

AdvancedStatsAssignment

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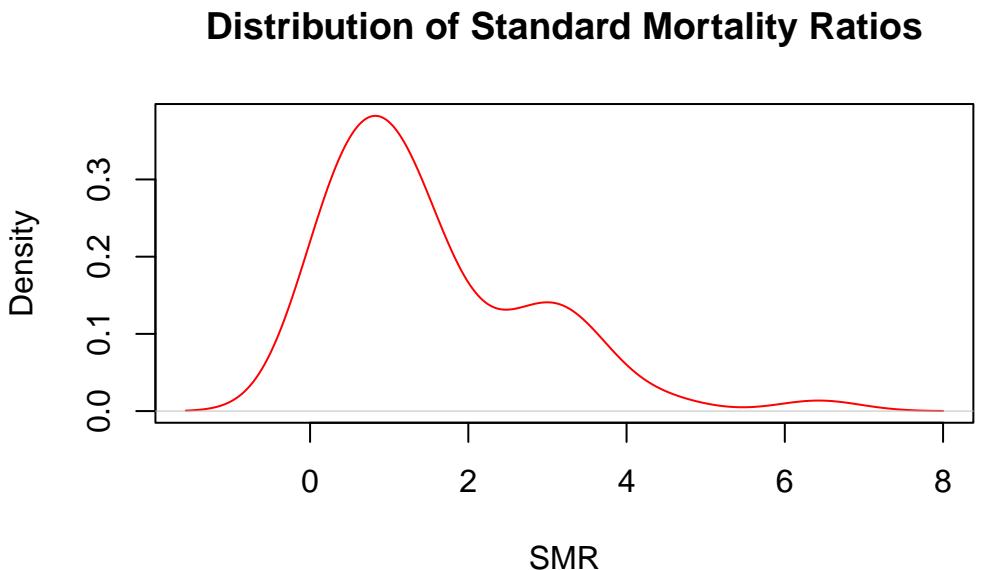
Question 1

```
source("ScotlandMap.R") # need to read in the Scotland Map function  
testdat = runif(56) # generate random numbers to use as observations  
ScotlandMap(testdat, figtitle = "Scotland random numbers")
```

Question 1 a)

```
ScotlandDF$SMR = ScotlandDF$Observed/ScotlandDF$Expected

plot(density(ScotlandDF$SMR), main = "Distribution of Standard Mortality Ratios",
      xlab = "SMR", ylab = "Density", col = "red")
```



```
source("ScotlandMap.R") # need to read in the ScotlandMap function
testdat = ScotlandDF$SMR # generate random numbers to use as observations
ScotlandMap(testdat, figtitle = "Scotland SMR by region")
```

Warning: OGR support is provided by the sf and terra packages among others

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Warning: OGR support is provided by the sf and terra packages among others

Warning: OGR support is provided by the sf and terra packages among others

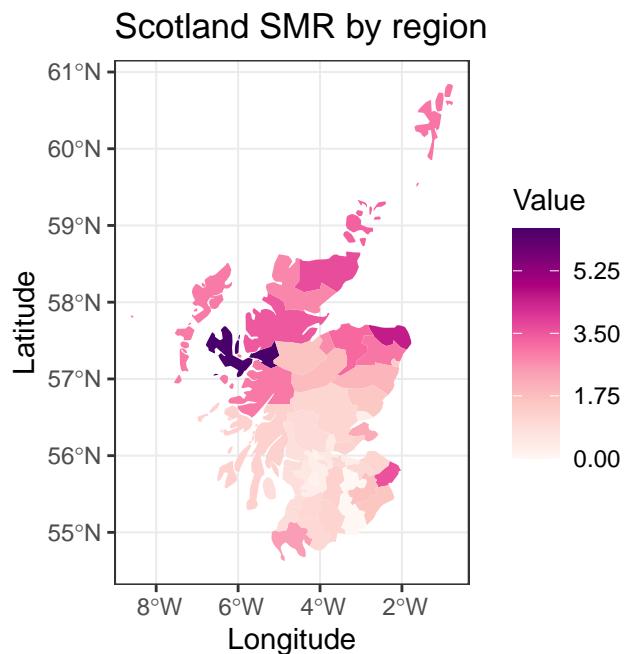
Warning: OGR support is provided by the sf and terra packages among others

OGR data source with driver: ESRI Shapefile

Source: "C:\AppliedDataScienceAndStatistics\Applied-Data-Science-and-Statistics\Term2\Advanced

with 56 features

It has 1 fields



Question 1 b)

β_0 is the intercept that represents the baseline for when all the other variables are 0 which can also be interpreted as the log number expected of cases per administrative area.

θ_i is the effect that captures the variation in the observed number of cases that cannot be explained by the expected numbers alone. θ_i also represents the deviation of the log observed number of cases from the log expected number of cases for area i.

In the Poisson model, θ_i represents the deviation of the observed number of cases in area i from the expected number of cases in area i, given the reference rates. In other words, it captures how much higher or lower the observed number of cases is compared to what we would expect based on the reference rates

The role of i in the estimation of the relative risk is to allow for variation in the risk of disease across different areas, over and above what is explained by the reference rates. By including a random effect for each area in the model, we are able to estimate the relative risk for each area, while accounting for the fact that some areas may have higher or lower risk due to factors that are not captured by the reference rates alone.

Question 1 c)

```
jags.mod.lipCancer = function() {
  # Priors
  beta0 ~ dnorm(0, 1/1000)
  tau ~ dgamma(1, 0.05)

  # Likelihood
  for (i in 1:N) {
    obs[i] ~ dpois(mu[i])
    log(mu[i]) = log(expo[i]) + beta0 + theta[i]
    theta[i] ~ dnorm(0, tau)
    RR[i] = exp(beta0) * exp(theta[i])
  }
}

# Parameters to monitor
jags.param.lipCancer = c("beta0", "theta", "tau", "RR")

# Data
jags.data.lipCancer <- list(N = nrow(ScotlandDF), obs = ScotlandDF$Observed,
                           expo = ScotlandDF$Expected)

## initial values, have to be for the stochastic for theta it will be a
## repetition because of the i
inits1 <- list(tau = 1, beta0 = 1, theta = rep(1, 56))
inits2 <- list(tau = 17.20806, beta0 = -0.5604756, theta = rep(19.38524,
  56))

## these initial values for inits2 came from these functions random
## generation set.seed(123) y <- rgamma(n = 1, shape = 1, rate = 0.05)
## value <- rnorm(1, mean = 0, sd = sqrt(1000)) tau_init <- 1/rgamma(n
## = 1, shape = 2, rate = 0.1)
```

```
jags.inits.lipCancer = list(inits1, inits2)

## fit the jags model

jags.mod.fit.lipCancer <- jags(data = jags.data.lipCancer, inits = jags.inits.lipCancer,
  parameters.to.save = jags.param.lipCancer, n.chains = 2, n.iter = 15000,
  n.burnin = 7500, n.thin = 1, model.file = jags.mod.lipCancer, DIC = FALSE)

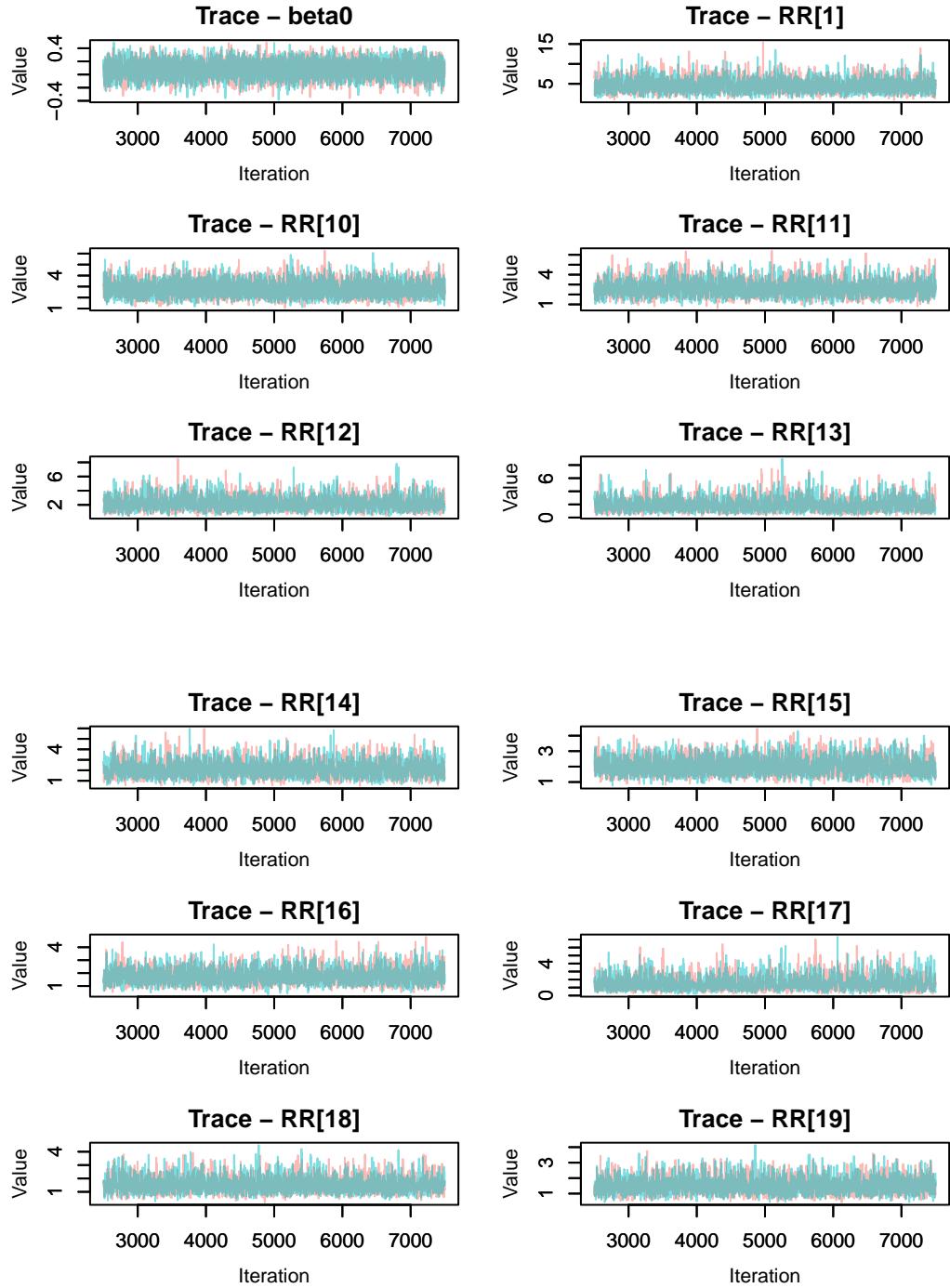
module glm loaded

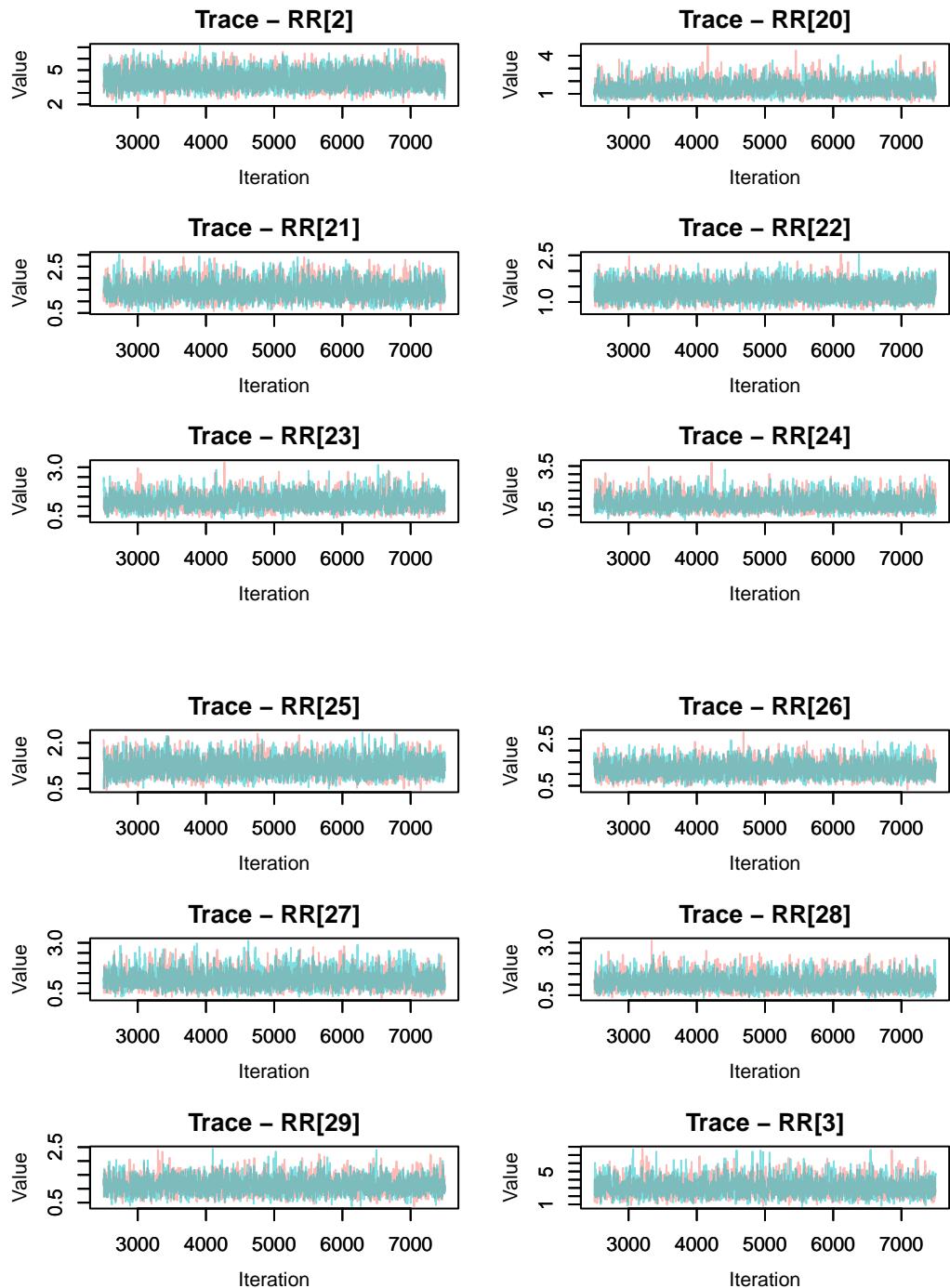
module dic loaded

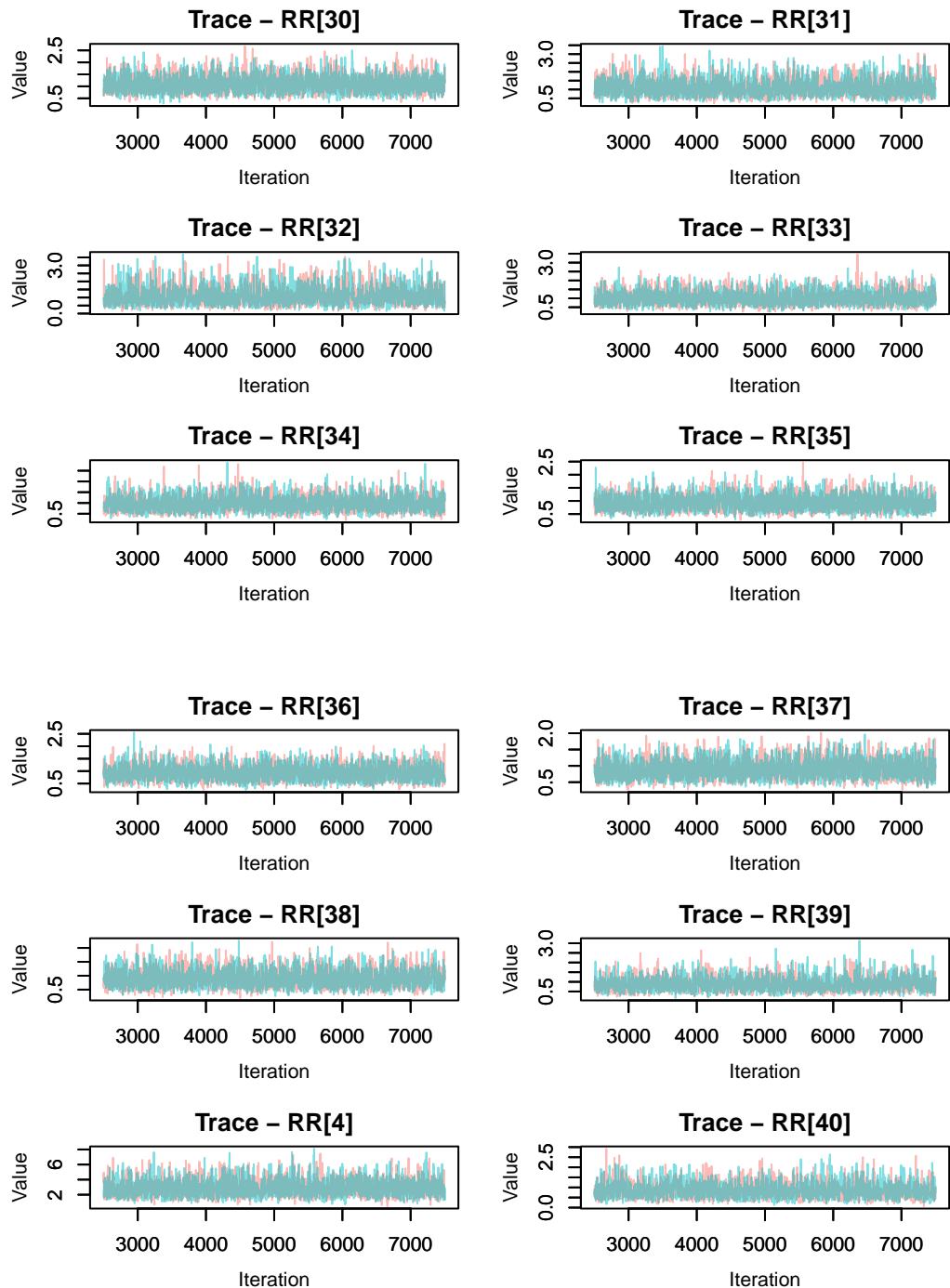
Compiling model graph
  Resolving undeclared variables
  Allocating nodes
Graph information:
  Observed stochastic nodes: 56
  Unobserved stochastic nodes: 58
  Total graph size: 450

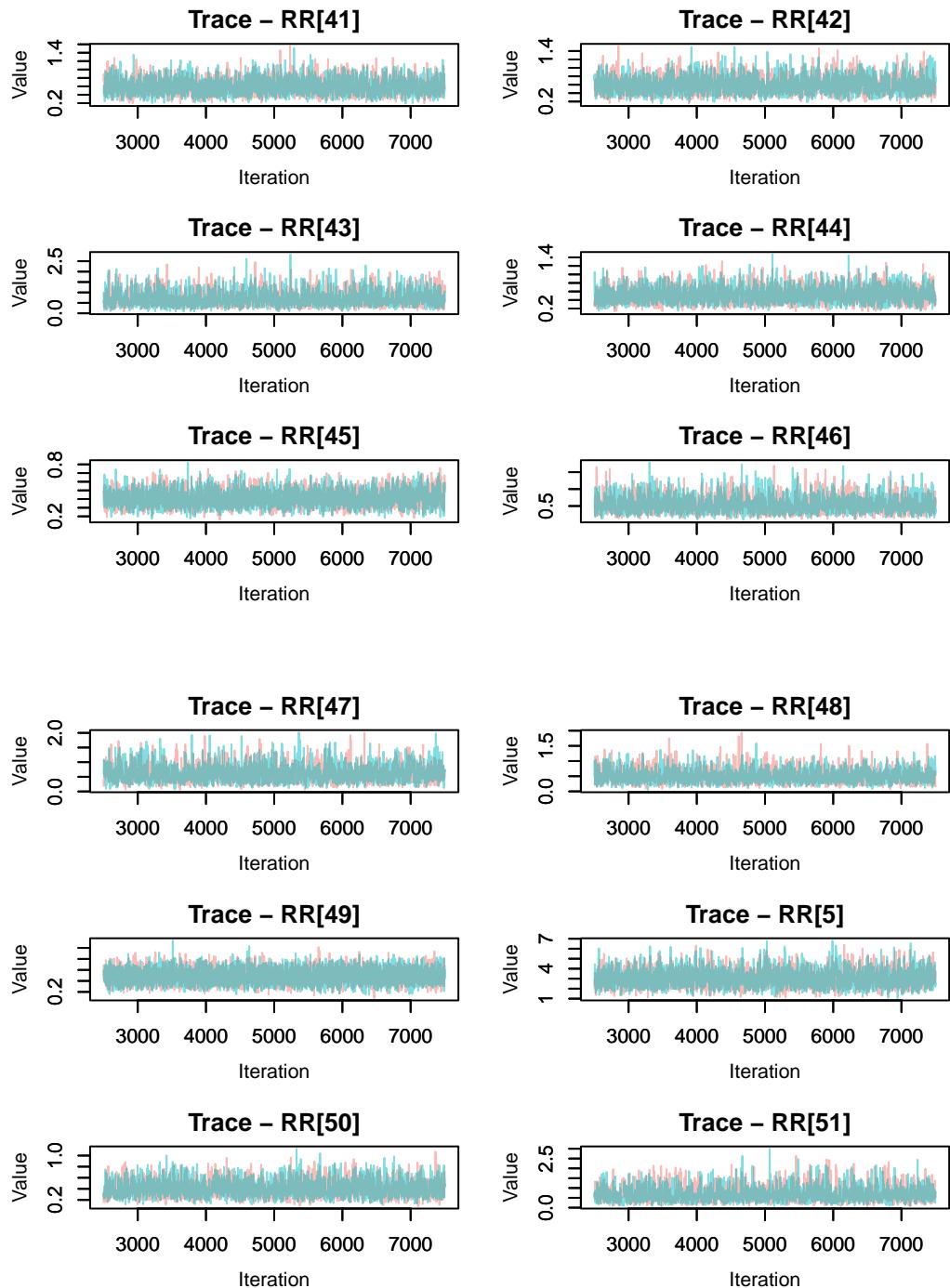
Initializing model

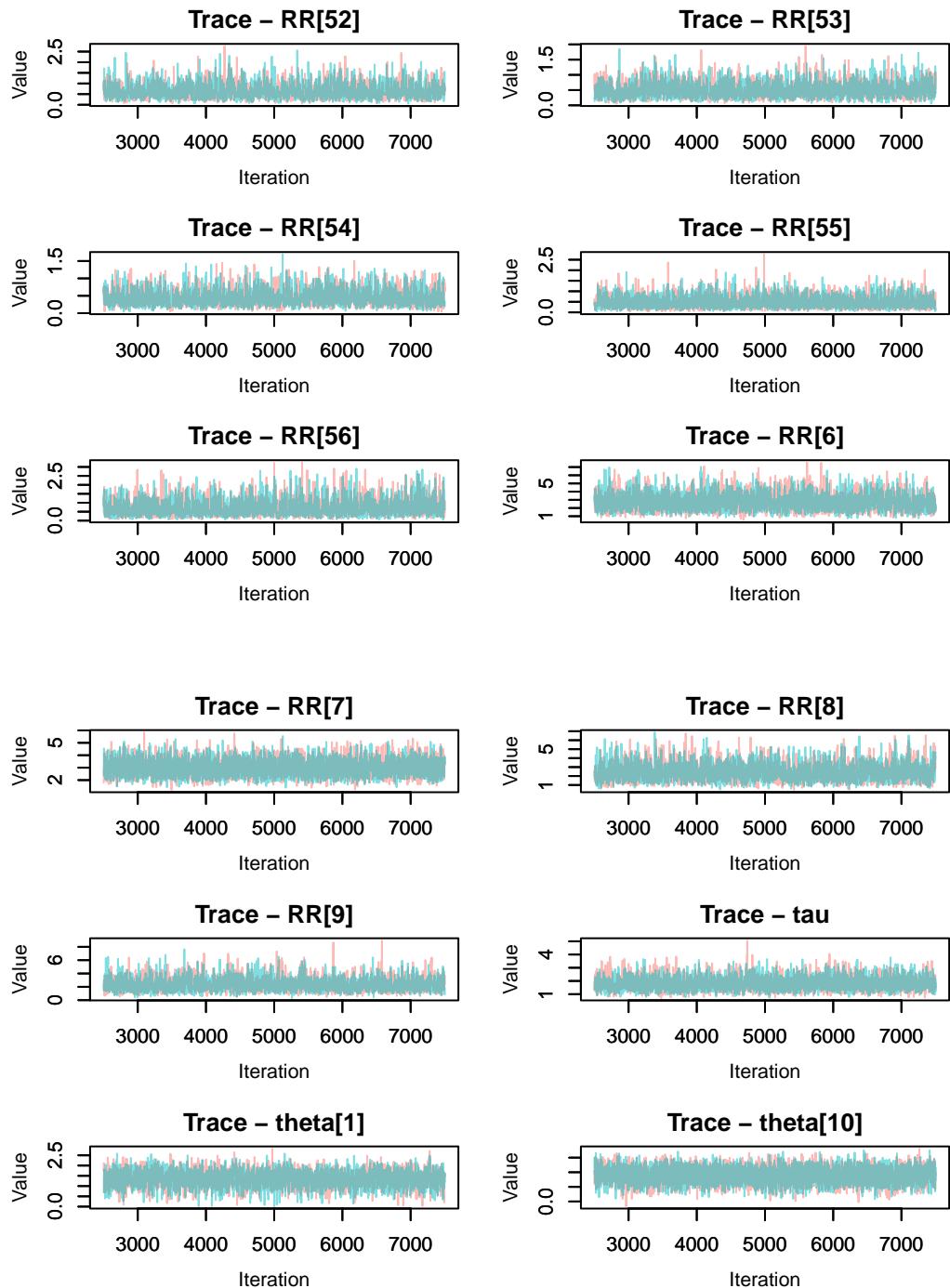
jagsfitlipCancer.mcmc <- as.mcmc(jags.mod.fit.lipCancer)
MCMCtrace(jagsfitlipCancer.mcmc, type = "trace", ind = TRUE, pdf = FALSE)
```

