apply(GoF,1,GoF_Test)

# Histogram of posterior model p-values
#hist(GoF_Summary,xlim=c(0,1))

# Percent of posterior models with p-value less than 0.05
mean(GoF_Summary < 0.05)

```

```
## [1] 0.49079
```

```
q1prob <- mean(b1>0)
```

The model does not fit the data well as seen from the Chi-square Goodness-of-Fit test. What is $P(\beta_1 > 0)$ in the following model? 0.98264

Question 2

```
HKdata <- read.table("HorseKicks.txt", header=T)

horse <- HKdata %>%
  mutate(deaths = rowSums(select(., GC:C15)), year = Year)

#plot(horse$year, horse$deaths)

#x <- seq(0, 20, length = 1001)
#curve(dexp(x, rate=1/5), from=0, to=20) #mean of 5
#curve(dexp(x, rate=1/15), from=0, to=20) #mean of 15

#q <- matrix(c(1,1,1876,1892), ncol=2)
#q
#solve(q)

n <- length(horse$deaths)
time <- horse$year
y <- horse$deaths

HorseModel <- "model {
  for(i in 1:n){
    y[i] ~ dpois(lambda[i])
    log(lambda[i]) <- beta[1] + beta[2] * time[i]
  }

  beta[1] = (118.2500)*log(lam76) - (117.2500)*log(lam92)
  beta[2] = -(0.0625)*log(lam76) + (0.0625)*log(lam92)
  lam76 ~ dexp(1/5)
  lam92 ~ dexp(1/15)

}

"

```

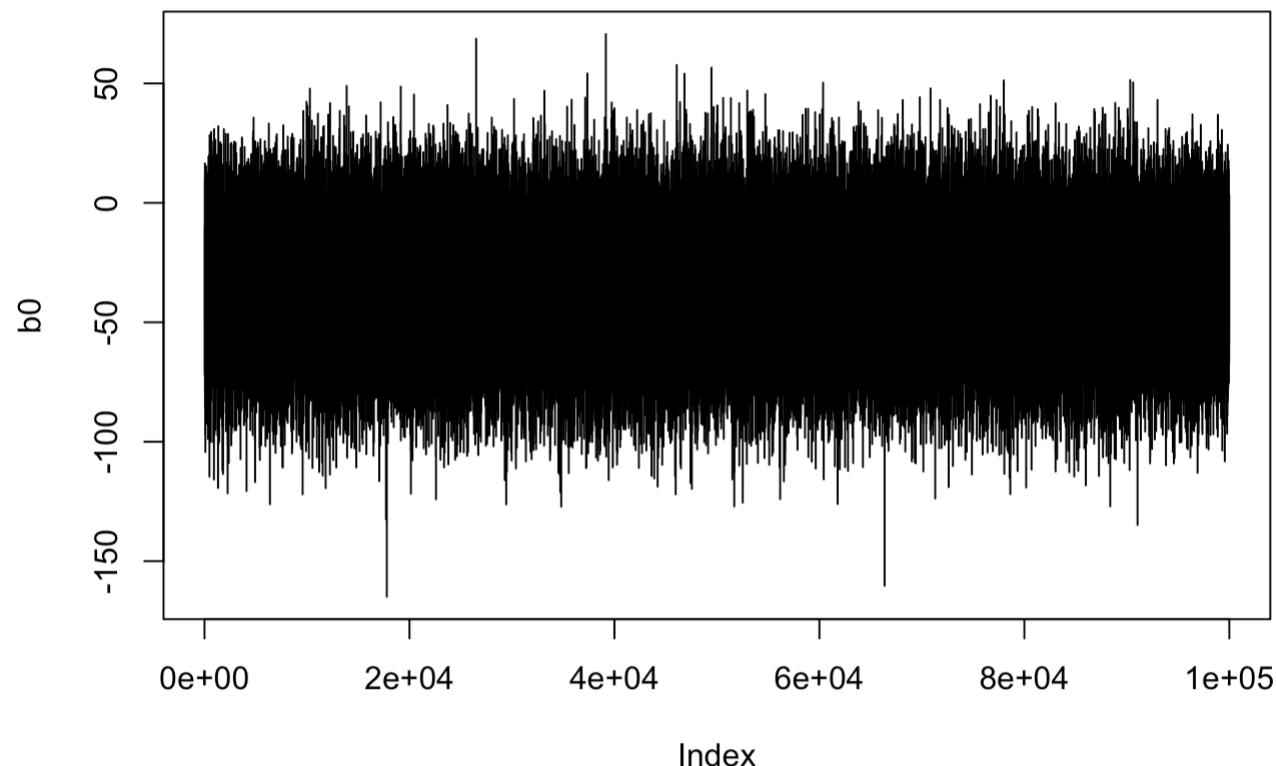
```
HorseModel.sim <- jags(
  data=c('y','time','n'),
  parameters.to.save=c('beta'),
  model.file=textConnection(HorseModel),
  n.iter=22000,
  n.burnin=2000,
  n.chains=5,
  n.thin=1
)
```

```
## Compiling model graph
## Resolving undeclared variables
## Allocating nodes
## Graph information:
##   Observed stochastic nodes: 20
##   Unobserved stochastic nodes: 2
##   Total graph size: 120
##
## Initializing model
```

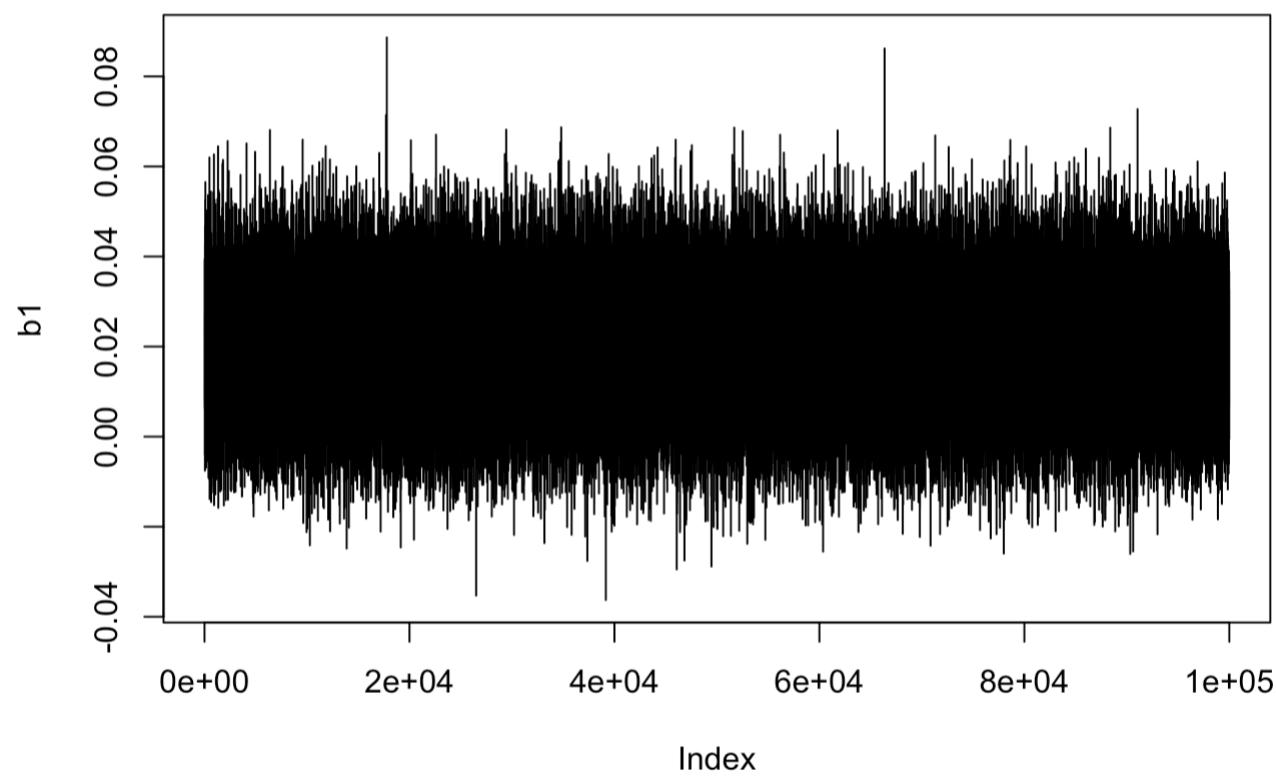
```
# 100,000 MCMC samples obtained
#head(HorseModel.sim$BUGSoutput$sims.matrix)