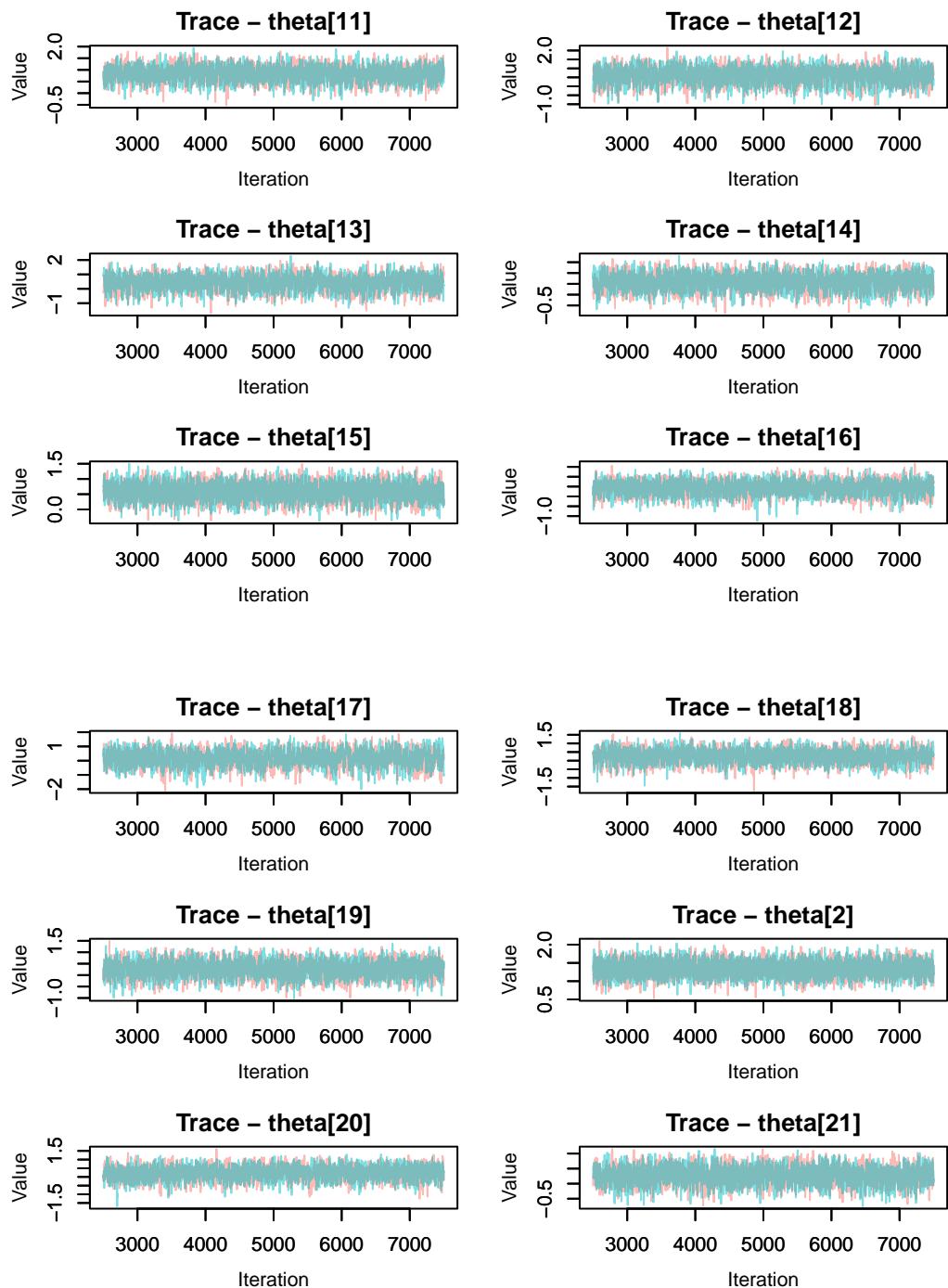


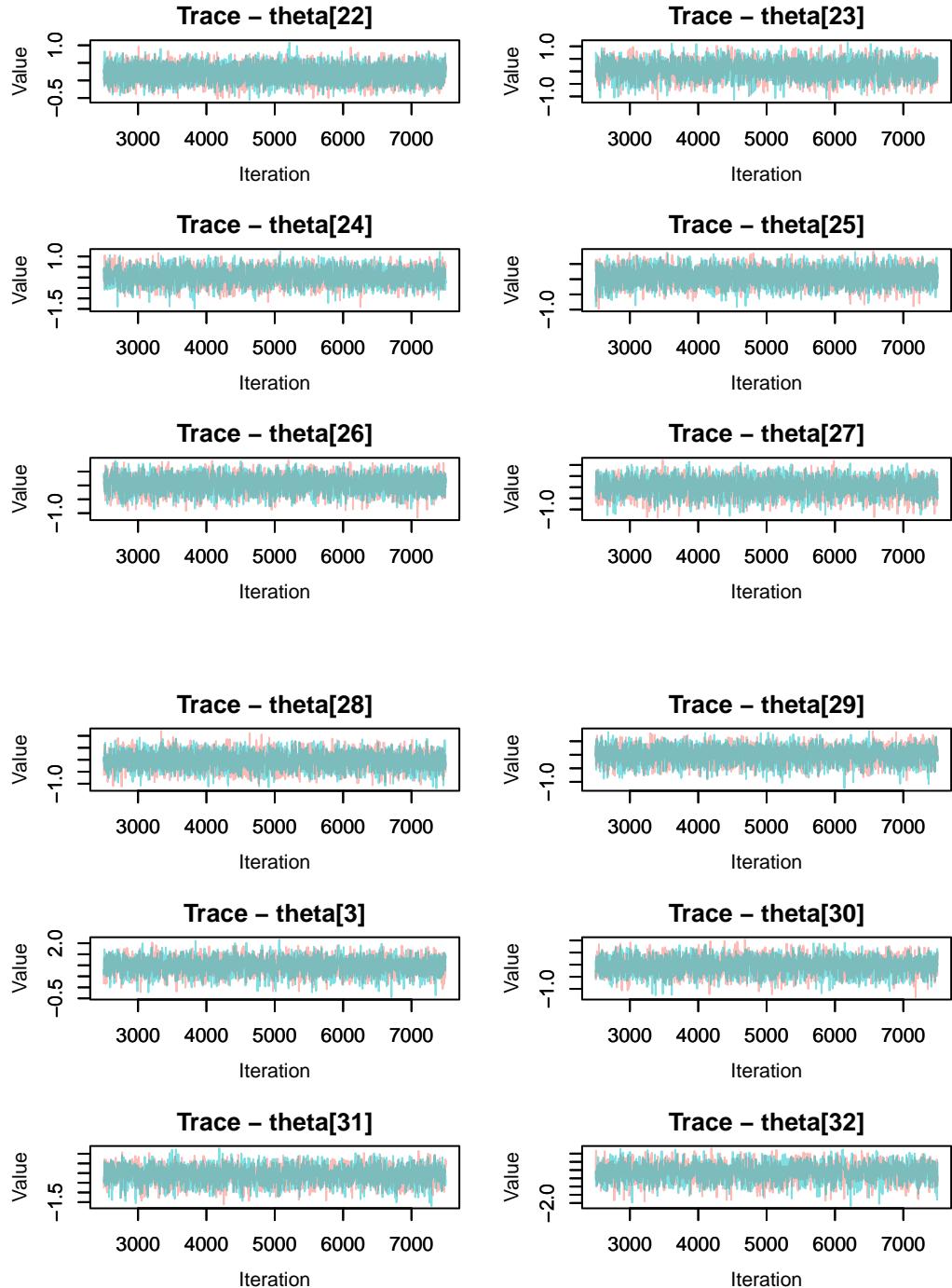


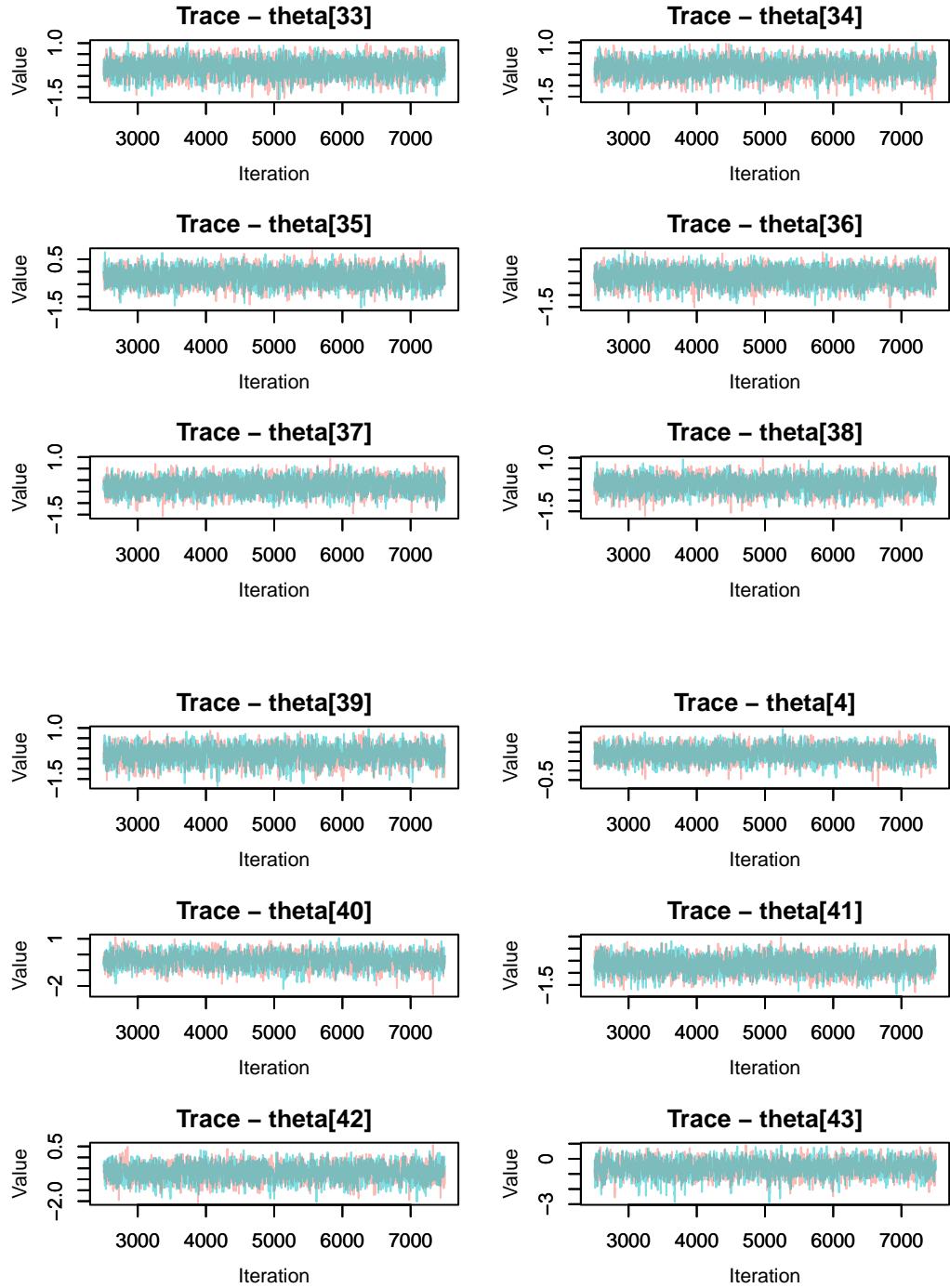


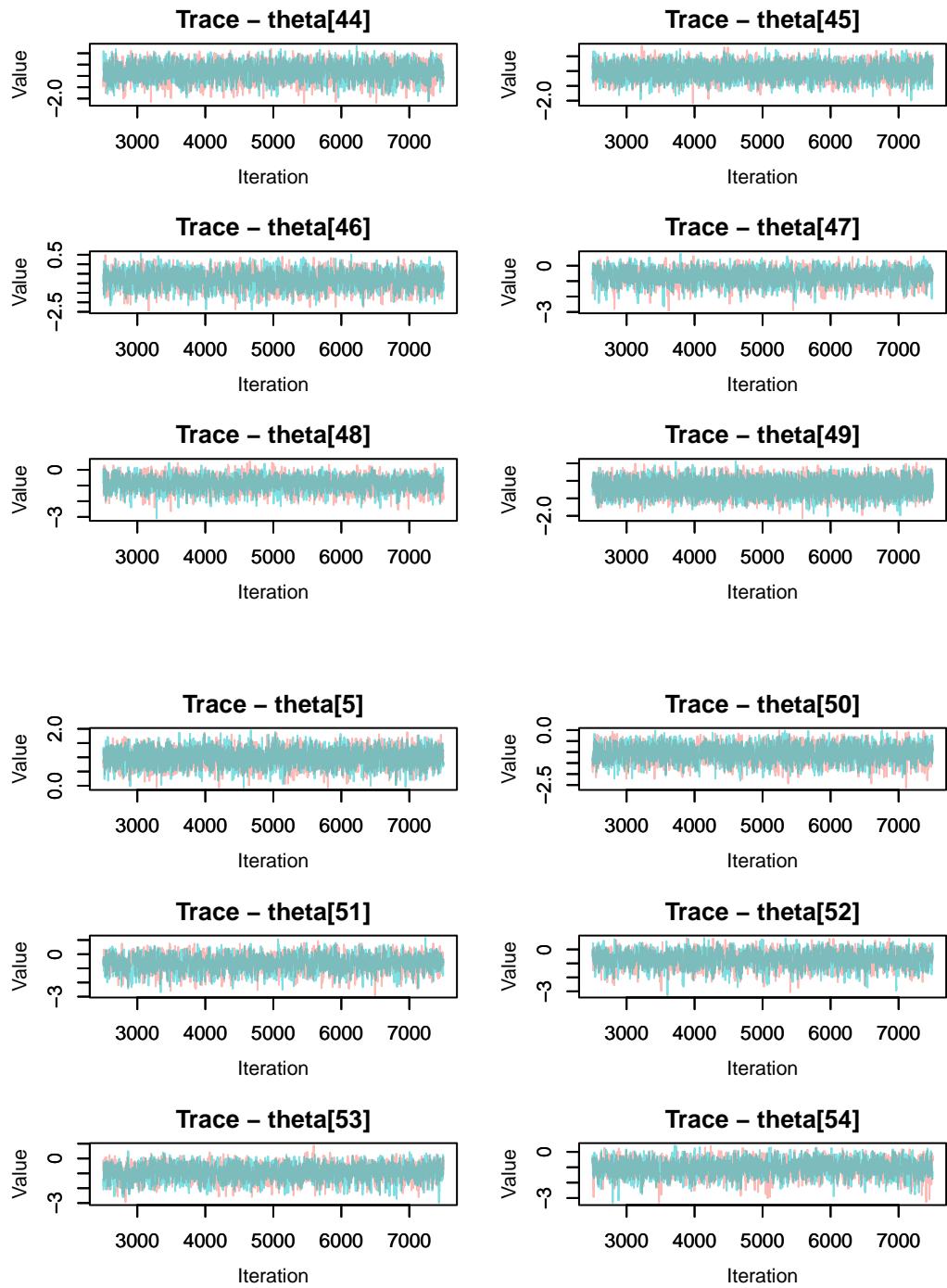


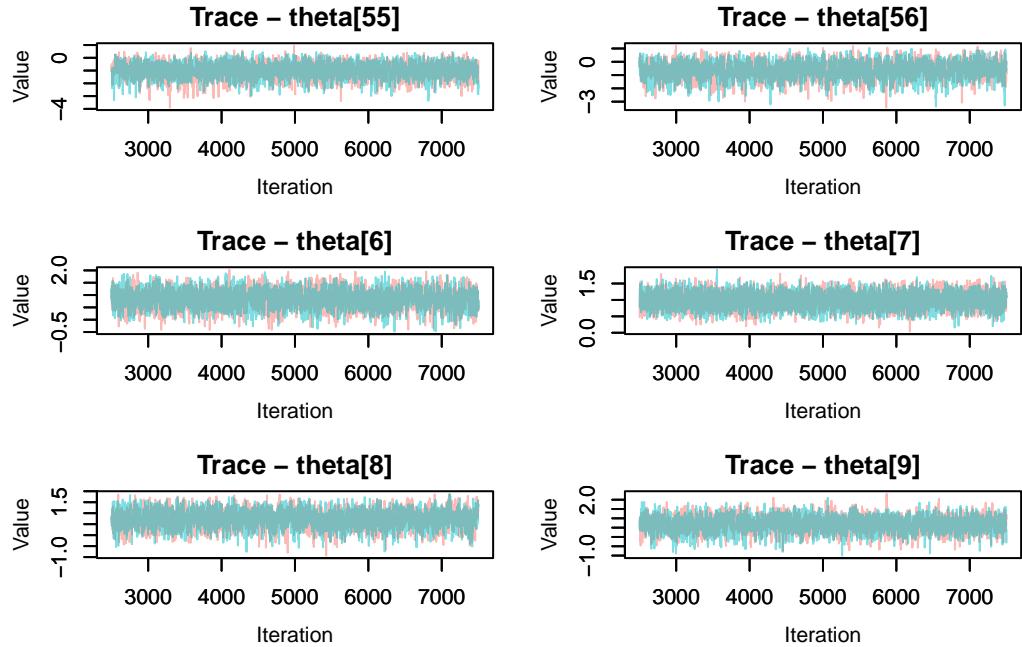












```
gelman.diag(jagsfitlipCancer.mcmc)
```

Potential scale reduction factors:

	Point est.	Upper C.I.
beta0	1	1.00
RR[1]	1	1.00
RR[10]	1	1.00
RR[11]	1	1.00
RR[12]	1	1.00
RR[13]	1	1.01
RR[14]	1	1.00
RR[15]	1	1.00
RR[16]	1	1.00
RR[17]	1	1.02
RR[18]	1	1.00
RR[19]	1	1.00
RR[2]	1	1.00
RR[20]	1	1.00
RR[21]	1	1.00
RR[22]	1	1.01
RR[23]	1	1.00

RR[24]	1	1.00
RR[25]	1	1.00
RR[26]	1	1.00
RR[27]	1	1.01
RR[28]	1	1.00
RR[29]	1	1.01
RR[3]	1	1.00
RR[30]	1	1.01
RR[31]	1	1.00
RR[32]	1	1.00
RR[33]	1	1.00
RR[34]	1	1.00
RR[35]	1	1.00
RR[36]	1	1.00
RR[37]	1	1.00
RR[38]	1	1.01
RR[39]	1	1.00
RR[4]	1	1.00
RR[40]	1	1.00
RR[41]	1	1.00
RR[42]	1	1.00
RR[43]	1	1.00
RR[44]	1	1.01
RR[45]	1	1.00
RR[46]	1	1.00
RR[47]	1	1.00
RR[48]	1	1.00
RR[49]	1	1.00
RR[5]	1	1.00
RR[50]	1	1.01
RR[51]	1	1.00
RR[52]	1	1.00
RR[53]	1	1.01
RR[54]	1	1.00
RR[55]	1	1.00
RR[56]	1	1.01
RR[6]	1	1.00
RR[7]	1	1.00
RR[8]	1	1.00
RR[9]	1	1.00
tau	1	1.01
theta[1]	1	1.00
theta[10]	1	1.00

theta[11]	1	1.00
theta[12]	1	1.00
theta[13]	1	1.01
theta[14]	1	1.00
theta[15]	1	1.00
theta[16]	1	1.00
theta[17]	1	1.02
theta[18]	1	1.00
theta[19]	1	1.00
theta[2]	1	1.00
theta[20]	1	1.00
theta[21]	1	1.00
theta[22]	1	1.00
theta[23]	1	1.00
theta[24]	1	1.00
theta[25]	1	1.00
theta[26]	1	1.00
theta[27]	1	1.01
theta[28]	1	1.00
theta[29]	1	1.02
theta[3]	1	1.00
theta[30]	1	1.01
theta[31]	1	1.00
theta[32]	1	1.00
theta[33]	1	1.00
theta[34]	1	1.00
theta[35]	1	1.00
theta[36]	1	1.01
theta[37]	1	1.00
theta[38]	1	1.01
theta[39]	1	1.00
theta[4]	1	1.00
theta[40]	1	1.00
theta[41]	1	1.00
theta[42]	1	1.00
theta[43]	1	1.00
theta[44]	1	1.00
theta[45]	1	1.00
theta[46]	1	1.00
theta[47]	1	1.00
theta[48]	1	1.00
theta[49]	1	1.00
theta[5]	1	1.00

```

theta[50]      1      1.00
theta[51]      1      1.00
theta[52]      1      1.00
theta[53]      1      1.01
theta[54]      1      1.00
theta[55]      1      1.00
theta[56]      1      1.01
theta[6]        1      1.00
theta[7]        1      1.01
theta[8]        1      1.01
theta[9]        1      1.00

```

Multivariate psrf

1.03

question 1.d)

we know have to monitor RR as well

```

## extract posterior RR
posRR <- substr(rownames(jags.mod.fit.lipCancer$BUGSoutput$summary), 1, 2) ==
  "RR"

RRRegions = jags.mod.fit.lipCancer$BUGSoutput$summary[posRR, 1]

ScotlandDF$RR = RRRegions

```

Checking the difference between the average RR and the SMR for each region

I firstly do RR/SMR and see how close it is to 1

`ScotlandDF$SMR/ScotlandDF$RR`

RR[1]	RR[2]	RR[3]	RR[4]	RR[5]	RR[6]	RR[7]	RR[8]
1.3818571	1.0690585	1.1948640	1.2285324	1.1391592	1.2147104	1.0750410	1.2426297
RR[9]	RR[10]	RR[11]	RR[12]	RR[13]	RR[14]	RR[15]	RR[16]
1.2587125	1.0932405	1.1311915	1.2631703	1.4023615	1.1565892	1.0697607	1.0975261
RR[17]	RR[18]	RR[19]	RR[20]	RR[21]	RR[22]	RR[23]	RR[24]
1.1773397	1.0874219	1.0691595	1.0686052	1.0253791	1.0158042	1.0059088	1.0120600
RR[25]	RR[26]	RR[27]	RR[28]	RR[29]	RR[30]	RR[31]	RR[32]
1.0067507	1.0012337	0.9879578	1.0036061	0.9951590	0.9898051	0.9596262	0.9484298

RR[33]	RR[34]	RR[35]	RR[36]	RR[37]	RR[38]	RR[39]	RR[40]
0.9737082	0.9667291	0.9677330	0.9605754	0.9553878	0.9466386	0.9293967	0.8876148
RR[41]	RR[42]	RR[43]	RR[44]	RR[45]	RR[46]	RR[47]	RR[48]
0.8985497	0.8664100	0.6733063	0.8015128	0.9111734	0.6896680	0.5988371	0.6558237
RR[49]	RR[50]	RR[51]	RR[52]	RR[53]	RR[54]	RR[55]	RR[56]
0.9281296	0.7597000	0.4599588	0.4549579	0.3700189	0.3403620	0.0000000	0.0000000

And now I plot it on the map to see how close the posterior is to SMR likelihood

```
comparison = ScotlandDF$SMR/ScotlandDF$RR

source("ScotlandMap.R") # need to read in the ScotlandMap function
testdat = comparison # generate random numbers to use as observations
ScotlandMap(testdat, figtitle = "Scotland SMR by RR comparison by region")
```

Warning: OGR support is provided by the sf and terra packages among others

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Warning: OGR support is provided by the sf and terra packages among others

Warning: OGR support is provided by the sf and terra packages among others

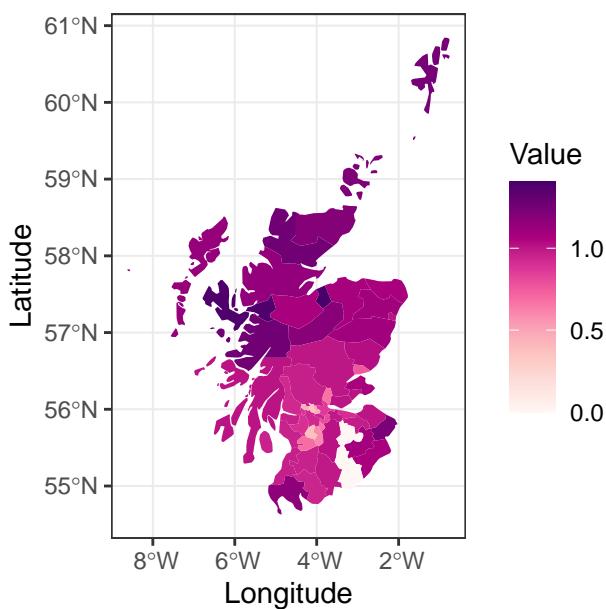
OGR data source with driver: ESRI Shapefile

Source: "C:\AppliedDataScienceAndStatistics\Applied-Data-Science-and-Statistics\Term2\Advanced

with 56 features

It has 1 fields

Scotland SMR by RR comparison by region



Question 1.e)

Now I will have to check when RR is > 1 using similarly the summary Confidence intervals

```
jags.mod.lipCancer = function() {
  # Priors
  beta0 ~ dnorm(0, 1/1000)
  tau ~ dgamma(1, 0.05)

  # Likelihood
  for (i in 1:N) {
    obs[i] ~ dpois(mu[i])
    log(mu[i]) = log(expo[i]) + beta0 + theta[i]
    theta[i] ~ dnorm(0, tau)
    RR[i] = exp(beta0) * exp(theta[i])
  }

  PRRAbove = ifelse(RR > 1, 1, 0)
}

# Parameters to monitor
```

```

jags.param.lipCancer = c("beta0", "theta", "tau", "RR", "PRRAbove")

# Data
jags.data.lipCancer <- list(N = nrow(ScotlandDF), obs = ScotlandDF$Observed,
                           expo = ScotlandDF$Expected)

## initial values, have to be for the stochastic for theta it will be a
## repetition because of the i
inits1 <- list(tau = 1, beta0 = 1, theta = rep(1, 56))
inits2 <- list(tau = 17.20806, beta0 = -0.5604756, theta = rep(19.38524,
                56))

## these initial values for inits2 came from these functions random
## generation set.seed(123) y <- rgamma(n = 1, shape = 1, rate = 0.05)
## value <- rnorm(1, mean = 0, sd = sqrt(1000)) tau_init <- 1/rgamma(n
## = 1, shape = 2, rate = 0.1)

jags.inits.lipCancer = list(inits1, inits2)

## fit the jags model

jags.mod.fit.lipCancer <- jags(data = jags.data.lipCancer, inits = jags.inits.lipCancer,
                                 parameters.to.save = jags.param.lipCancer, n.chains = 2, n.iter = 15000,
                                 n.burnin = 7500, n.thin = 1, model.file = jags.mod.lipCancer, DIC = FALSE)

```

Compiling model graph
 Resolving undeclared variables
 Allocating nodes
 Graph information:
 Observed stochastic nodes: 56
 Unobserved stochastic nodes: 58
 Total graph size: 453

Initializing model

```

## to see which regions RR are in the 95% C.I we will have to see if
## the 2.5% is small or equal to 1 and if 97.5% is equal or greater
## than 1

```

```

## extract posterior RR
posProbRR <- substr(rownames(jags.mod.fit.lipCancer$BUGSoutput$summary),
  1, 2) == "RR"

# jags.mod.fit.lipCancer$BUGSoutput$summary [posProbRR,1] ##mean
lowerCI = jags.mod.fit.lipCancer$BUGSoutput$summary [posProbRR, 3] # 2.5 percentile
upperCI = jags.mod.fit.lipCancer$BUGSoutput$summary [posProbRR, 7] # 97.5 percentile

```

Since we know that the 97,5 percentile is always bigger than the the 2,5 percentile to check if the 95% CI of RR is lower than 1, meaning there is no excessive risk, all we have to do is check if a region 97,5% percentile is smaller than 1

```

ScotlandDF$AboveRR = upperCI
ScotlandDF$isAboveRR = 0

for (i in 1:nrow(ScotlandDF)) {

  if (ScotlandDF$AboveRR[i] > 1) {
    ScotlandDF$isAboveRR[i] = 1
  }

  if (upperCI[i] < 1) {
    print(ScotlandDF>Name[i])
  }
}

[1] "Renfrew"
[1] "Falkirk"
[1] "Motherwell"
[1] "Edinburgh"
[1] "Hamilton"
[1] "Glasgow"
[1] "Dundee"
[1] "Strathkelvin"

```

Here is the list of the regions where we are 95% certain that RR is bellow 1

So now to map the regions with and without excess risk of lip cancer

```

source("ScotlandMap.R") # need to read in the ScotlandMap function
testdat = ScotlandDF$isAboveRR # generate random numbers to use as observations
ScotlandMap(testdat, figtitle = "Scotland regions with excess lip cancer")

```

```
Warning: OGR support is provided by the sf and terra packages among others
```

```
Warning: OGR support is provided by the sf and terra packages among others
```

```
Warning: OGR support is provided by the sf and terra packages among others
```

```
Warning: OGR support is provided by the sf and terra packages among others
```

```
Warning: OGR support is provided by the sf and terra packages among others
```

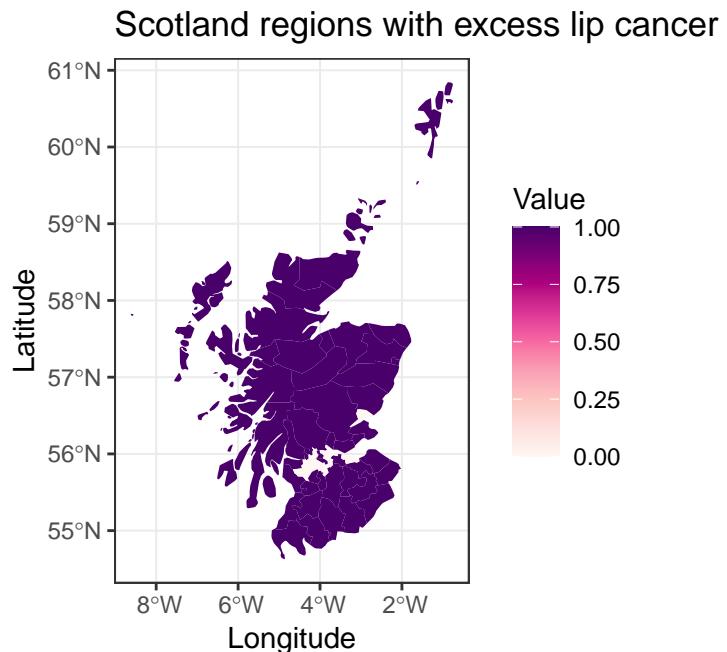
```
Warning: OGR support is provided by the sf and terra packages among others
```

```
OGR data source with driver: ESRI Shapefile
```

```
Source: "C:\AppliedDataScienceAndStatistics\Applied-Data-Science-and-Statistics\Term2\Advanced
```

```
with 56 features
```

```
It has 1 fields
```



```
source("ScotlandMap.R") # need to read in the ScotlandMap function  
testdat = as.integer(!ScotlandDF$isAboveRR) # generate random numbers to use as observati
```

```
ScotlandMap(testdat, figtitle = "Scotland regions without excess of lip cancer")
```

Warning: OGR support is provided by the sf and terra packages among others

Warning: OGR support is provided by the sf and terra packages among others

Warning: OGR support is provided by the sf and terra packages among others

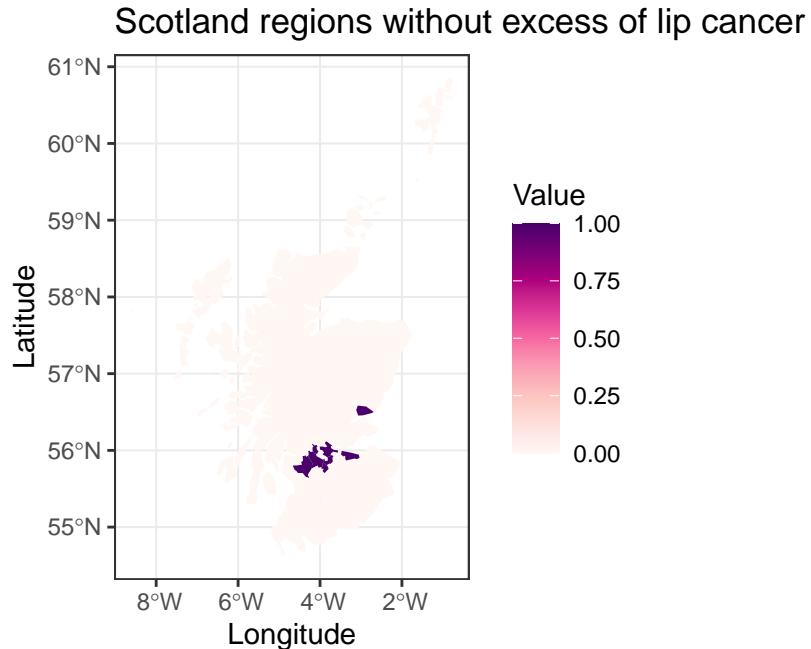
Warning: OGR support is provided by the sf and terra packages among others

Warning: OGR support is provided by the sf and terra packages among others
Warning: OGR support is provided by the sf and terra packages among others

OGR data source with driver: ESRI Shapefile

Source: "C:\AppliedDataScienceAndStatistics\Applied-Data-Science-and-Statistics\Term2\Advanced
with 56 features

It has 1 fields



Here I have decided to map separately without and without the risk of lip cancer due to the default colour scheme of the above risk cancer regions making it very hard to see which regions have risk below 1.

Question 1f)

For the new priors I have chosen to utilize the previous posterior values for β_0 and τ as they represent our newly updated beliefs about the values derived from the data after the first model.

Here, we have used the posterior distributions from the previous model of the same data to update our prior beliefs about the parameters β_0 and τ and as such this new model has information about our previous analysis. The mean of the posterior distributions is an approximated value of the most likely values for β_0 and τ from the observed data.