b0 <- HorseModel.sim$BUGSoutput$sims.matrix[,1]
b1 <- HorseModel.sim$BUGSoutput$sims.matrix[,2]

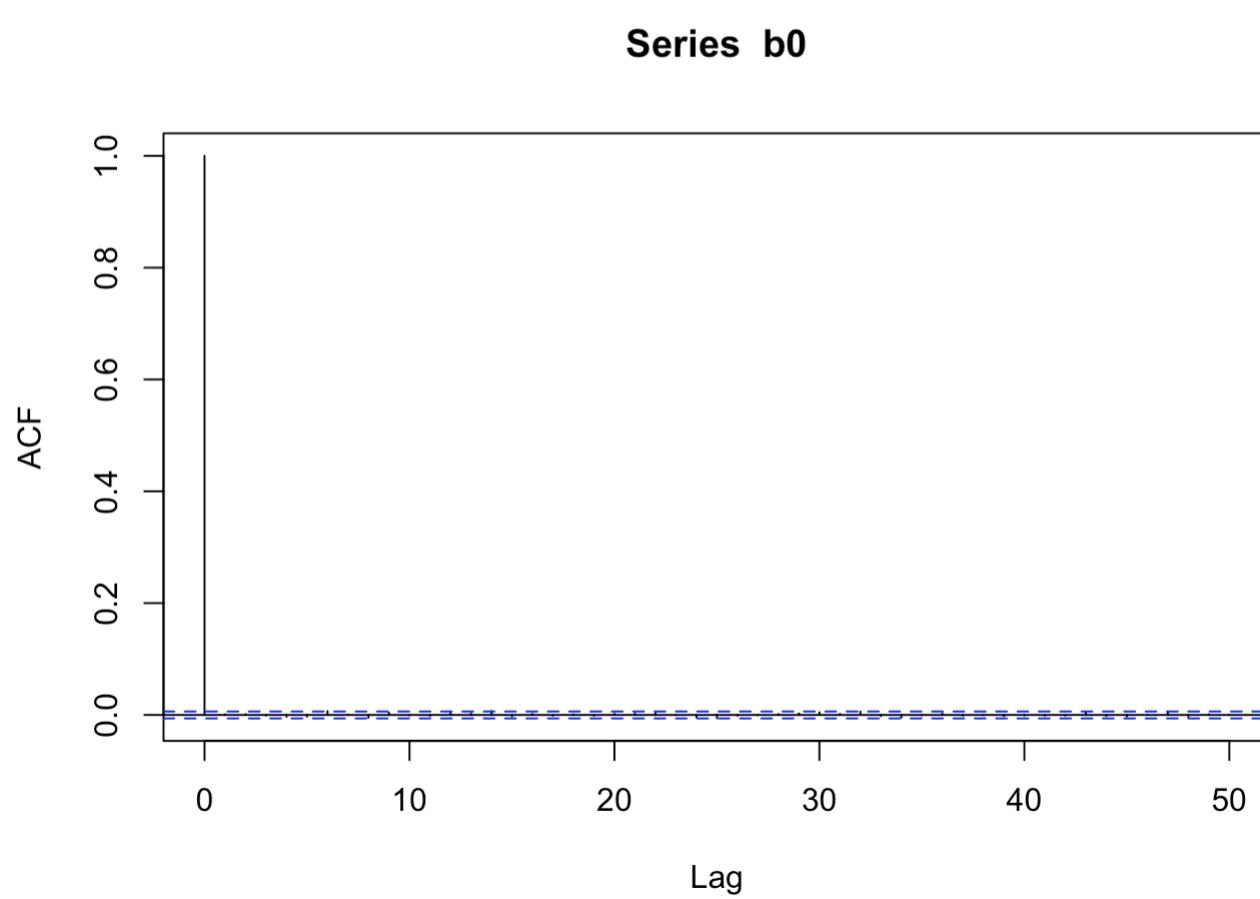
plot(b0, type="l")
```



```
plot(b1,type="l")
```

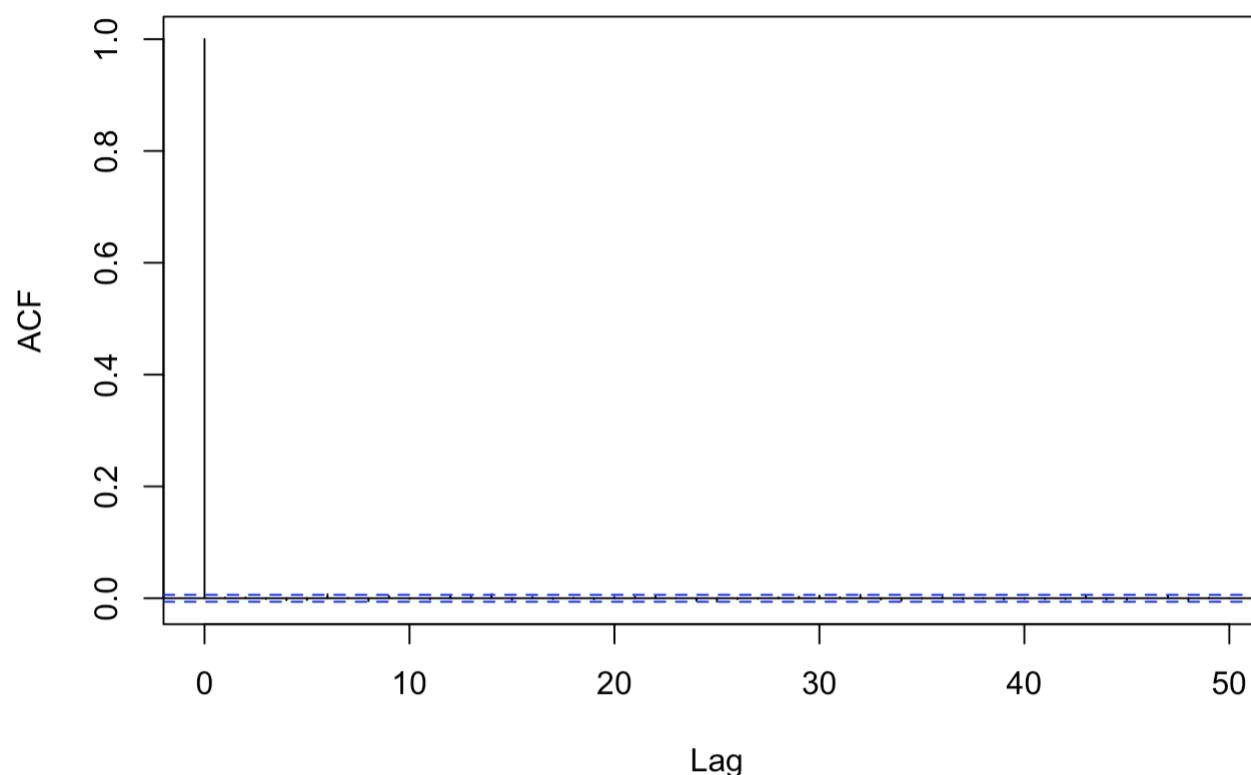


```
acf(b0)
```



```
acf(b1)
```

Series b1



```
gelman.diag(HorseModel.sim$BUGSoutput)
```

```
## Potential scale reduction factors:  
##  
##          Point est. Upper C.I.  
## beta[1]      1      1  
## beta[2]      1      1  
## deviance     1      1  
##  
## Multivariate psrf  
##  
## 1
```

```
HorseModel.sim$BUGSoutput$DIC
```

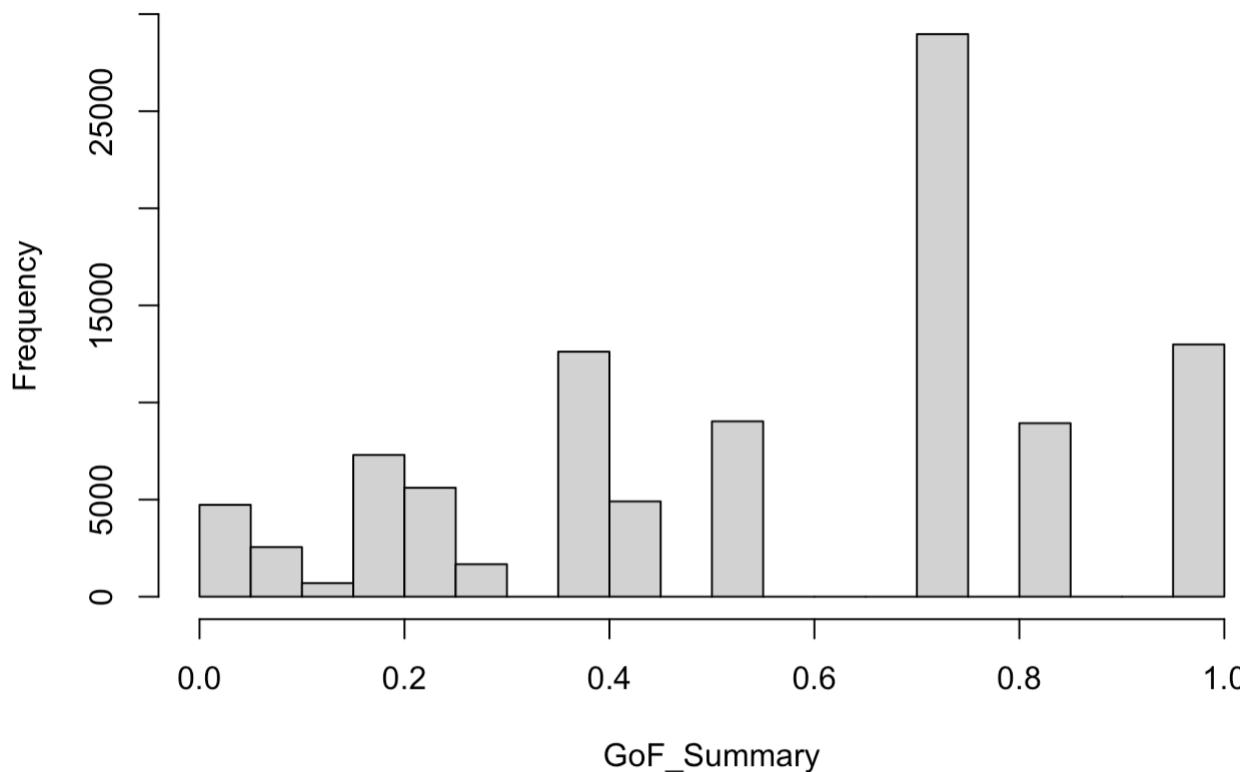
```
## [1] 120.8834
```

```
effectiveSize(HorseModel.sim)
```

```
## beta[1]  beta[2]  deviance  
## 43799.65 43791.95 42538.03
```

```
# Calculating the fitted quantiles for each posterior model  
# and adjusting for a discrete model  
GoF <- matrix(NA, ncol=length(time), nrow=length(b0))  
for (i in 1:length(b0)) {  
  for (j in 1:length(time)) {  
    vals <- ppois(c(y[j]-1,y[j]),exp(b0[i]+b1[i]*(time[j])))  
    GoF[i,j] <- runif(1,vals[1],vals[2])  
  }  
}  
  
# Function requires fitted quantiles and returns a p-value  
GoF_Test <- function(fitted_quantiles) {  
  n <- length(fitted_quantiles)  
  K <- round((n)^(0.4))  
  mK <- table(cut(fitted_quantiles,(0:K)/K))  
  np <- n/K  
  RB <- sum(((mK-np)^2)/np)  
  return(1-pchisq(RB,K-1))  
}  
  
# Calculating the p-values for each posterior model  
GoF_Summary <- apply(GoF,1,GoF_Test)  
  
# Histogram of posterior model p-values  
hist(GoF_Summary,xlim=c(0,1))
```

Histogram of GoF_Summary



```
# Percent of posterior models with p-value less than 0.05  
mean(GoF_Summary < 0.05)
```

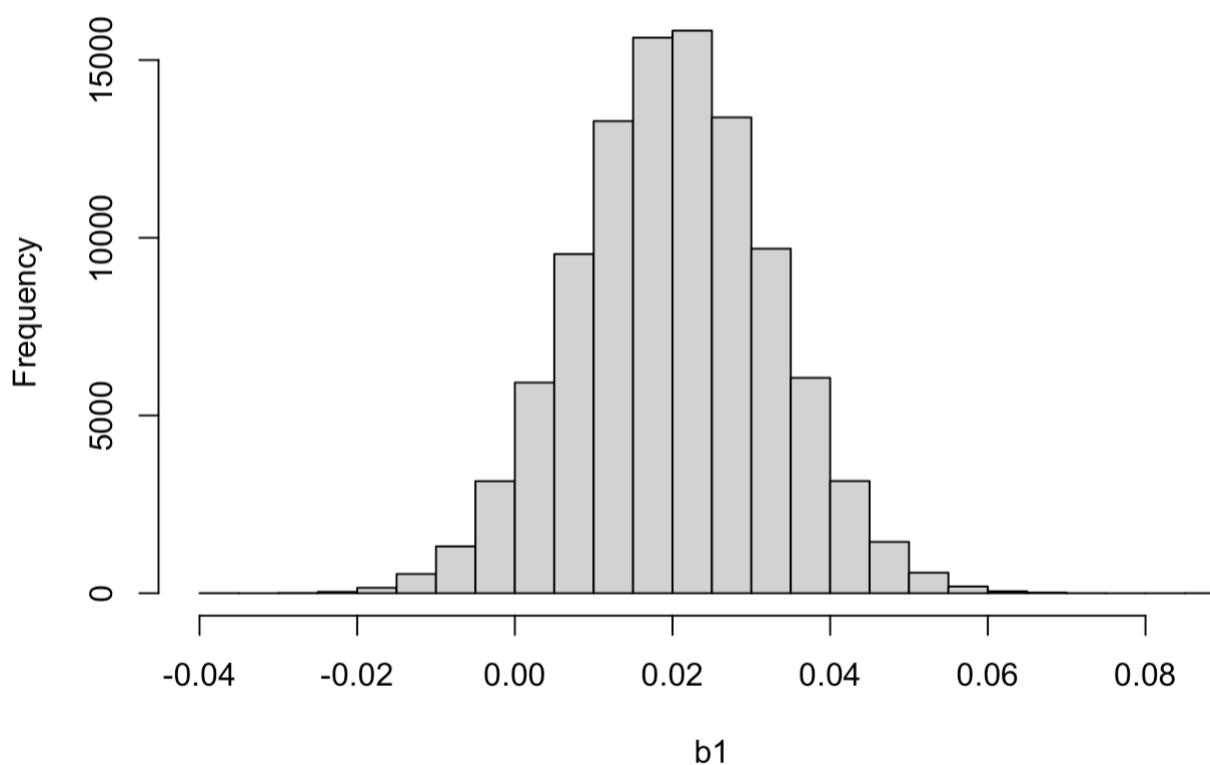
```
## [1] 0.0473
```

```
mean(b1)
```

```
## [1] 0.02011894
```

```
hist(b1)
```

Histogram of b1



```
#lam76 <- rexp(100000,1/5)  
#lam92 <- rexp(100000,1/15)  
#b0prior <- (118.2500)*log(lam76) - (117.2500)*log(lam92)  
#b1prior <- -(0.0625)*log(lam76) + (0.0625)*log(lam92)  
#plot(b0prior,b1prior,xlim=c(-15,7),ylim=c(-.03,.03),pch='.',ylab='b1',xlab='b0')  
#par(new=T)  
#plot(HorseModel.sim$BUGSoutput$sims.matrix[,1],HorseModel.sim$BUGSoutput$sims.matrix[,2],  
#      xlim=c(-15,20),ylim=c(-.03,.03),col=4,pch='.',ylab='',xlab='')  
  
lambda1880 <- exp(b0+b1*(1880))  
PPD1880 <- rpois(length(lambda1880),lambda1880)  
quantile(PPD1880,c(0.025,0.975))
```

```
## 2.5% 97.5%  
## 3 15
```

```

lambda1890 <- exp(b0+b1*(1890))
PPD1890 <- rpois(length(lambda1890), lambda1890)
quantile(PPD1890,c(0.025,0.975))

```

```

## 2.5% 97.5%
##      5     18

```

Time does affect the rate of death by horse kicks. Our model fits the data well, as seen from the Chi-square Goodness-of-Fit test, and our b1 value is positive. This means that our slope is increasing over time. Thus, there are more deaths per year as time goes on.

Question 3

```

gauge <- read.table("table78.txt",header=T)
#head(gauge)

#plot(gauge$Gauge, gauge$Strength)
#plot(log(gauge$Gauge), gauge$Strength)

#z <- matrix(c(1,1,1.609438,5.579730), ncol=2)
#z
#solve(z)

logGauge <- log(gauge$Gauge)
n <- length(gauge$Strength)
y <- gauge$Strength

GaugeModel <- "model {
  for(i in 1:n){
    y[i] ~ dlnorm(mu[i],1/(sigma)^2)
    mu[i] <- beta0 + beta1 * logGauge[i]
  }

  sigma ~ dexp(1/2)
  mu1.6 ~ dnorm(1.7128,0.2)
  mu5.5 ~ dnorm(3.5272,0.2)
  beta0 = (1.4053702)*mu1.6 - (0.4053702)*mu5.5
  beta1 = -(0.2518706)*mu1.6 + (0.2518706)*mu5.5
}

"

```

```

GaugeModel.sim <- jags(
  data=c('y', 'n', 'logGauge'),
  parameters.to.save=c('beta0','beta1','sigma'),
  model.file=textConnection(GaugeModel),
  n.iter=22000,
  n.burnin=2000,
  n.chains=5,
  n.thin=1
)

```