We will first start by gathering the previous posteriors to use as the new model priors.

```
# Extracting the posterior mean for each variable  
beta0PosteriorMean <- mean(as.numeric(jags.mod.fit.lipCancer$BUGSoutput$sims.list$beta0))  
tauPosteriorMean <- mean(as.numeric(jags.mod.fit.lipCancer$BUGSoutput$sims.list$tau))  
  
beta0PosteriorSD = sd(as.numeric(jags.mod.fit.lipCancer$BUGSoutput$sims.list$beta0))  
tauPosteriorSD = sd(as.numeric(jags.mod.fit.lipCancer$BUGSoutput$sims.list$tau))  
  
beta0PosteriorMean  
  
[1] 0.08214692  
  
beta0PosteriorSD  
  
[1] 0.1160699  
  
tauPosteriorMean  
  
[1] 1.806577  
  
tauPosteriorSD  
  
[1] 0.4481229
```

Here I will supply the values of the mean and sd from both beta0 and tau manually since JAGS model function does not have a global scope to see all variables in the system

```

jags.mod.lipCancerNew = function(beta0PosteriorMean) {

  ## calcs for prior gamma alpha = ( $x_{bar}^2 / s^2$ ) beta = ( $s^2 /$ 
  ##  $x_{bar}$ )
  shape <- (1.811285/0.45581)^2
  rate <- ((0.45581)^2)/1.811285

  # Priors
  beta0 ~ dnorm(0.08064184, 0.1167079)

  tau ~ dgamma(shape, rate)

  # Likelihood
  for (i in 1:N) {
    obs[i] ~ dpois(mu[i])
    log(mu[i]) = log(expo[i]) + beta0 + theta[i]
    theta[i] ~ dnorm(0, tau)
    RR[i] = exp(beta0) * exp(theta[i])
  }
}

# Parameters to monitor
jags.param.lipCancerNew = c("beta0", "theta", "tau", "RR")

# Data
jags.data.lipCancerNew <- list(N = nrow(ScotlandDF), obs = ScotlandDF$Observed,
  expo = ScotlandDF$Expected)

## initial values, have to be for the stochastic for theta it will be a
## repetition because of the i
inits1 <- list(tau = 1, beta0 = 1, theta = rep(1, 56))
inits2 <- list(tau = 17.20806, beta0 = -0.5604756, theta = rep(19.38524,
  56))

## these initial values for inits2 came from these functions random
## generation set.seed(123) y <- rgamma(n = 1, shape = 1, rate = 0.05)
## value <- rnorm(1, mean = 0, sd = sqrt(1000)) tau_init <- 1/rgamma(n
## = 1, shape = 2, rate = 0.1)

```

```

jags.inits.lipCancerNew = list(inits1, inits2)

## fit the jags model

jags.mod.fit.lipCancerNew <- jags(data = jags.data.lipCancerNew, inits = jags.inits.lipCancerNew,
parameters.to.save = jags.param.lipCancerNew, n.chains = 2, n.iter = 15000,
n.burnin = 7500, n.thin = 1, model.file = jags.mod.lipCancerNew, DIC = FALSE)

```

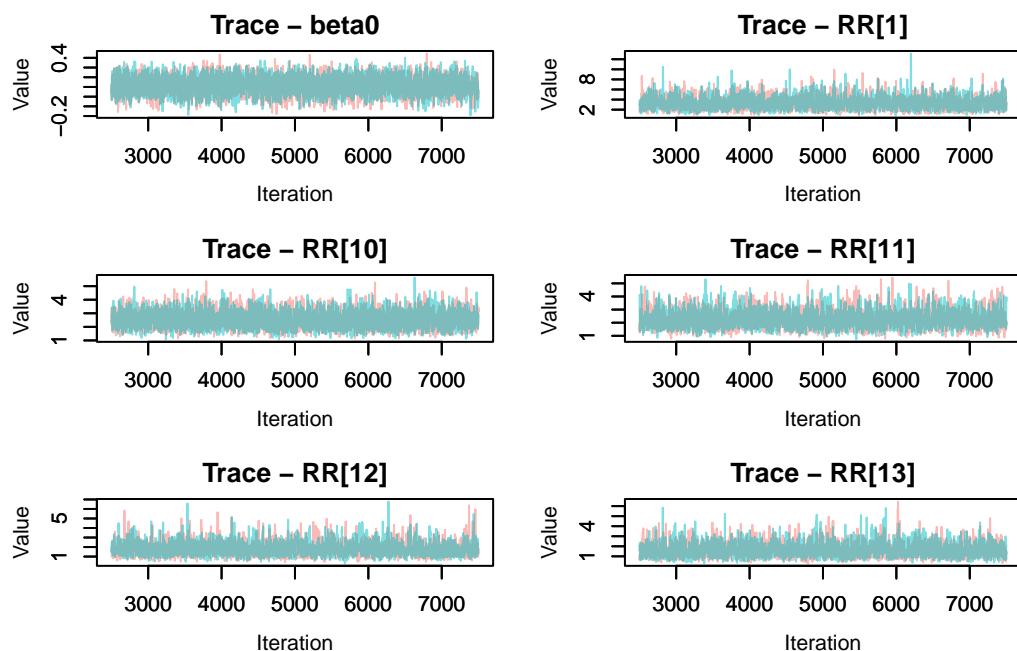
Compiling model graph
 Resolving undeclared variables
 Allocating nodes
 Graph information:
 Observed stochastic nodes: 56
 Unobserved stochastic nodes: 58
 Total graph size: 455

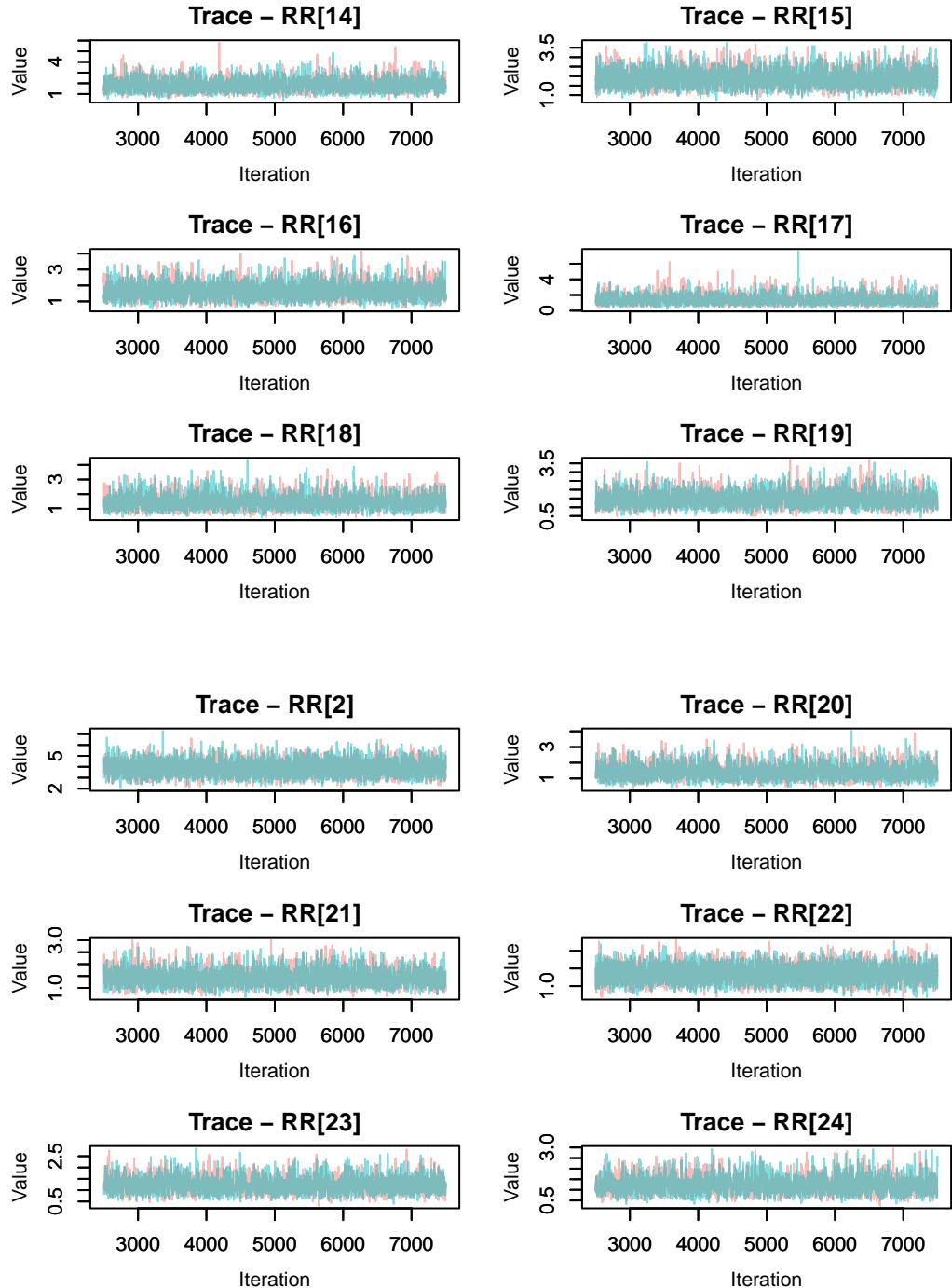
Initializing model

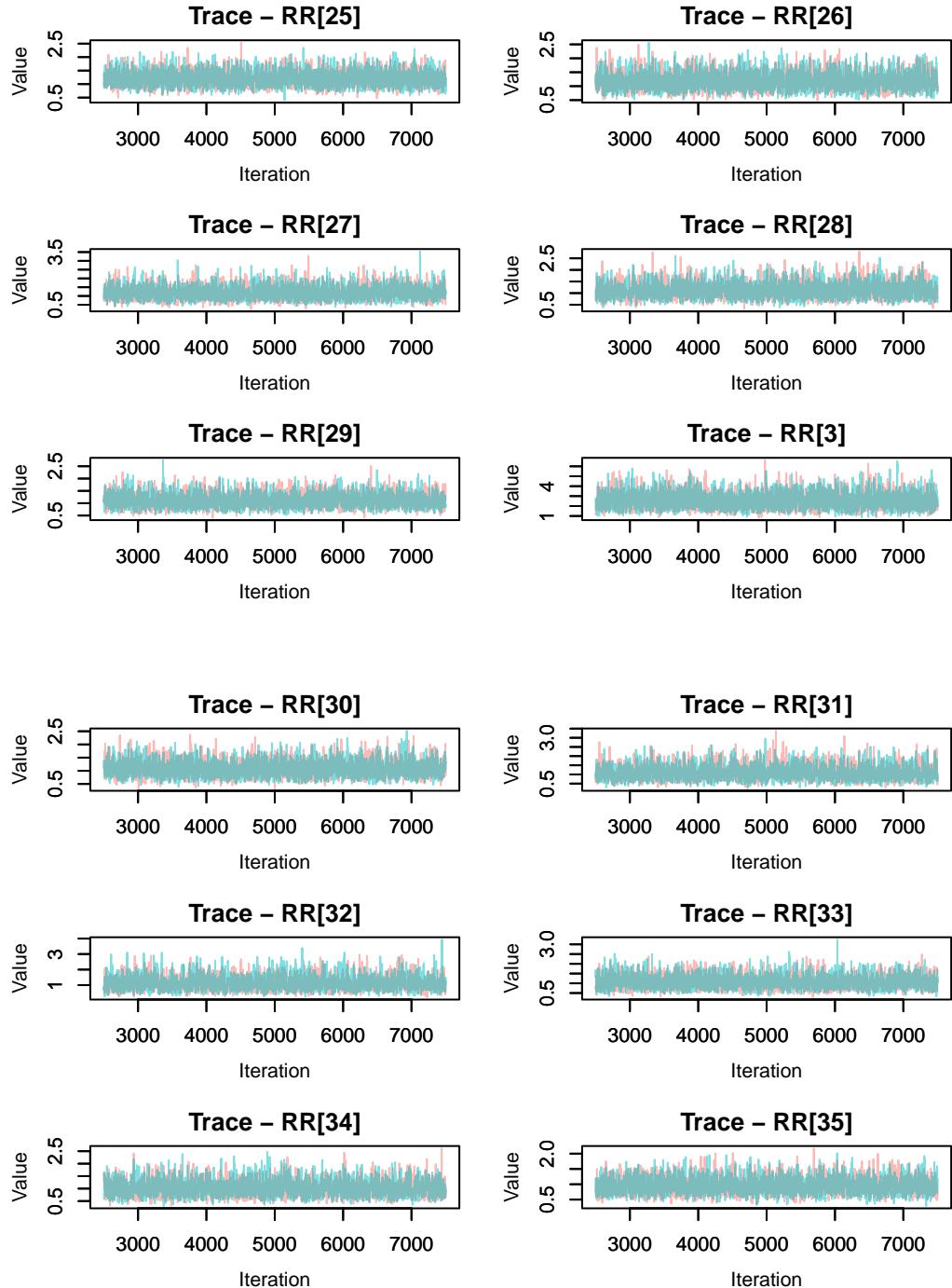
```

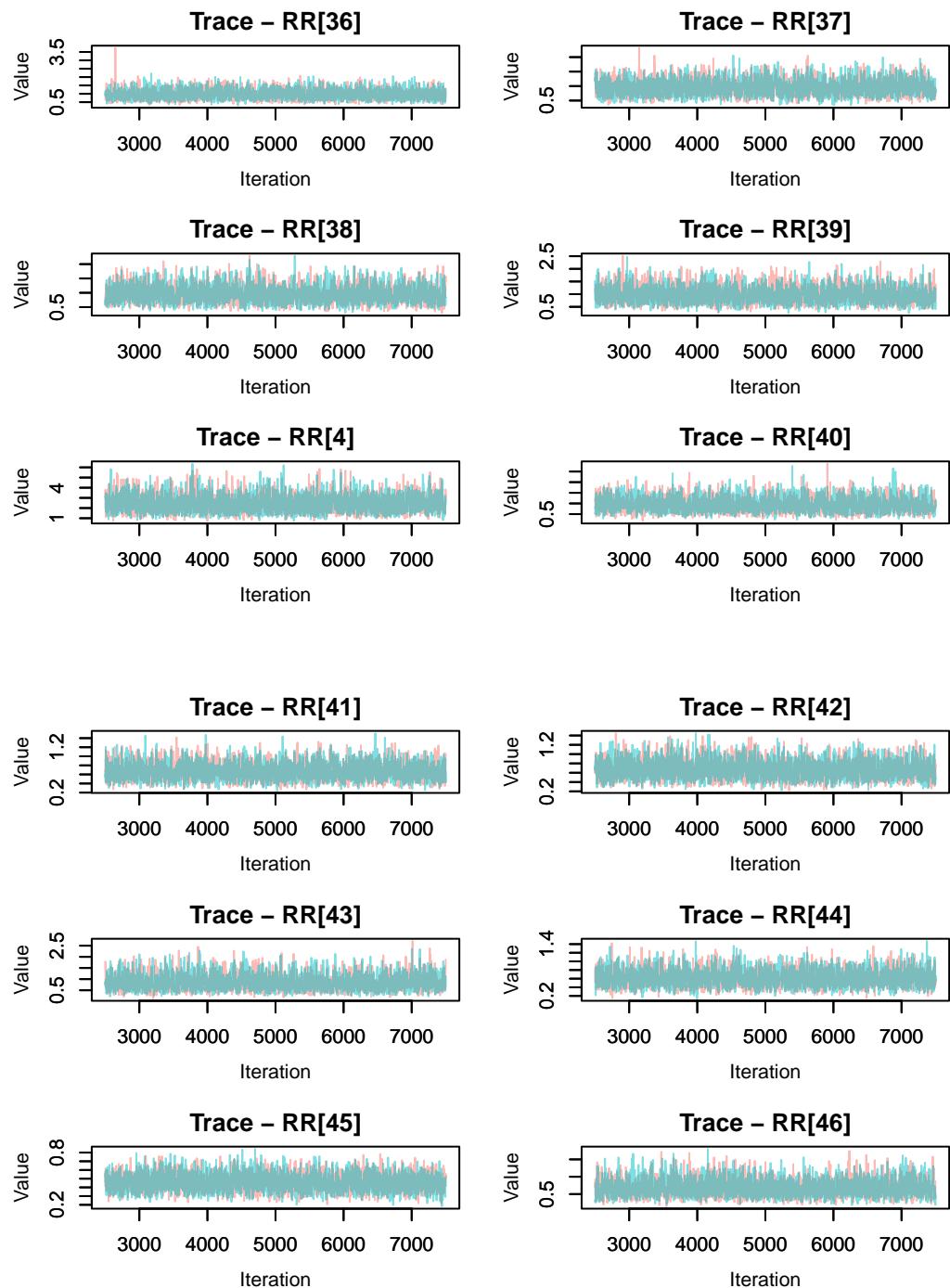
jagsfitlipCancerNew.mcmc <- as.mcmc(jags.mod.fit.lipCancerNew)
MCMCTrace(jagsfitlipCancerNew.mcmc, type = "trace", ind = TRUE, pdf = FALSE)

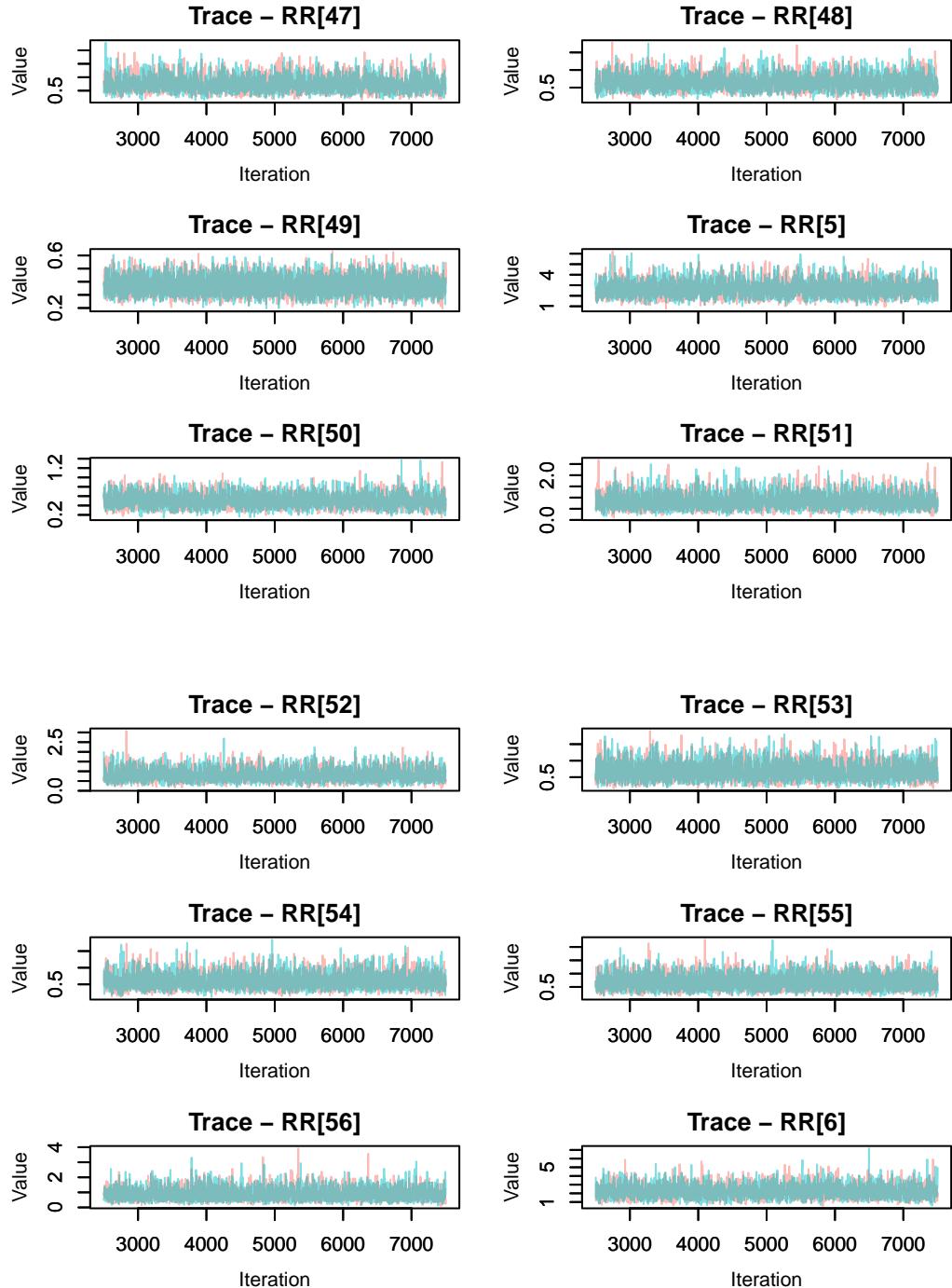
```