```

## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 214
##    Unobserved stochastic nodes: 3
##    Total graph size: 458
##
## Initializing model

```

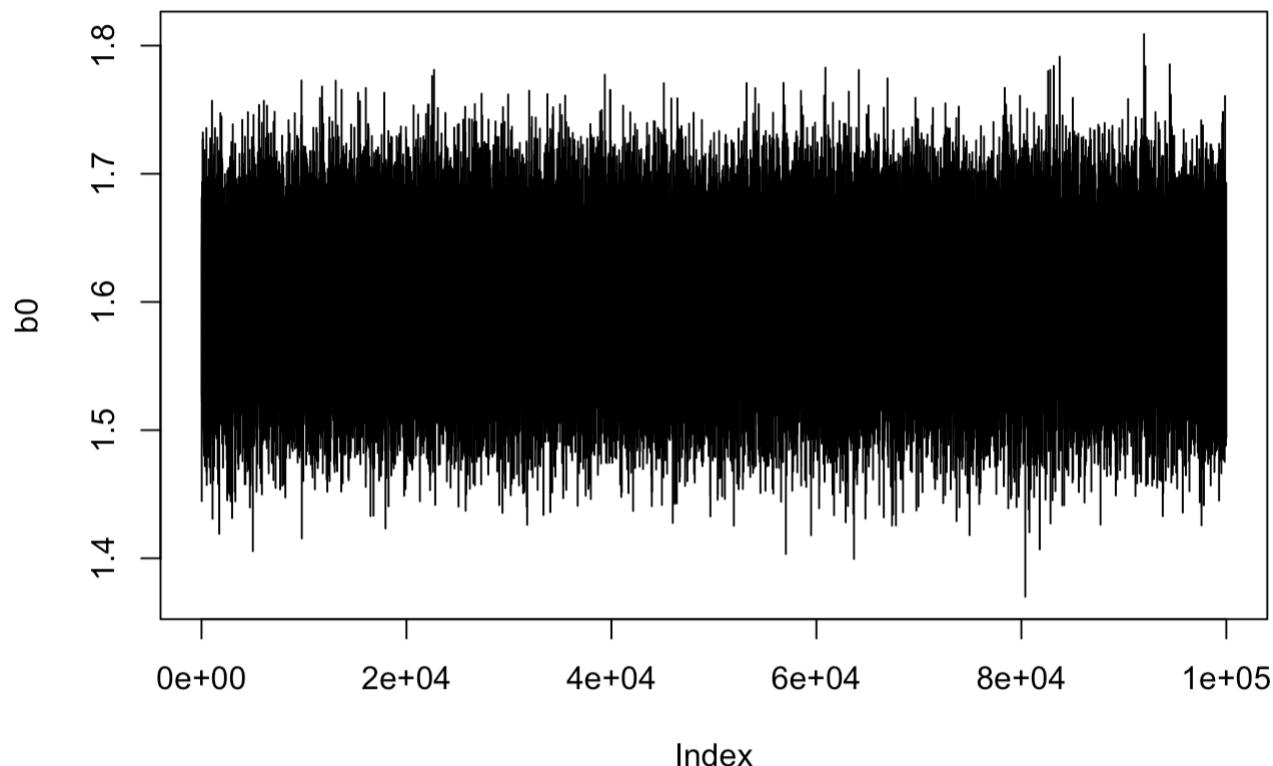
```

#head(GaugeModel.sim$BUGSoutput$sims.matrix)

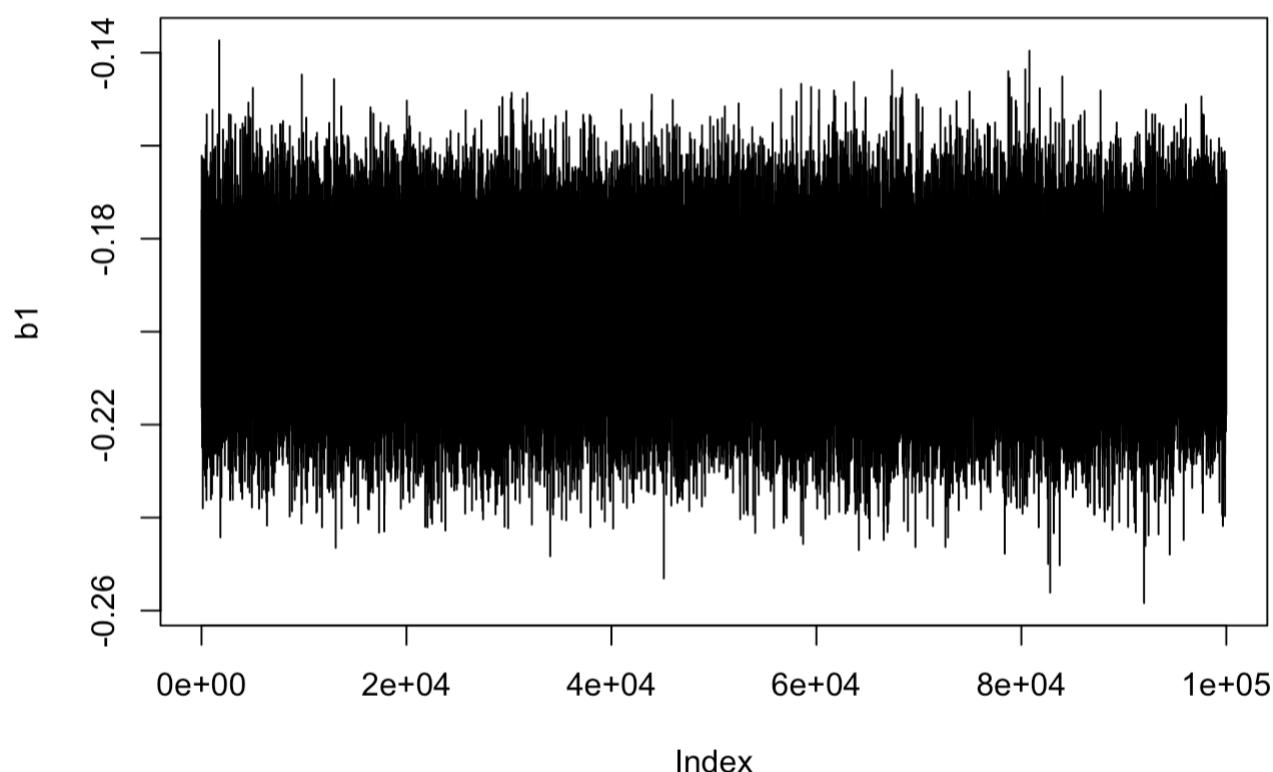
b0 <- GaugeModel.sim$BUGSoutput$sims.matrix[,1]
b1 <- GaugeModel.sim$BUGSoutput$sims.matrix[,2]
sigma <- GaugeModel.sim$BUGSoutput$sims.matrix[,4]

plot(b0,type="l")

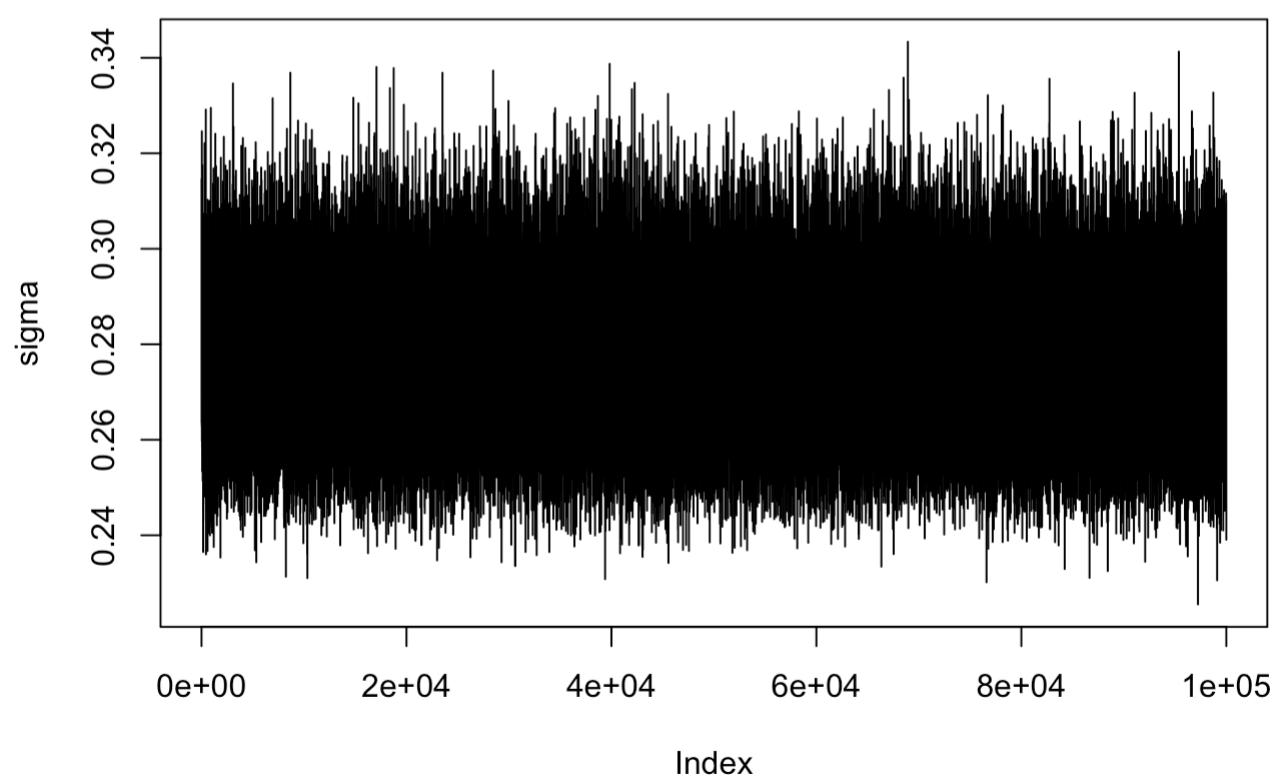
```



```
plot(b0,type="l")
```



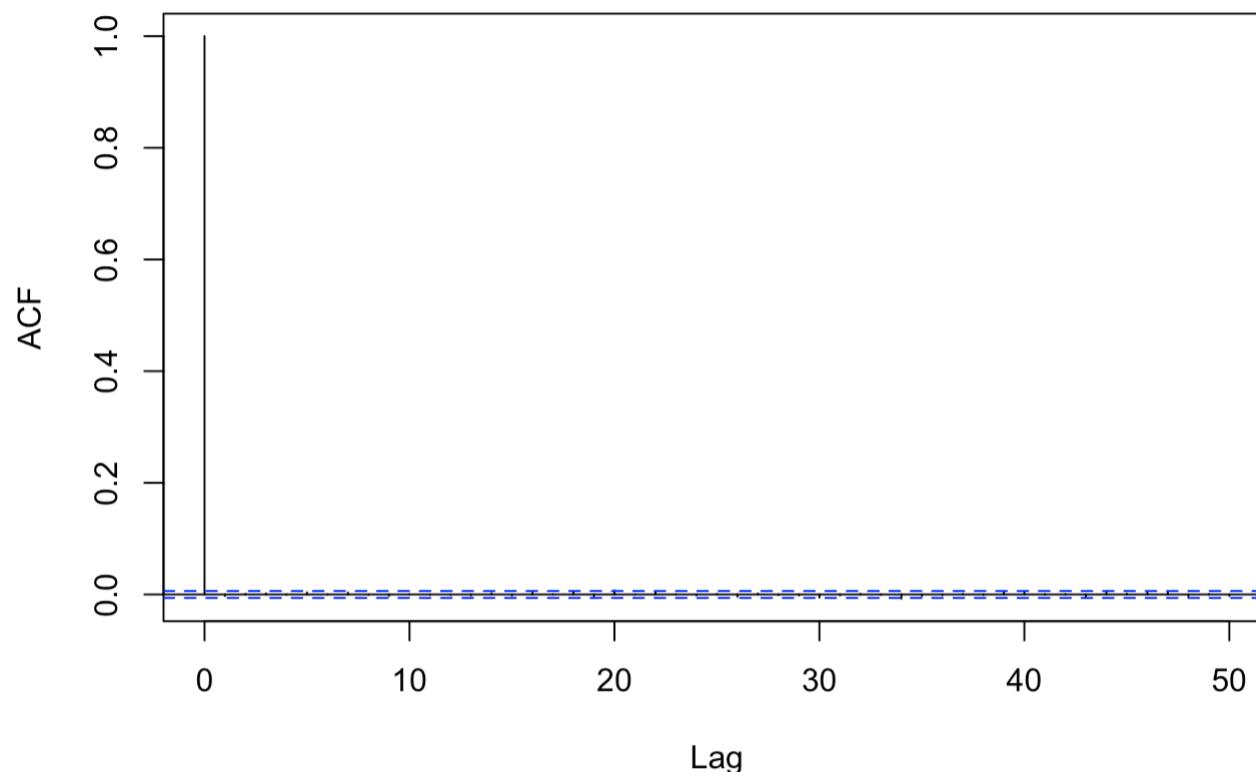
```
plot(b1,type="l")
```



Index

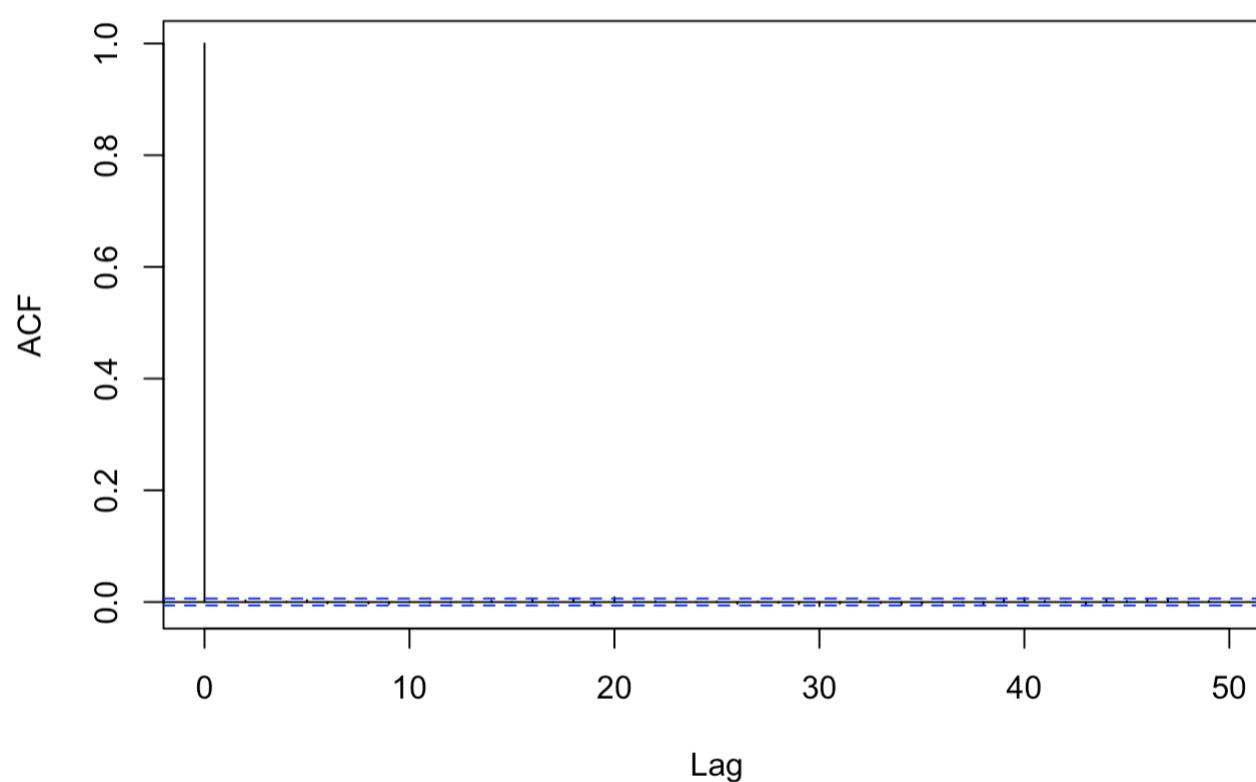
acf(b0)

Series b0



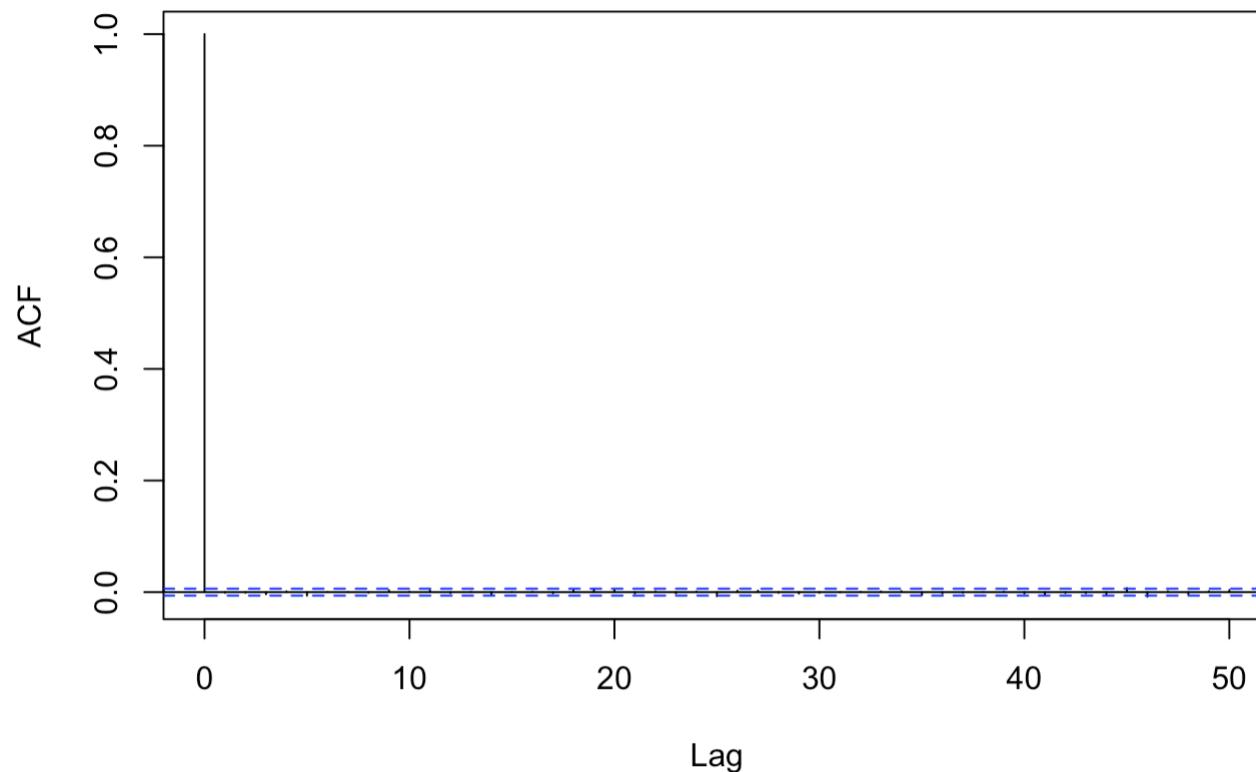
acf(b1)

Series b1



acf(sigma)

Series sigma



```
gelman.diag(GaugeModel.sim$BUGSoutput)
```

```
## Potential scale reduction factors:  
##  
##          Point est. Upper C.I.  
## beta0          1          1  
## beta1          1          1  
## deviance       1          1  
## sigma          1          1  
##  
## Multivariate psrf  
##  
## 1
```