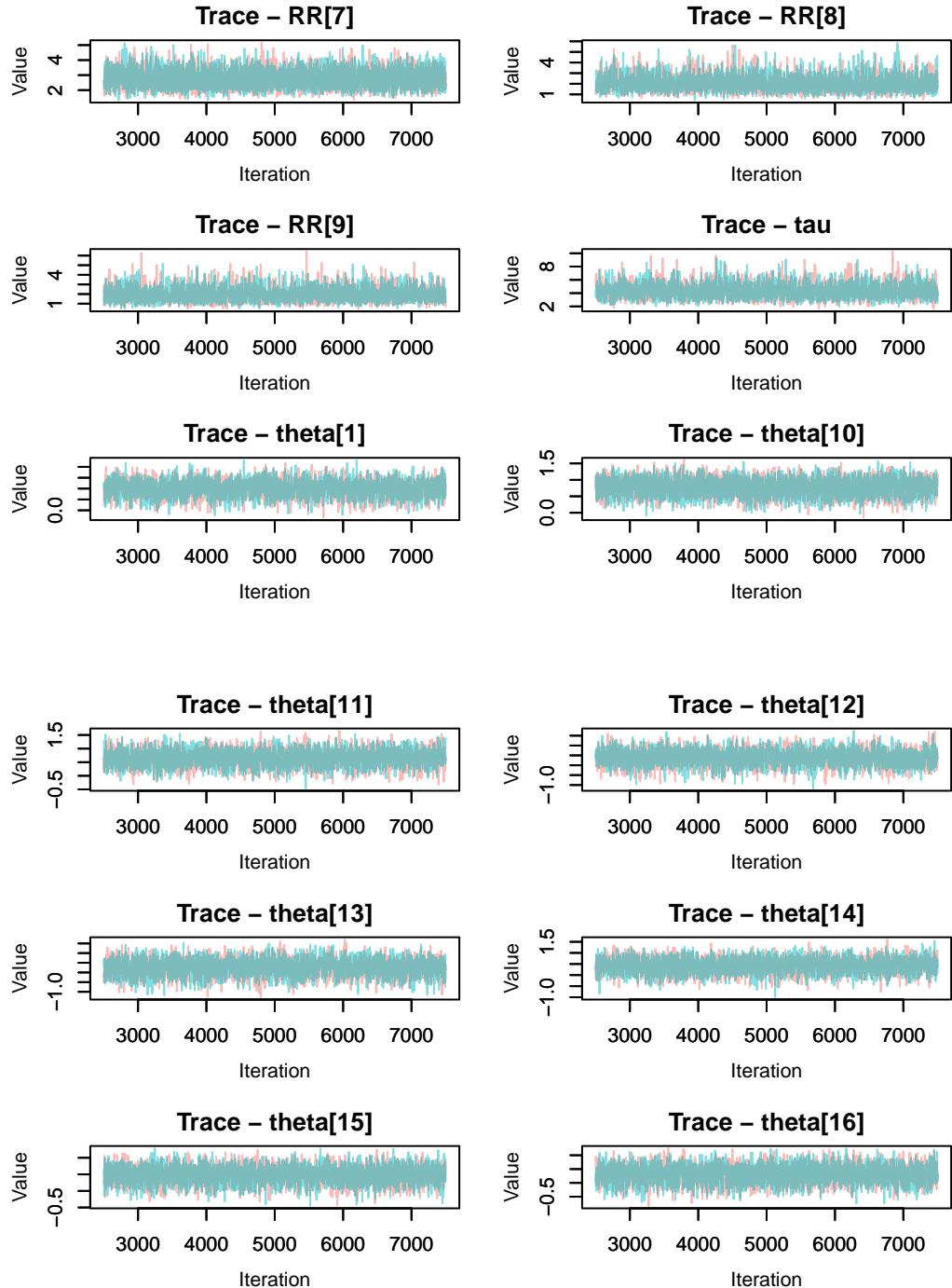


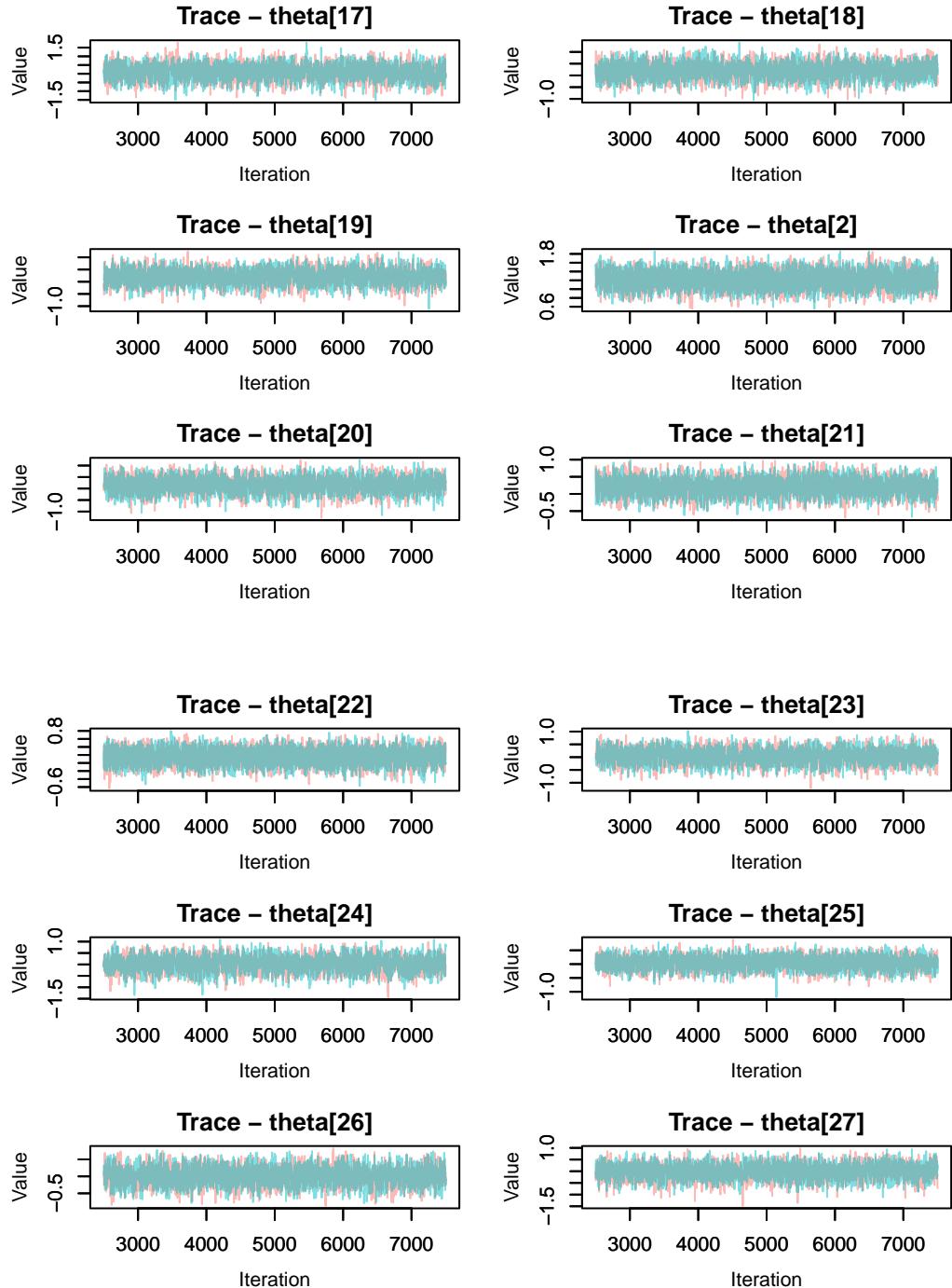


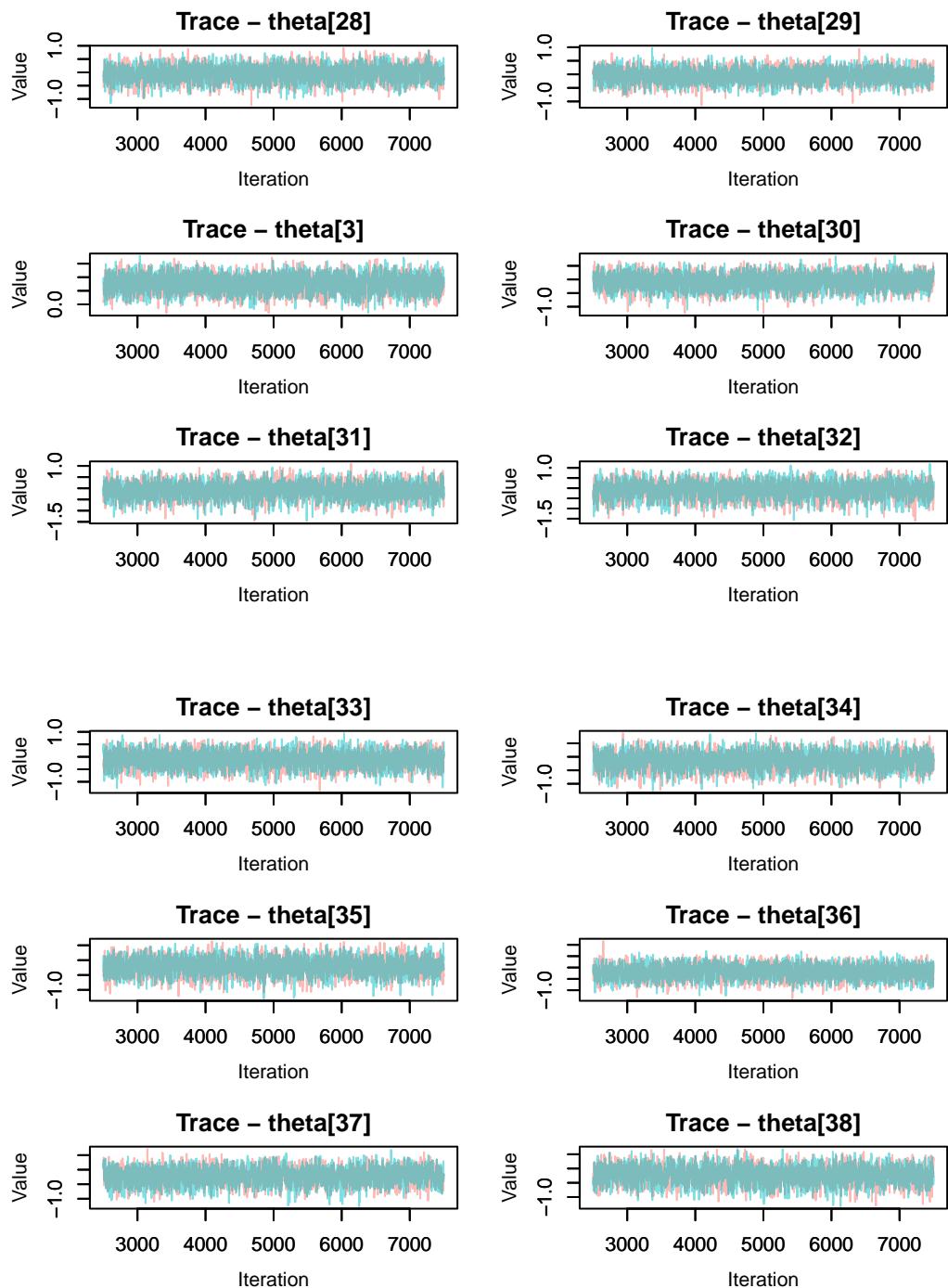


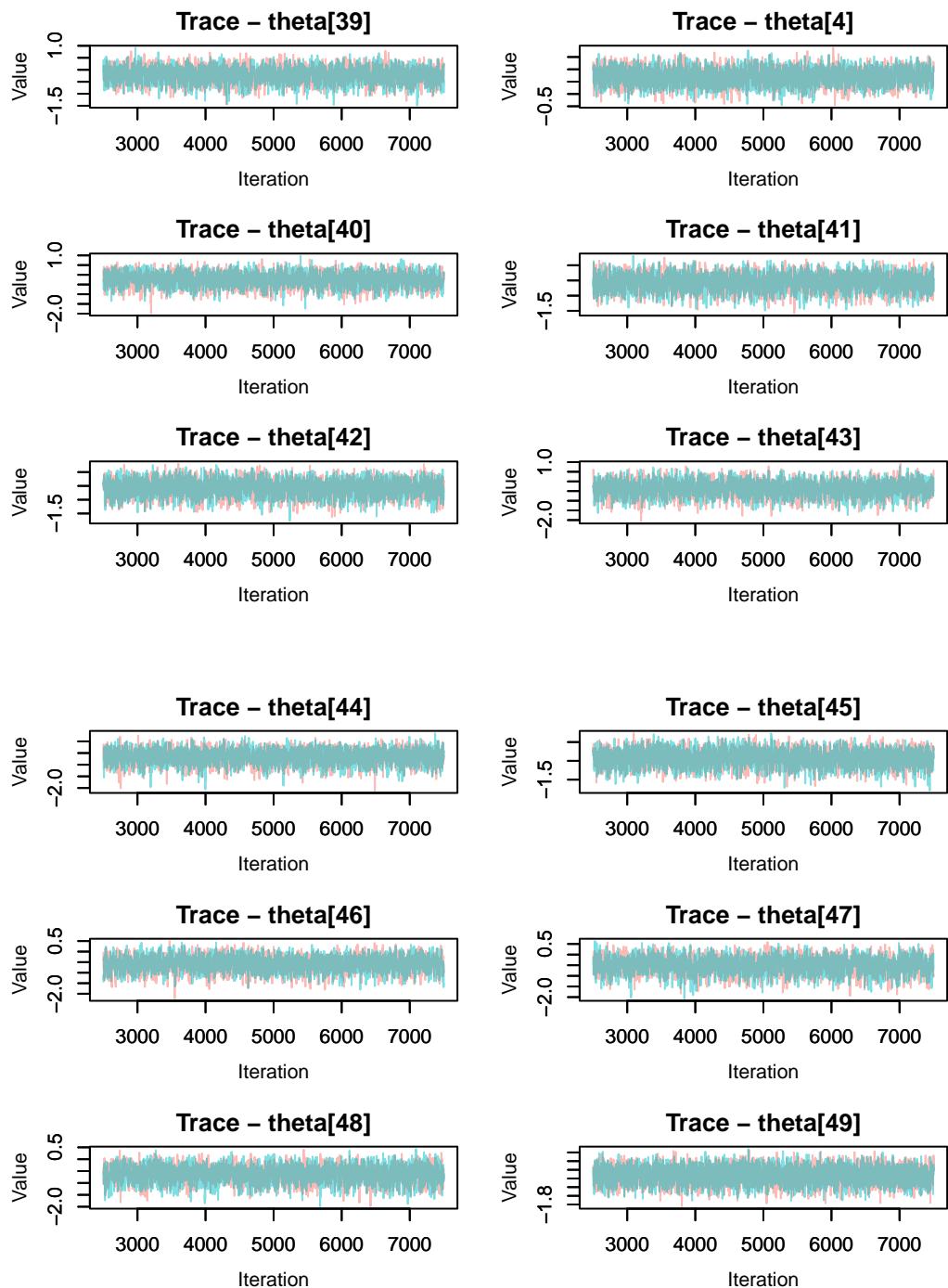


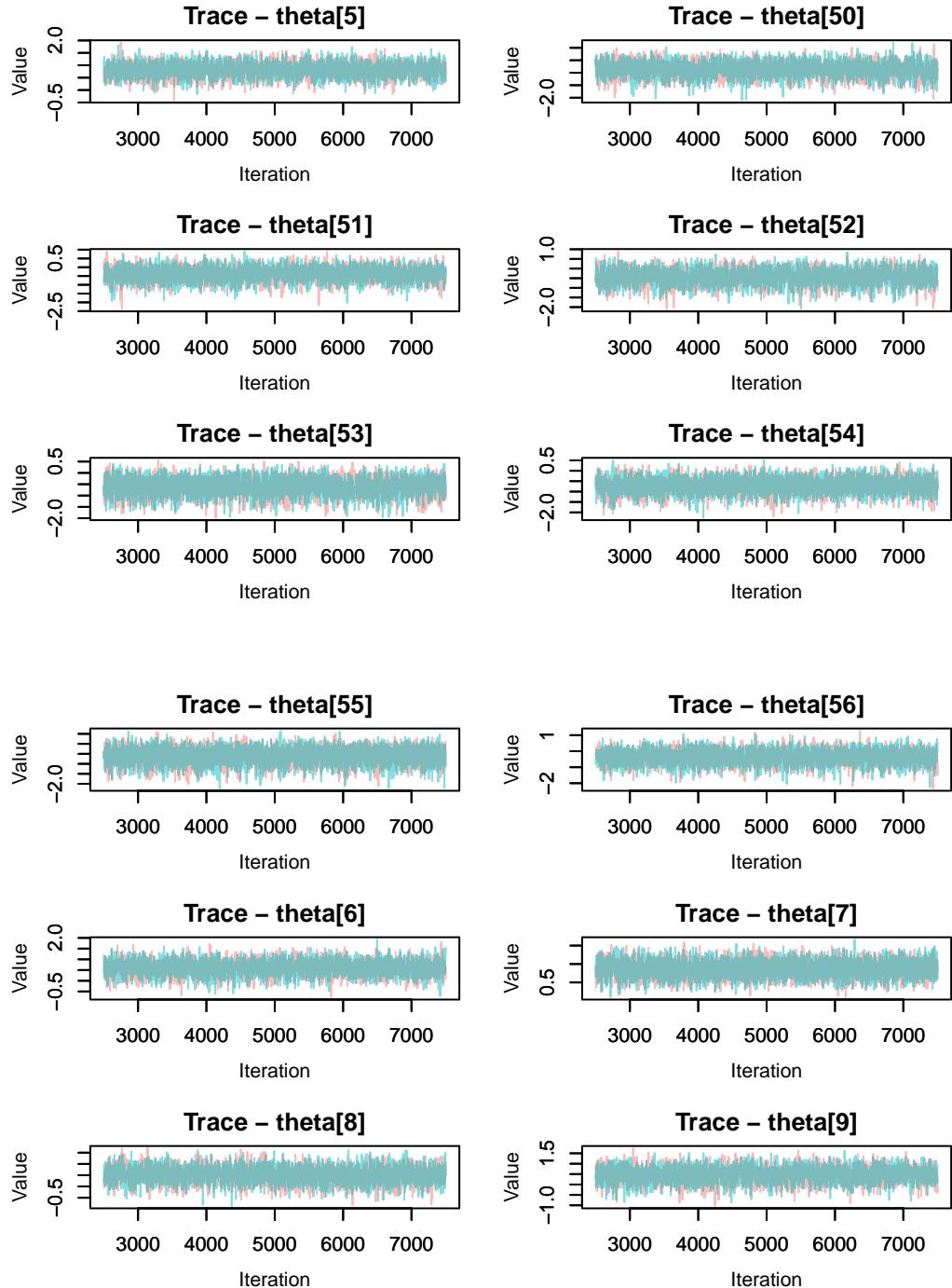












```
gelman.diag(jagsfitlipCancer.mcmc)
```

Potential scale reduction factors:

	Point est.	Upper C.I.
beta0	1	1.00
RR[1]	1	1.00
RR[10]	1	1.00
RR[11]	1	1.00
RR[12]	1	1.00
RR[13]	1	1.01
RR[14]	1	1.00
RR[15]	1	1.00
RR[16]	1	1.00
RR[17]	1	1.02
RR[18]	1	1.00
RR[19]	1	1.00
RR[2]	1	1.00
RR[20]	1	1.00
RR[21]	1	1.00
RR[22]	1	1.01
RR[23]	1	1.00
RR[24]	1	1.00
RR[25]	1	1.00
RR[26]	1	1.00
RR[27]	1	1.01
RR[28]	1	1.00
RR[29]	1	1.01
RR[3]	1	1.00
RR[30]	1	1.01
RR[31]	1	1.00
RR[32]	1	1.00
RR[33]	1	1.00
RR[34]	1	1.00
RR[35]	1	1.00
RR[36]	1	1.00
RR[37]	1	1.00
RR[38]	1	1.01
RR[39]	1	1.00
RR[4]	1	1.00
RR[40]	1	1.00
RR[41]	1	1.00
RR[42]	1	1.00
RR[43]	1	1.00
RR[44]	1	1.01

RR[45]	1	1.00
RR[46]	1	1.00
RR[47]	1	1.00
RR[48]	1	1.00
RR[49]	1	1.00
RR[5]	1	1.00
RR[50]	1	1.01
RR[51]	1	1.00
RR[52]	1	1.00
RR[53]	1	1.01
RR[54]	1	1.00
RR[55]	1	1.00
RR[56]	1	1.01
RR[6]	1	1.00
RR[7]	1	1.00
RR[8]	1	1.00
RR[9]	1	1.00
tau	1	1.01
theta[1]	1	1.00
theta[10]	1	1.00
theta[11]	1	1.00
theta[12]	1	1.00
theta[13]	1	1.01
theta[14]	1	1.00
theta[15]	1	1.00
theta[16]	1	1.00
theta[17]	1	1.02
theta[18]	1	1.00
theta[19]	1	1.00
theta[2]	1	1.00
theta[20]	1	1.00
theta[21]	1	1.00
theta[22]	1	1.00
theta[23]	1	1.00
theta[24]	1	1.00
theta[25]	1	1.00
theta[26]	1	1.00
theta[27]	1	1.01
theta[28]	1	1.00
theta[29]	1	1.02
theta[3]	1	1.00
theta[30]	1	1.01
theta[31]	1	1.00

theta[32]	1	1.00
theta[33]	1	1.00
theta[34]	1	1.00
theta[35]	1	1.00
theta[36]	1	1.01
theta[37]	1	1.00
theta[38]	1	1.01
theta[39]	1	1.00
theta[4]	1	1.00
theta[40]	1	1.00
theta[41]	1	1.00
theta[42]	1	1.00
theta[43]	1	1.00
theta[44]	1	1.00
theta[45]	1	1.00
theta[46]	1	1.00
theta[47]	1	1.00
theta[48]	1	1.00
theta[49]	1	1.00
theta[5]	1	1.00
theta[50]	1	1.00
theta[51]	1	1.00
theta[52]	1	1.00
theta[53]	1	1.01
theta[54]	1	1.00
theta[55]	1	1.00
theta[56]	1	1.01
theta[6]	1	1.00
theta[7]	1	1.01
theta[8]	1	1.01
theta[9]	1	1.00