```
GaugeModel.sim$BUGSoutput$DIC
```

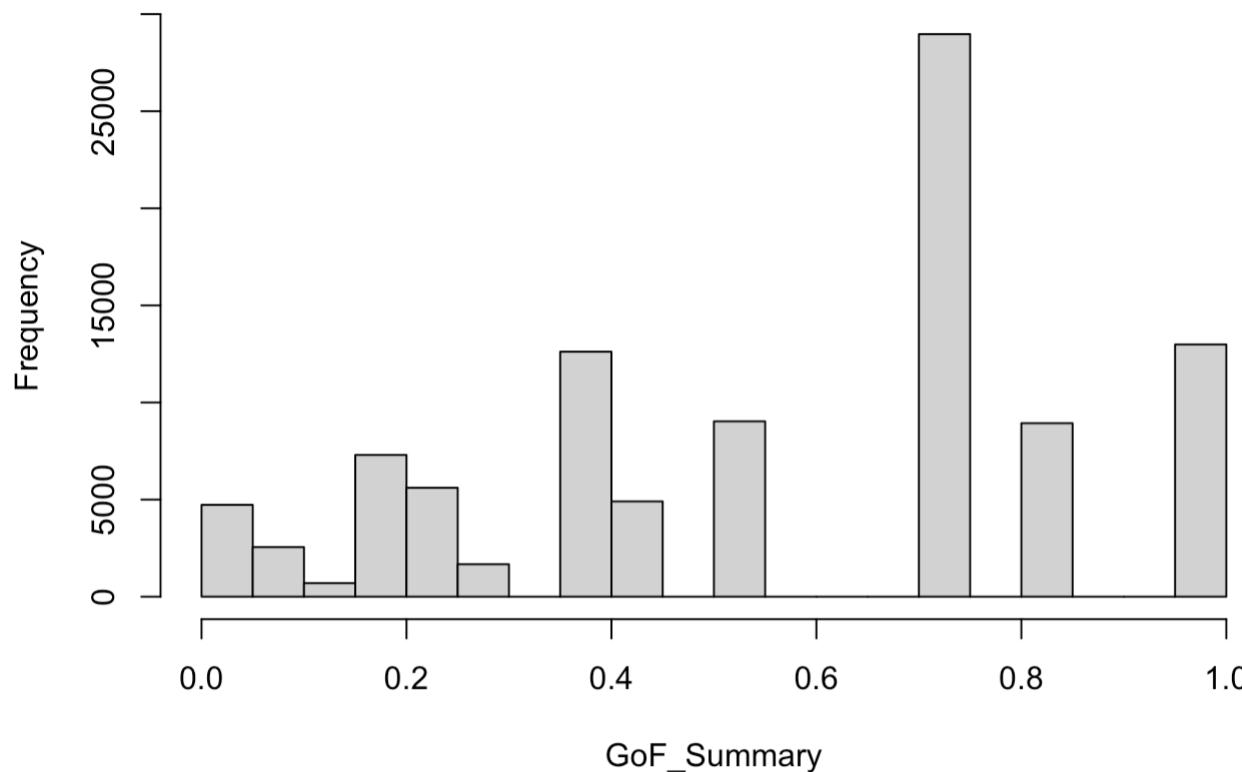
```
## [1] 471.6606
```

```
effectiveSize(GaugeModel.sim)
```

```
##    beta0    beta1 deviance    sigma  
## 44127.74 42289.71 40160.25 57195.98
```

```
GoF <- matrix(NA, ncol=n, nrow=length(b0))  
for (i in 1:length(b0)) {  
  for (j in 1:n) {  
    GoF[i,j] <- plnorm(y[j], b0[i]+b1[i]*logGauge[j], sd=sigma[i])  
  }  
}  
  
GoF_Test <- function(fitted_quantiles) {  
  n <- length(fitted_quantiles)  
  K <- round((n)^(0.4))  
  mK <- table(cut(fitted_quantiles, (0:K)/K))  
  np <- n/K  
  RB <- sum(((mK-np)^2)/np)  
  return(1-pchisq(RB, K-1))  
}  
  
GoF <- apply(GoF, 1, GoF_Test)  
  
hist(GoF_Summary, xlim=c(0,1))
```

Histogram of GoF_Summary

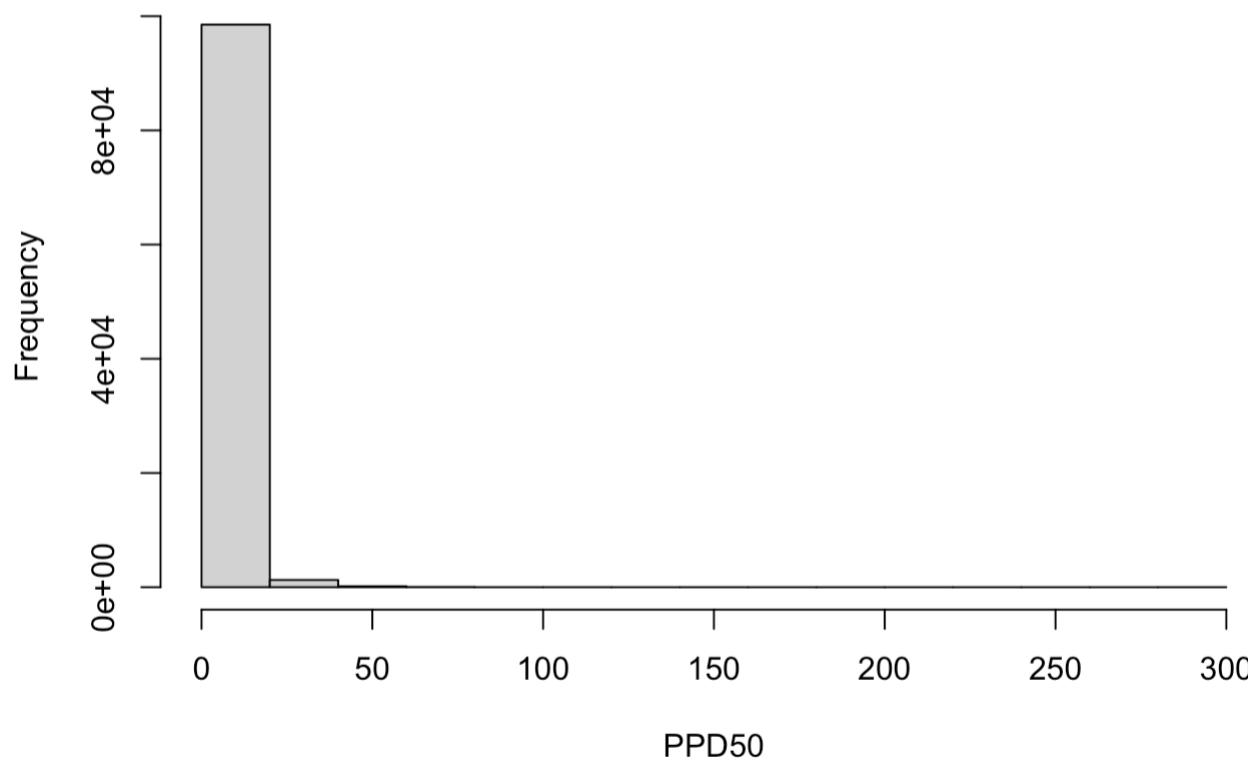


```
# Percent of posterior models with p-value less than 0.05  
mean(GoF_Summary < 0.05)
```

```
## [1] 0.0473
```

```
# PPD for gauge length 50mm  
mu50 <- b0+b1*(log(50))  
PPD50 <- rlnorm(length(mu50),mu50)  
hist(PPD50)
```

Histogram of PPD50



```
#summary(PPD50)  
estimate <- mean(PPD50)  
#quantile(PPD50,c(0.025,0.975))  
less.than.5 <- quantile(PPD50,c(0.05,1))
```

Model fits quite well, as seen from the Chi-square Goodness-of-Fit diagnostics.

estimate: 3.7621285

uncertainty such that less than 5% of the population has a smaller value: (0.4415513, 292.3085559)