Multivariate psrf

1.03

As we can see everything still converges so we will now extract the new RR posterior values and map the two posterior RRs we have

```
## extract posterior RR
posRRNew <- substr(rownames(jags.mod.fit.lipCancerNew$BUGSoutput$summary) ,
  1, 2) == "RR"
```

```
RRRegionsNew = jags.mod.fit.lipCancerNew$BUGSoutput$summary[posRRNew, 1]

ScotlandDF$RRNew = RRRegionsNew

source("ScotlandMap.R") # need to read in the ScotlandMap function
testdat = ScotlandDF$RR # generate random numbers to use as observations
ScotlandMap(testdat, figtitle = "Scotland SMR by region")
```

Warning: OGR support is provided by the sf and terra packages among others

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Warning: OGR support is provided by the sf and terra packages among others

Warning: OGR support is provided by the sf and terra packages among others

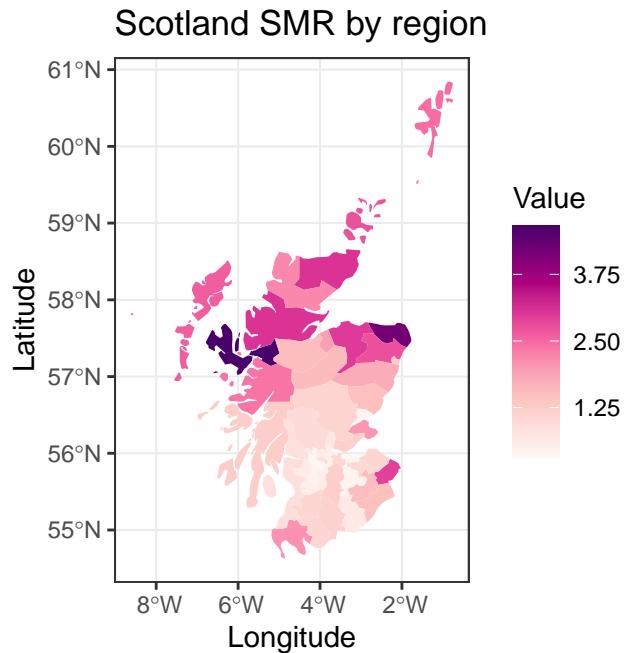
Warning: OGR support is provided by the sf and terra packages among others

OGR data source with driver: ESRI Shapefile

Source: "C:\AppliedDataScienceAndStatistics\Applied-Data-Science-and-Statistics\Term2\Advanced

with 56 features

It has 1 fields



```
source("ScotlandMap.R") # need to read in the ScotlandMap function
testdat = ScotlandDF$RRNew # generate random numbers to use as observations
ScotlandMap(testdat, figtitle = "Scotland SMR by region")
```

Warning: OGR support is provided by the sf and terra packages among others

Warning: OGR support is provided by the sf and terra packages among others

Warning: OGR support is provided by the sf and terra packages among others

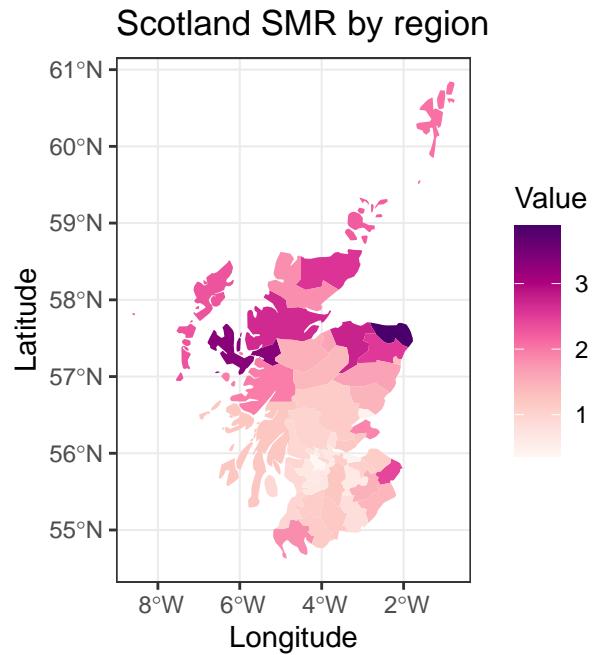
Warning: OGR support is provided by the sf and terra packages among others

Warning: OGR support is provided by the sf and terra packages among others

Warning: OGR support is provided by the sf and terra packages among others

OGR data source with driver: ESRI Shapefile

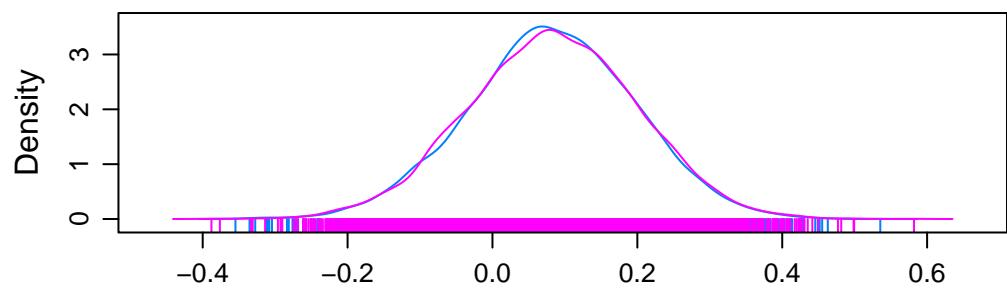
Source: "C:\AppliedDataScienceAndStatistics\Applied-Data-Science-and-Statistics\Term2\Advanced Data Science\Datasets\ScotlandMap\Scotland.shp"
with 56 features
It has 1 fields



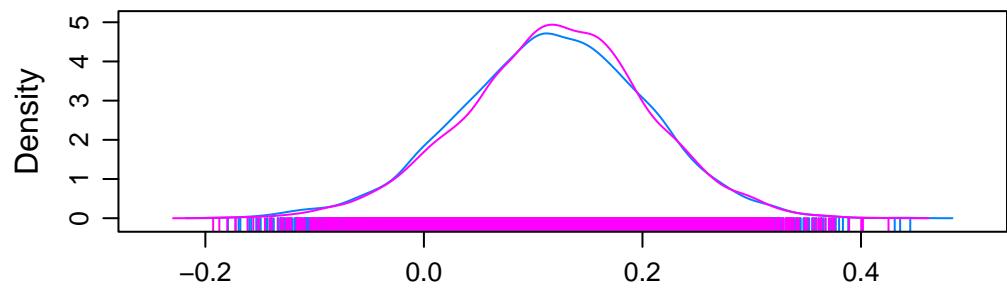
As we can see from both maps there seems to be higher risk in some of the regions within the latitudes of 57 and 58 degrees from the new updated posteriors.

```
jags.mod.fit.mcmc <- as.mcmc(jags.mod.fit.lipCancer)
jags.mod.fit.mcmcNew <- as.mcmc(jags.mod.fit.lipCancerNew)

densityplot(jags.mod.fit.mcmc[, "beta0"])
```

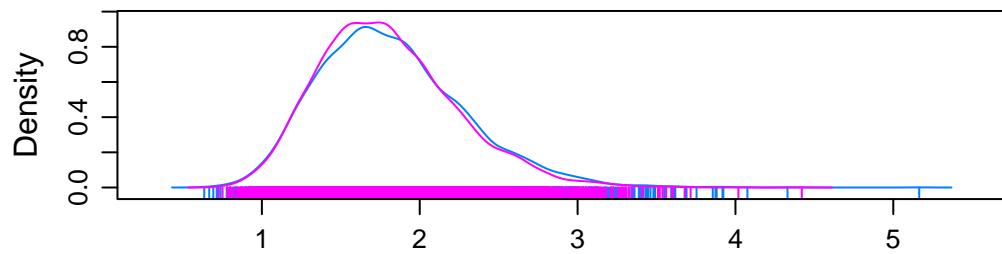


```
densityplot(jags.mod.fit.mcmcNew[, "beta0"])
```

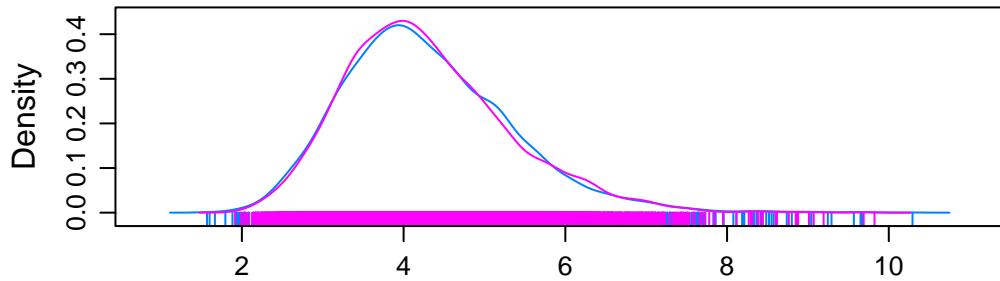


Plotting β_0 density plots to better identify any patterns changes in the summaries we can see that in the updated model the bell curve is not as flat as it reaches a maximum density of close to 5 while the previous model didn't reach density 4 at its peak of the bell curve, however that means that the new bell curve is narrower.

```
densityplot(jags.mod.fit.mcmc[, "tau"])
```



```
densityplot(jags.mod.fit.mcmcNew[, "tau"])
```



Again plotting τ density plots to better identify any patterns changes in the summaries we can see that the opposite has occurred from β_0 as the curve is more stretched and more skewed to the right than the previous model.

Question 2 a)

```
jags.mod.infantDeath <- function(){
  for(i in 1:12){
    r[i] ~ dbin(theta[i],n[i])
    logit(theta[i]) <- logit.theta[i]
    logit.theta[i] ~ dnorm(mu, tau)
  }
  mu ~ dnorm(0,0.001)
  tau <- 1/sigma^2
  sigma ~ dunif(0,100)
}

# Parameters to monitor
jags.param.infantDeath <- c("mu", "sigma", "theta", "tau")

## initial values
```

```

inits1 <- list('mu' = 1, 'sigma' = 1, 'theta'=rep(1,12))
inits2 <- list('mu'= 0,'sigma'=50,'theta'= rep(20,12))

jags.inits = list(inits1,inits2)

## data

jags.data.infantDeath <- list(r = surgicalDF$r, n = surgicalDF$n)

## fit the jags model

jags.mod.fit.infantDeath <- jags(data = jags.data.infantDeath, #inits = jags.inits,
parameters.to.save = jags.param.infantDeath, n.chains = 2, n.iter = 10000,
n.burnin = 5000,n.thin=1,model.file = jags.mod.infantDeath, DIC=FALSE)

```

```

Compiling model graph
Resolving undeclared variables
Allocating nodes
Graph information:
Observed stochastic nodes: 12
Unobserved stochastic nodes: 14
Total graph size: 57

```

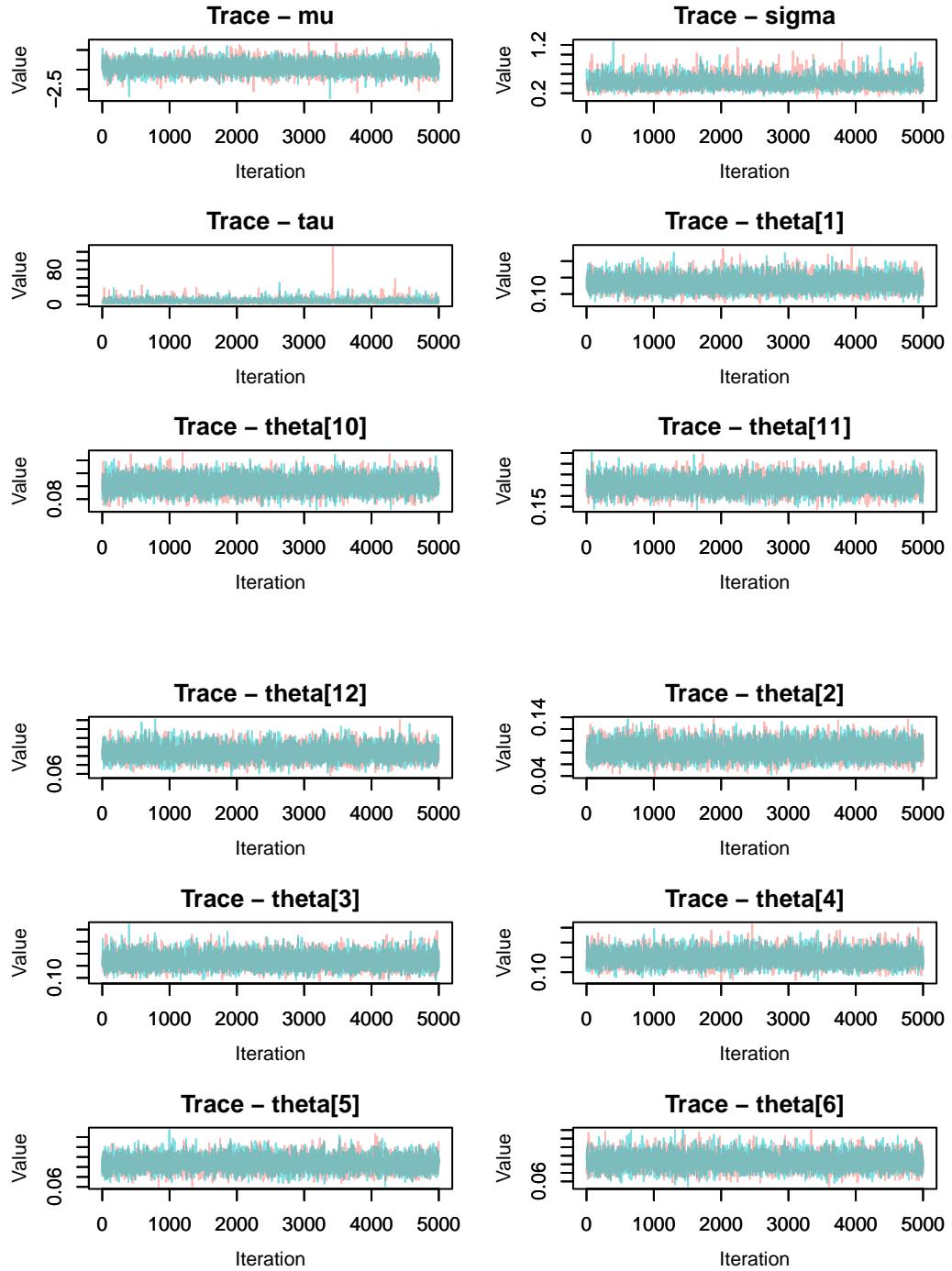
Initializing model

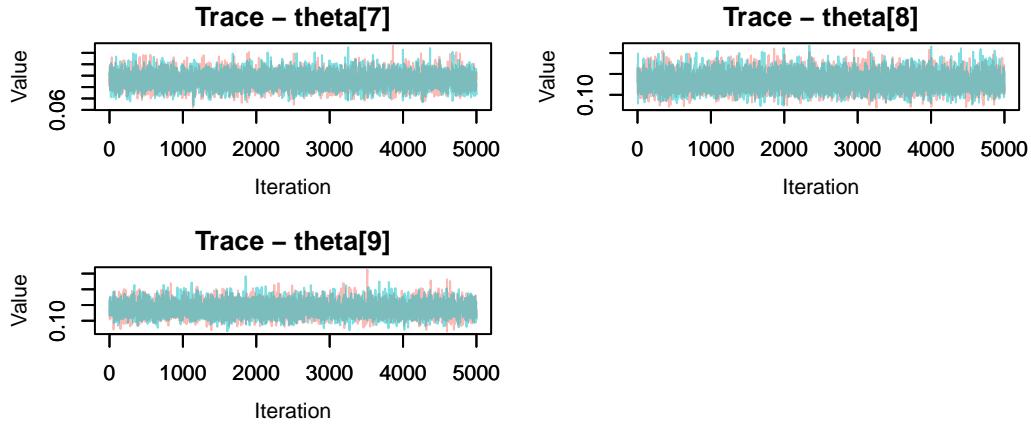
Now that we have the fitted the model we will observe the plots to check for possible convergence during the recorded 5000 iterations.

```

jagsfitinfantDeath.mcmc <- as.mcmc(jags.mod.fit.infantDeath)
MCMCtrace(jagsfitinfantDeath.mcmc, type = "trace", ind = TRUE, pdf = FALSE)

```





As we can see from the plots, there seems to be no visible patterns on the chains and all parameters have stable oscillation around a common value. We can also observe that the chains seem to be well mixed with each other as it is difficult to distinguish between chains.

However visualization alone is not enough to fully access the convergence so we will use the Gelman-Rubin diagnostics to check for convergence.

```
gelman.diag(jagsfitinfantDeath.mcmc)
```

Potential scale reduction factors:

	Point est.	Upper C.I.
mu	1.00	1.00
sigma	1.01	1.01
tau	1.03	1.03
theta[1]	1.00	1.00
theta[10]	1.00	1.00
theta[11]	1.00	1.00
theta[12]	1.00	1.00
theta[2]	1.00	1.00
theta[3]	1.00	1.00
theta[4]	1.00	1.00

```

theta[5]      1.00      1.00
theta[6]      1.00      1.00
theta[7]      1.00      1.00
theta[8]      1.00      1.00
theta[9]      1.00      1.00

```

Multivariate psrf

1.01

As we can see from the Upper Confidence Interval, the values of all parameters are approximately 1, indicating that the parameters have indeed converged.

Question 2 b)

```

jags.mod.infantDeath <- function(){
  for(i in 1:12){
    r[i] ~ dbin(theta[i],n[i])
    rpred[i] ~ dbin(theta[i],n[i])

    logit(theta[i]) <- logit.theta[i]
    logit.theta[i] ~ dnorm(mu, tau)

    #mid p-value
    p[i] = ifelse(rpred[i] > r[i], 1, ifelse(rpred[i] == r[i], 0.5, 0))
  }

  mu ~ dnorm(0,0.001)
  tau <- 1/sigma^2
  sigma ~ dunif(0,100)

}

# Parameters to monitor
jags.param.infantDeath <- c("mu", "sigma", "theta", "tau", "p")

## initial values
inits1 <- list('tau' = 100, 'sigma' = 20, 'theta'=c(10,-5,-25))

```

```

inits2 <- list('tau'=100000,'sigma'=-100,'theta'=c(-100,100,500))

jags.inits = list(inits1,inits2)

## data

jags.data.infantDeath <- list(r = surgicalDF$r, n = surgicalDF$n)

## fit the jags model

jags.mod.fit.infantDeath <- jags(data = jags.data.infantDeath, #inits = jags.inits,
parameters.to.save = jags.param.infantDeath, n.chains = 2, n.iter = 10000,
n.burnin = 5000,n.thin=1,model.file = jags.mod.infantDeath, DIC=FALSE)

```

Compiling model graph
Resolving undeclared variables
Allocating nodes
Graph information:
Observed stochastic nodes: 12
Unobserved stochastic nodes: 26
Total graph size: 118

Initializing model

```
mid_p_summary <- jags.mod.fit.infantDeath$BUGSoutput$summary[grep("p\\\[\\d+\\]",  

rownames(jags.mod.fit.infantDeath$BUGSoutput$summary)), ]
```

```
mid_p_summary_means <- subset(mid_p_summary, select = "mean")
```

```
mid_p_summary
```

	mean	sd	2.5%	25%	50%	75%	97.5%	Rhat	n.eff
p[1]	0.47230	0.4828105	0	0	0.5	1	1	1.000922	10000
p[2]	0.65205	0.4623064	0	0	1.0	1	1	1.001085	8100
p[3]	0.32720	0.4535534	0	0	0.0	1	1	1.000922	10000
p[4]	0.41080	0.4750957	0	0	0.0	1	1	1.002058	1300
p[5]	0.54455	0.4845759	0	0	1.0	1	1	1.000940	10000
p[6]	0.56535	0.4794031	0	0	1.0	1	1	1.001065	9000
p[7]	0.51955	0.4889956	0	0	0.5	1	1	1.000899	10000
p[8]	0.46635	0.4815245	0	0	0.5	1	1	1.001951	1400

```

p[9] 0.44350 0.4812285    0   0 0.0    1      1 1.002046 1300
p[10] 0.55080 0.4871787   0   0 1.0    1      1 1.000990 10000
p[11] 0.22360 0.4046226   0   0 0.0    0      1 1.001146 6100
p[12] 0.55480 0.4836531   0   0 1.0    1      1 1.000909 10000

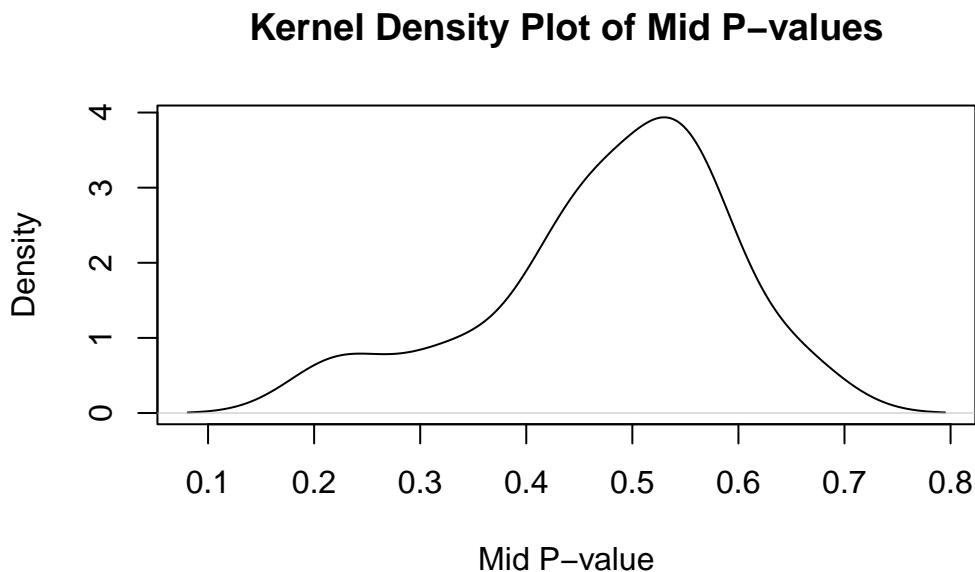
```

As we can see from the average mid p-value, the probability that the predicted mortality is higher than the registered mortality, it seems that hospital 3, 4 and 11 have mean values significantly lower than 0,5 meaning they have unusually higher mortality rate compared to the predicted mortality rate

```

# Plot kernel density of mid p-values
plot(density(mid_p_summary_means), main = "Kernel Density Plot of Mid P-values",
      xlab = "Mid P-value")

```



Question 2 c)

```

jags.mod.infantDeathUniform <- function(){

  for(i in 1:12){

    theta[i] ~ dunif(0, 1) ## new theta definition
  }
}

```

```

r[i] ~ dbin(theta[i],n[i])
rpred[i] ~ dbin(theta[i],n[i])

p[i] =ifelse(rpred[i] > r[i], 1, ifelse(rpred[i] == r[i], 0.5, 0))
}

mu ~ dnorm(0,0.001)
tau <- 1/sigma^2
sigma ~ dunif(0,100)
}

# Parameters to monitor
jags.param.infantDeathUniform <- c("mu", "sigma", "theta", "tau", "p")

## initial values
inits1 <- list('mu' = 1, 'sigma' = 1, 'theta'=rep(1,12))
inits2 <- list('mu'= 0,'sigma'=50,'theta'= rep(20,12))

jags.inits = list(inits1,inits2)

## data

jags.data.infantDeathUniform <- list(r = surgicalDF$r, n = surgicalDF$n)

## fit the jags model

jags.mod.fit.infantDeathUniform <- jags(data = jags.data.infantDeathUniform, #inits = jags
parameters.to.save = jags.param.infantDeathUniform, n.chains = 2, n.iter = 10000,
n.burnin = 5000,n.thin=1,model.file = jags.mod.infantDeathUniform, DIC=FALSE)

Compiling model graph
Resolving undeclared variables
Allocating nodes
Graph information:
Observed stochastic nodes: 12
Unobserved stochastic nodes: 26
Total graph size: 106

Initializing model

```

After having checked for convergence we will now use box plots to compare the theta mortality rates from the first and the last model.

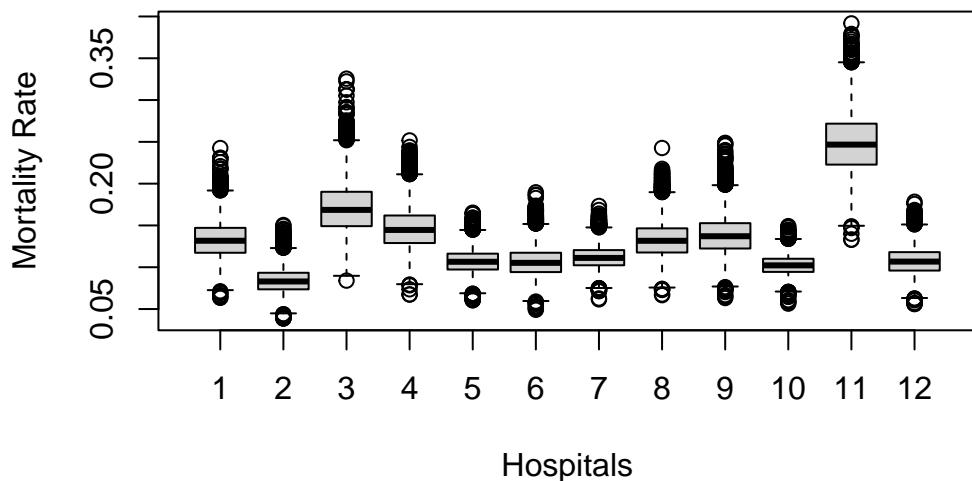
```

# Extract posterior samples of theta
theta.samples <- jags.mod.fit.infantDeath$BUGSoutput$sims.list$theta
theta.samplesUniform <- jags.mod.fit.infantDeathUniform$BUGSoutput$sims.list$theta

# Create boxplot
boxplot(theta.samples, xlab = "Hospitals", ylab = "Mortality Rate", main = "Posterior Dist

```

Posterior Distribution of Theta for the 1st model

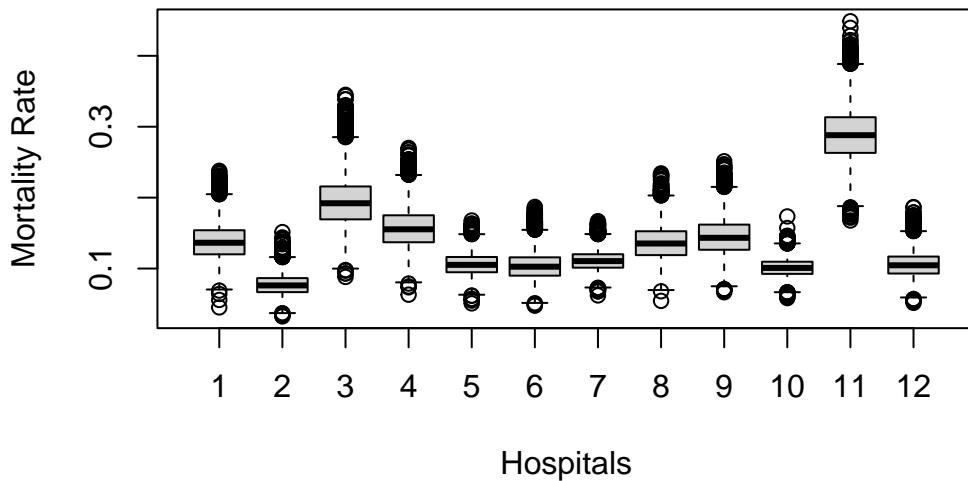


```

# Create boxplot
boxplot(theta.samplesUniform, xlab = "Hospitals", ylab = "Mortality Rate",
        main = "Posterior Distribution of Theta For uniform dist model")

```

Posterior Distribution of Theta For uniform dist model



From the 2 box plots it seems that the changes are mainly in increasing the overall mortality rate theta in the last model as the trends remain identical but all values seem to have a slightly constant increase in value. This means that our new independent fixed effect model has a very similar effect captured compared to the previous mortality rate effect.

Question 2 d)

```
mid_p_summaryUniform <- jags.mod.fit.infantDeathUniform$BUGSoutput$summary[grep("p\\\[\\d+",  
rownames(jags.mod.fit.infantDeathUniform$BUGSoutput$summary)), ]  
  
mid_p_summary_meansUniform <- subset(mid_p_summaryUniform, select = "mean")  
  
mid_p_summaryUniform
```

	mean	sd	2.5%	25%	50%	75%	97.5%	Rhat	n.eff
p[1]	0.51790	0.4848743	0	0	0.5	1	1	1.000935	10000
p[2]	0.52230	0.4855680	0	0	0.5	1	1	1.000941	10000
p[3]	0.51890	0.4830798	0	0	0.5	1	1	1.001138	6300
p[4]	0.52090	0.4841349	0	0	0.5	1	1	1.000909	10000
p[5]	0.52560	0.4882812	0	0	1.0	1	1	1.001353	3300

```

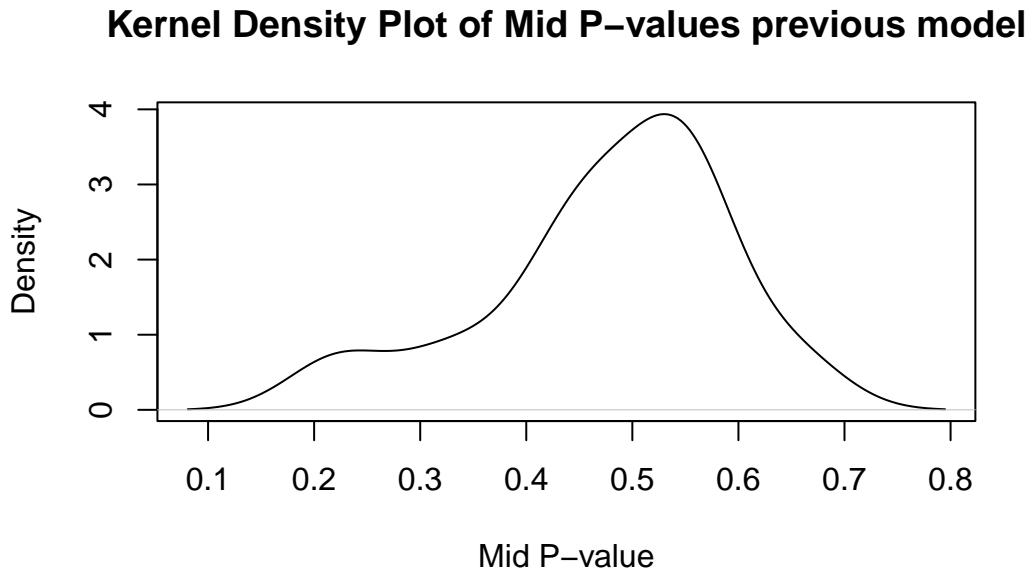
p[6] 0.52900 0.4840273 0 0 0.5 1 1 1.001114 7000
p[7] 0.50290 0.4890455 0 0 0.5 1 1 1.000917 10000
p[8] 0.51315 0.4844332 0 0 0.5 1 1 1.000966 10000
p[9] 0.51250 0.4842698 0 0 0.5 1 1 1.000922 10000
p[10] 0.51355 0.4906276 0 0 0.5 1 1 1.000907 10000
p[11] 0.50785 0.4864021 0 0 0.5 1 1 1.001362 3200
p[12] 0.52300 0.4865128 0 0 0.5 1 1 1.001401 3000

```

```

# Plot kernel density of mid p-values
plot(density(mid_p_summary_means), main = "Kernel Density Plot of Mid P-values previous model",
      xlab = "Mid P-value")

```

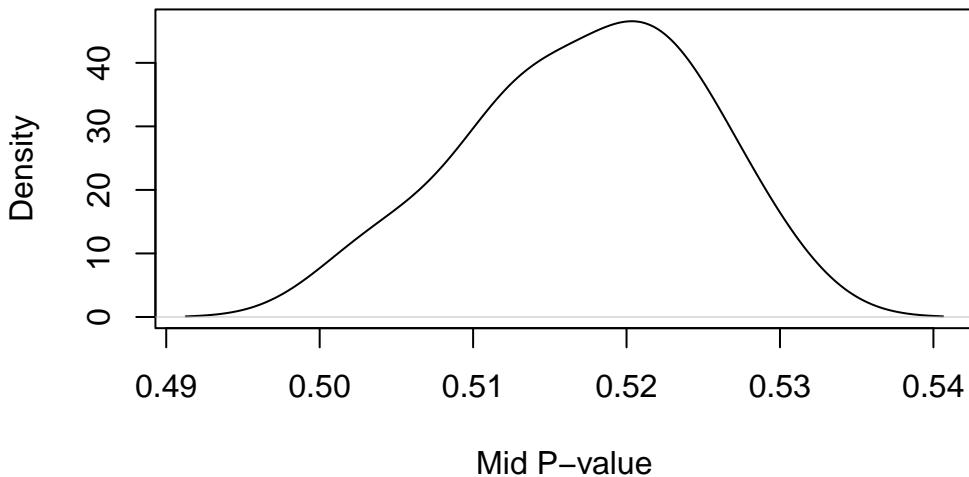


```

# Plot kernel density of mid p-values
plot(density(mid_p_summary_meansUniform), main = "Kernel Density Plot of Mid P-values Uniform",
      xlab = "Mid P-value")

```

Kernel Density Plot of Mid P-values Uniform dist



As we can see from the graph, it seems that the previous model mid p-values have an higher mean and are more skewed to the left, as compared to the new model that is skewed to the right, meaning that the newer model has smaller mid p-values.

This indicates that the fixed effects model is a better fit for the data. This means that the unusual mortality rates can be better explained by the fixed effects model, which assumes that each hospital has its own fixed effect on the mortality rate, rather than the random effects model, which assumes that the effects vary randomly across hospitals.

Question B - classification

Question B.1

Group 0 is characterised for always having $x_1 > -1.65$ and $x_2 < 2.05$ with the majority of the occurrences of group 0 having

```
## I am just going to split the dataframe in two so its easier to show
## an histogram of each variable for both groups

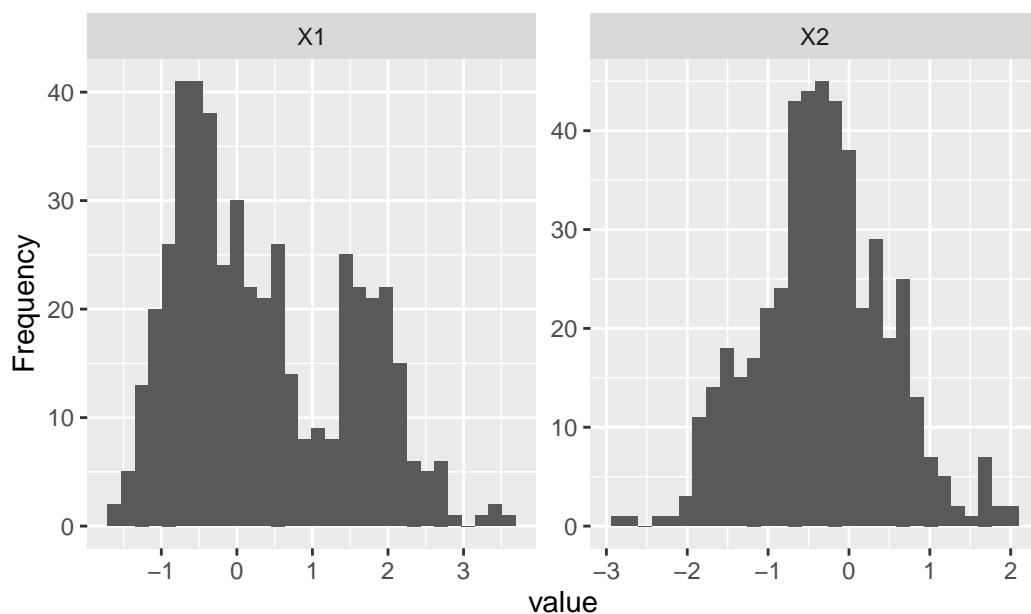
group0 = subset(classificationDF, Group == 0)
group1 = subset(classificationDF, Group == 1)
```

```

## removing the id variable from both of these new data frames so they
## are not included in the histograms
group0 = group0 %>%
  select(-(1))
group1 = group1 %>%
  select(-(1))

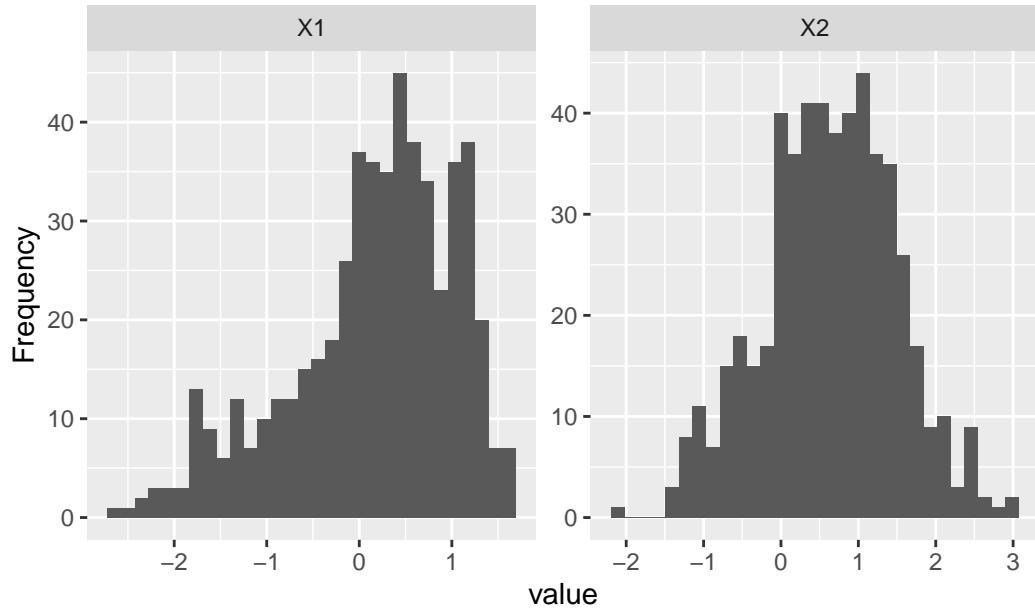
plot_histogram(group0)

```



As we can see from the histograms from group 0 it seems that X2 seems to follow a normal distribution that is very slightly skewed to the left and has mean -0,5. X1 is clearly skewed to the right possibly following a normal distribution and again mean equal to -0,5.

```
plot_histogram(group1)
```



Group 1 histograms reveal that X_2 is normally distributed with mean equal to 0,5 and slightly skewed to the left. The variable X_1 also seems to follow a normal distribution that has a very prolonged skewness to the left and mean 0,5,0

Question B.2

Both LDA and QDA assume normality which seems to hold from what we can see from the histograms on question B.1

Starting with Linear discriminant analysis (LDA) we can easily see from the initial graph that we can see that the any sensible decision boundary is highly non-linear. As analysed from histograms this data violates the initial assumption of homogeneity of variance (homoscedasticity). The non-linearity of the data would also lead to LDA having terrible performance. As such we can conclude that LDA is not suitable for this data.

Secondly, quadratic discriminant analysis (QDA) follow the assumption of normality of each of the variables which does seem to hold even with how highly non-linear the data is. However judging from the plot with the observations, it does seem that QDA does not have enough flexibility to account for all the variability in what is the theoretical Bayes decision boundary due to the highly non-linear nature of the data. As such we can conclude that QDA is not suitable for this data.

Thirdly, K-nearest neighbour classification (KNN) has no assumptions made about the shape of the decision, as such as we choose a adequate level of smoothness to prevent overfitting KNN classification is an adequate method for the data.

Support Vector Machines (SVM) are most commonly used for binary classification, which holds true for our data. The high non-linear decision boundary however requires a careful selection of a non linear kernel function to ensure that the boundary becomes non-linear when converted back to the regular space. As such I deem SVM an appropriate method to classify the data.

Finally, Random forest also do not make any assumptions about the underlying distribution present on the data set. A random forest would also have the added bonus of letting us understand which of the variables X1 or X2 has the biggest impact on the classification of data points which could be useful for future applications of this model. As such I deem Random forest an appropriate method to classify the data.

Question B.3

```
# make this example reproducible
set.seed(26041999)
# use 80% of dataset as training set and 20% as test set
sample = sample.split(classificationDF$Group, SplitRatio = 0.8)
## note that the column selected above can be any column.
train = classificationDF[sample, ]
test = classificationDF[!sample, ]

# split the data using the indices returned by the createDataPartition
# function
X_train = train[, c("X1", "X2")]
y_train = train$Group
X_test = test[, c("X1", "X2")]
y_test = test$Group

# check the dimensions
dim(train)
```

```
[1] 800    4
```

```
dim(test)
```

```
[1] 200    4
```

Question B.4

The 3 method I will be using are Random forest, KNN and SVM as deemed to be the most appropriate methods for this data.

Random Forest

For random Forest we will tune the number of variables randomly split for each of the random samples, as such we will try if only 1 split variable or both variables give a better accuracy

```
# Random Search for best number of variables
control <- trainControl(method = "repeatedcv", number = 10, repeats = 3,
    search = "random")

rf_random <- train(Group ~ ., data = trainNum, method = "rf", metric = "Accuracy",
    tuneLength = 15, trControl = control)
print(rf_random)
```

Random Forest

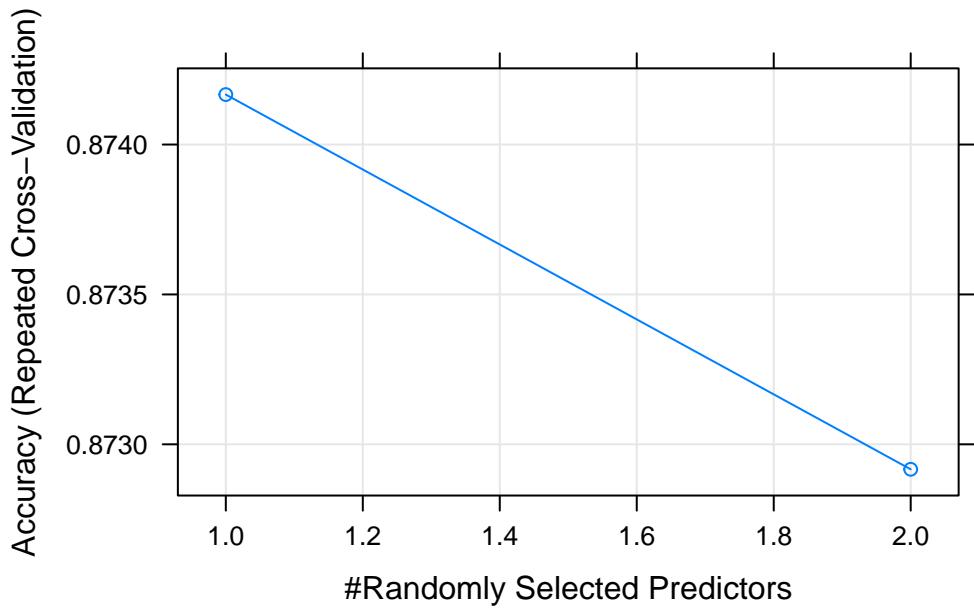
```
800 samples
 2 predictor
 2 classes: '0', '1'
```

```
No pre-processing
Resampling: Cross-Validated (10 fold, repeated 3 times)
Summary of sample sizes: 720, 720, 720, 720, 720, 720, ...
Resampling results across tuning parameters:
```

mtry	Accuracy	Kappa
1	0.8741667	0.7478208
2	0.8729167	0.7452588

```
Accuracy was used to select the optimal model using the largest value.
The final value used for the model was mtry = 1.
```

```
plot(rf_random)
```



As we can see the accuracy is almost identical with a difference of less than 0,1% and is actually variable depending on the randomly selected values during the training process due to the nature of the random search as such I will try both mtry = 1 and mtry = 2.

```
# Train the model
rf_model <- randomForest(Group ~ ., data = trainNum, tuneGrid = data.frame(mtry = 1))

# Make predictions on the test data
predictions <- predict(rf_model, testNum)

confusionMatrix(as.factor(predictions), as.factor(y_test))
```

Confusion Matrix and Statistics

		Reference	
		Prediction	
		0	1
Prediction		0	79
		1	16
		20	85

Accuracy : 0.82
 95% CI : (0.7596, 0.8706)
 No Information Rate : 0.525

```
P-Value [Acc > NIR] : <2e-16
```

```
Kappa : 0.6398
```

```
McNemar's Test P-Value : 0.6171
```

```
Sensitivity : 0.8316  
Specificity : 0.8095  
Pos Pred Value : 0.7980  
Neg Pred Value : 0.8416  
Prevalence : 0.4750  
Detection Rate : 0.3950  
Detection Prevalence : 0.4950  
Balanced Accuracy : 0.8206
```

```
'Positive' Class : 0
```

```
# Train the model  
rf_model <- randomForest(Group ~ ., data = trainNum, tuneGrid = data.frame(mtry = 2))  
  
# Make predictions on the test data  
predictions <- predict(rf_model, testNum)  
  
## Manually making the cut at 0,5 of prediction for the groups  
## predictions <- ifelse(predictions >= 0.5, 1, 0)  
  
confusionMatrix(as.factor(predictions), as.factor(y_test))
```

Confusion Matrix and Statistics

Reference		
Prediction	0	1
0	80	21
1	15	84

```
Accuracy : 0.82  
95% CI : (0.7596, 0.8706)  
No Information Rate : 0.525  
P-Value [Acc > NIR] : <2e-16
```

```

Kappa : 0.6402

McNemar's Test P-Value : 0.4047

Sensitivity : 0.8421
Specificity : 0.8000
Pos Pred Value : 0.7921
Neg Pred Value : 0.8485
Prevalence : 0.4750
Detection Rate : 0.4000
Detection Prevalence : 0.5050
Balanced Accuracy : 0.8211

'Positive' Class : 0

```

As we can see from the summary tables both fine tuned values lead to approximately the same result of 82% accuracy which is actually lower than the random search was predicting.

KNN - K-nearest neighbour

First we make a graph displaying the accuracy for each k from 1 to 30 to see which K is the most appropriate by giving us the best accuracy.

```

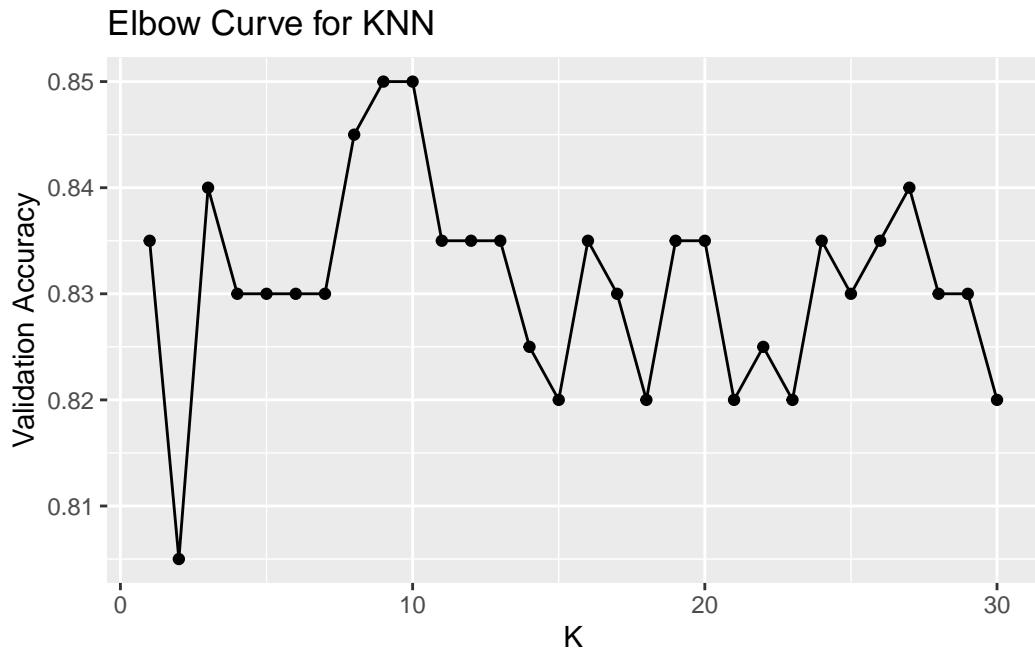
# Define range of K values to test
k_range <- 1:30

# Empty list to store validation accuracy scores
accuracy_scores <- c()

# Train and evaluate KNN model for each value of K
for (k in k_range) {
  knn <- knn(X_train, X_test, y_train, k = k)
  accuracy_scores <- c(accuracy_scores, sum(knn == y_test)/length(y_test))
}

# Plot the elbow curve
df <- data.frame(k = k_range, accuracy = accuracy_scores)
ggplot(df, aes(x = k, y = accuracy)) + geom_line() + geom_point() + xlab("K") +
  ylab("Validation Accuracy") + ggtitle("Elbow Curve for KNN")

```



As we can see from the graph, $k = 9$ is the one that give us the most accuracy and most other values have not been as highly accurate.

```
# fit the model
fit = knn(train = X_train, test = X_test, cl = y_train, k = 9)
# fit = knn(xTrain,xTest,yTrain,k=3)

# produce the confusion matrix when numbers are used as class labels we
# might need
confusion = confusionMatrix(as.factor(fit), as.factor(y_test))

confusion
```

Confusion Matrix and Statistics

		Reference	
Prediction	0	1	
0	82	17	
1	13	88	

Accuracy : 0.85
95% CI : (0.7928, 0.8965)

```

No Information Rate : 0.525
P-Value [Acc > NIR] : <2e-16

Kappa : 0.6998

McNemar's Test P-Value : 0.5839

Sensitivity : 0.8632
Specificity : 0.8381
Pos Pred Value : 0.8283
Neg Pred Value : 0.8713
Prevalence : 0.4750
Detection Rate : 0.4100
Detection Prevalence : 0.4950
Balanced Accuracy : 0.8506

'Positive' Class : 0

```

```

test$predicted_group = fit
test$correct_prediction = test$predicted_group == test$Group

# plot the data points
p = ggplot() + geom_point(data = train, aes(x = X1, y = X2, color = "Training"),
                           size = 3) + geom_point(data = test, aes(x = X1, y = X2, color = correct_prediction,
                           shape = factor(correct_prediction), size = 3) + scale_color_manual(values = c("red",
                           "blue", "green"), labels = c("Incorrect", "Correct", "Training")) + scale_shape_manual(
                           16)) + labs(x = "X1", y = "X2", color = "", shape = "") + ggtitle("KNN Classification")

# display the plot
print(p)

```

SVM - Support Vector Machines

Since we don't have a linear kernel due to the nature of the data we have a choice of using either a polynomial kernel or a radial kernel, however there is no simple test to differentiate which kernel function has the best performance for this data, as such I would be fine tuning both kernel functions and then see which kernel function has the best performance.

However since the polynomial fine tuning does not converge I will use the non tuned kernels to show that the radial kernel is better suited to the data.

Startin with the polynomial kernel

```

mdlSVMPoly = svm(Group ~ .,
                  data = train,
                  type = 'C-classification',
                  kernel = 'polynomial',
                  #cost = svmPolynoml_tuned$bestTune$C,
                  #sigma = svmPolynoml_tuned$bestTune$sigma
                  )

# Test model on testing data
yTestPredPoly = predict(mdlSVMPoly, newdata=test)
# yTestPred = mdl %>% predict(xTest)
confusionMatrix(as.factor(yTestPredPoly), as.factor(y_test)) # predicted/true

```

Confusion Matrix and Statistics

		Reference
Prediction	0	1
0	59	18
1	36	87

Accuracy : 0.73
 95% CI : (0.6628, 0.7902)
 No Information Rate : 0.525
 P-Value [Acc > NIR] : 2.343e-09

 Kappa : 0.4537

 Mcnemar's Test P-Value : 0.0207

 Sensitivity : 0.6211
 Specificity : 0.8286
 Pos Pred Value : 0.7662
 Neg Pred Value : 0.7073
 Prevalence : 0.4750
 Detection Rate : 0.2950
 Detection Prevalence : 0.3850
 Balanced Accuracy : 0.7248

 'Positive' Class : 0

As we can see this kernel function only has an average accuracy of 73% which is significantly

lower than the other methods.

```
mdlSVM = svm(Group ~ .,
              data = train,
              type = 'C-classification',
              kernel = 'radial')

# Test model on testing data
yTestPred = predict(mdlSVM, newdata=test)
# yTestPred = mdl %>% predict(xTest)
confusionMatrix(as.factor(yTestPred), as.factor(y_test)) # predicted/true
```

Confusion Matrix and Statistics

		Reference
Prediction	0	1
0	80	20
1	15	85

Accuracy : 0.825
95% CI : (0.7651, 0.875)
No Information Rate : 0.525
P-Value [Acc > NIR] : <2e-16

Kappa : 0.65

McNemar's Test P-Value : 0.499

Sensitivity : 0.8421
Specificity : 0.8095
Pos Pred Value : 0.8000
Neg Pred Value : 0.8500
Prevalence : 0.4750
Detection Rate : 0.4000
Detection Prevalence : 0.5000
Balanced Accuracy : 0.8258

'Positive' Class : 0

As we can see, the Radial kernel function even when not fine tuned has a significantly better accuracy than the polynomial kernel by almost 10%, such gap would have not been narrowed

by the fine tuning of the parameters alone and as such a Radial kernel function is the most appropriate for this data, as such we will be fine tuning the hyper parameters of the model.

Firstly I will start by fine tuning the common constant C and the sigma parameter which is specific to the radial kernel SVM

```
fitControl = trainControl(## 10-fold CV
                           method = "repeatedcv",
                           number = 10,
                           ## repeated ten times
                           repeats = 10)

param_grid <- expand.grid(C = seq(0.1, 10, length = 10),
                           sigma = seq(0.1, 1, length = 10))

svmRadial_tuned = train(Group ~ .,
                        data = trainNum,
                        method = 'svmRadial',
                        trControl = fitControl,
                        tuneGrid = param_grid)

svmRadial_tuned
```

Support Vector Machines with Radial Basis Function Kernel

```
800 samples
 2 predictor
 2 classes: '0', '1'
```

```
No pre-processing
Resampling: Cross-Validated (10 fold, repeated 10 times)
Summary of sample sizes: 720, 720, 720, 720, 720, ...
Resampling results across tuning parameters:
```

C	sigma	Accuracy	Kappa
0.1	0.1	0.774125	0.5474824
0.1	0.2	0.804375	0.6082202
0.1	0.3	0.816750	0.6330858
0.1	0.4	0.828500	0.6568911
0.1	0.5	0.838000	0.6759468
0.1	0.6	0.841625	0.6832838

0.1	0.7	0.845875	0.6917003
0.1	0.8	0.847625	0.6951959
0.1	0.9	0.848625	0.6972030
0.1	1.0	0.851000	0.7020040
1.2	0.1	0.814625	0.6288121
1.2	0.2	0.852000	0.7037885
1.2	0.3	0.863125	0.7263778
1.2	0.4	0.865750	0.7317670
1.2	0.5	0.868250	0.7368202
1.2	0.6	0.868625	0.7376100
1.2	0.7	0.870375	0.7411153
1.2	0.8	0.872875	0.7461434
1.2	0.9	0.873375	0.7471350
1.2	1.0	0.874500	0.7493192
2.3	0.1	0.825875	0.6514549
2.3	0.2	0.858125	0.7162464
2.3	0.3	0.863500	0.7271185
2.3	0.4	0.867250	0.7348227
2.3	0.5	0.869500	0.7393521
2.3	0.6	0.871750	0.7438767
2.3	0.7	0.873375	0.7471450
2.3	0.8	0.875875	0.7520855
2.3	0.9	0.878250	0.7567092
2.3	1.0	0.880625	0.7612476
3.4	0.1	0.834375	0.6686225
3.4	0.2	0.862625	0.7252902
3.4	0.3	0.864750	0.7297386
3.4	0.4	0.867500	0.7353467
3.4	0.5	0.869875	0.7401243
3.4	0.6	0.875250	0.7509467
3.4	0.7	0.875000	0.7503502
3.4	0.8	0.878125	0.7563653
3.4	0.9	0.881875	0.7636264
3.4	1.0	0.886500	0.7726123
4.5	0.1	0.843875	0.6875661
4.5	0.2	0.864000	0.7280358
4.5	0.3	0.865750	0.7317767
4.5	0.4	0.867375	0.7350838
4.5	0.5	0.871500	0.7433916
4.5	0.6	0.873500	0.7474097
4.5	0.7	0.876250	0.7526861
4.5	0.8	0.882250	0.7643886
4.5	0.9	0.887375	0.7743615

4.5	1.0	0.891750	0.7829283
5.6	0.1	0.847375	0.6944760
5.6	0.2	0.865125	0.7302821
5.6	0.3	0.867000	0.7342874
5.6	0.4	0.868625	0.7375996
5.6	0.5	0.873250	0.7469459
5.6	0.6	0.874375	0.7490668
5.6	0.7	0.880000	0.7600253
5.6	0.8	0.886000	0.7716813
5.6	0.9	0.892750	0.7850086
5.6	1.0	0.893875	0.7871524
6.7	0.1	0.851625	0.7029540
6.7	0.2	0.865000	0.7300621
6.7	0.3	0.867875	0.7360572
6.7	0.4	0.870375	0.7411338
6.7	0.5	0.873750	0.7479047
6.7	0.6	0.875500	0.7512072
6.7	0.7	0.884250	0.7683498
6.7	0.8	0.890125	0.7798265
6.7	0.9	0.893625	0.7867012
6.7	1.0	0.896125	0.7916334
7.8	0.1	0.853250	0.7062708
7.8	0.2	0.866875	0.7338577
7.8	0.3	0.868000	0.7363082
7.8	0.4	0.871375	0.7431444
7.8	0.5	0.874125	0.7485991
7.8	0.6	0.877000	0.7541060
7.8	0.7	0.886500	0.7726783
7.8	0.8	0.892375	0.7842332
7.8	0.9	0.895500	0.7904077
7.8	1.0	0.896250	0.7918742
8.9	0.1	0.855750	0.7113351
8.9	0.2	0.867250	0.7346342
8.9	0.3	0.868500	0.7372914
8.9	0.4	0.871125	0.7426332
8.9	0.5	0.873750	0.7478349
8.9	0.6	0.879375	0.7587404
8.9	0.7	0.889375	0.7783491
8.9	0.8	0.891875	0.7831710
8.9	0.9	0.896125	0.7916140
8.9	1.0	0.895875	0.7911165
10.0	0.1	0.855875	0.7115987
10.0	0.2	0.867375	0.7349059

```

10.0  0.3      0.869375  0.7390316
10.0  0.4      0.871250  0.7428916
10.0  0.5      0.873750  0.7477788
10.0  0.6      0.882125  0.7641143
10.0  0.7      0.890875  0.7812984
10.0  0.8      0.893750  0.7869032
10.0  0.9      0.896625  0.7926159
10.0  1.0      0.895875  0.7910950

```

Accuracy was used to select the optimal model using the largest value.
The final values used for the model were sigma = 0.9 and C = 10.

This is the non-converging polynomial SVM where I would fine tuning the common constant C and the specific fine tuning parameters from the polynomial function, degree and scale.

```

# Set up the tuning grid
tuningGrid <- expand.grid(degree = c(2, 3, 4), C = 10^(0:2), scale = c(0.1,
1, 10))

# Set up the control parameters
fitControl <- trainControl(method = "repeatedcv", number = 10, repeats = 3,
classProbs = TRUE)
## I had to convert the variable names from scientific notation to
## decimal because it is the only way for this to work for this kernel
trainNumTest = trainNum

levels(trainNumTest$Group) <- make.names(levels(trainNumTest$Group))

# Train the SVM with polynomial kernel
svmPoly_tuned <- train(Group ~ ., data = trainNumTest, method = "svmPoly",
tuneGrid = tuningGrid, trControl = fitControl, minstep = 1e-08)

# Print the results
svmPoly_tuned

```

Now that we have the fine tuned parameters I will be using these to fit a model for the Radial kernel.

```

mdlSVM = svm(Group ~ .,
              data = train,

```

```

    type = 'C-classification',
    kernel = 'radial',
    cost = svmRadial_tuned$bestTune$C,
    sigma = svmRadial_tuned$bestTune$sigma)

# Test model on testing data
yTestPred = predict(mdlSVM, newdata=test)
# yTestPred = mdl %>% predict(xTest)
confusionMatrix(as.factor(yTestPred), as.factor(y_test)) # predicted/true

```

Confusion Matrix and Statistics

		Reference
Prediction	0	1
0	83	23
1	12	82

Accuracy : 0.825
 95% CI : (0.7651, 0.875)
 No Information Rate : 0.525
 P-Value [Acc > NIR] : < 2e-16

 Kappa : 0.651

 Mcnemar's Test P-Value : 0.09097

 Sensitivity : 0.8737
 Specificity : 0.7810
 Pos Pred Value : 0.7830
 Neg Pred Value : 0.8723
 Prevalence : 0.4750
 Detection Rate : 0.4150
 Detection Prevalence : 0.5300
 Balanced Accuracy : 0.8273

 'Positive' Class : 0

As we can see from the fine tuned model summary, the usage of C and sigma managed to improve the model by approximately 0,5% making this model slightly better than the previously untuned model.

Question B.5

In our data we have 475 observations belonging to the group 0 and the remaining 525 belonging to group 1, since there is only a small difference in number of observations between both groups, accuracy will be a sensible metric to compare all 3 different methods.

From the 3 final fine tuned models we can see that the Radial kernel SVM has an accuracy of 83%, the KNN with k=9 has an accuracy of 85% and the random forest has an accuracy of 82%, as such with overall accuracy in mind we can determine that KNN with 9 clusters is the better predictive model.

This also holds true if we were to compare the specificity of the 3 models as KNN has the highest value of 83,81% compared to the 80,00% from random forest and 78,10% from SVM.

However for sensitivity the SVM has 88,42% which beats both the SVM 86,32% and the random forest 84,32%.

To conclude unless there was a specific need to focus on the specificity of the model which is not given for this dataset the best method for classification is the K-nearest neighbour classification.