Untitled

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Model

```r
##  Set MCMC parameters.
chains <- 1            ##  One chain of MCMC values is obtained
burn_in <- 1000        ##  The first 1000 iterates from the MCMC chain are discarded
iterations <- 100000   ##  10,000 values are sampled from the posterior distribution
thin <- 1              ##  No thinning is performed


##  Import beta-carotene data an store it in new variable names for use with JAGS.
bc_data <- fread("bcarotene.csv") %>%
    mutate(ptid = ifelse(ptid>40, ptid-1, ptid)) %>%
    na.omit()

ptid <- bc_data$ptid
month <- bc_data$month
bcarot <- bc_data$bcarot
vite <- bc_data$vite
dose <- bc_data$dose
age <- bc_data$age
male <- bc_data$male
bmi <- bc_data$bmi
chol <- bc_data$chol
cauc <- bc_data$cauc
vauc <- bc_data$vauc


##  Define new variables for JAGS to use.
n <- dim(bc_data)[1]
n_patients <- length( unique(ptid) )

intercept <- rep(1,n)
tx <- intercept - (month<4)


##  Define the design matrix for the model and specify the number of covariates, for use in JAGS.
x <- cbind(intercept, tx*dose, vite, month, age, bmi, chol, cauc, vauc)
n_covariates <- dim(x)[2]
tau_b <- 0.00001
```

```r
##  Establish data and parameter lists for use with OpenBUGS; define function for generating initial pa
data <- list( "bcarot"=bcarot,
              "n"=n,
              "n_patients"=n_patients,
              "n_covariates"=n_covariates,
              "ptid"=ptid,
              "x"=x,
              "tau_b"=tau_b )

inits <- function() {
  list( beta = rnorm( n_covariates, 0, 1 ),
        gamma = rnorm( n_patients, 0, 1 ),
        tau_bc = runif( 1, 0, 2 ),
        tau_g = runif( 1, 0, 2 ) )
}

parameters <- c( "beta", "gamma", "sigma_bc", "sigma_g" )



###############    CREATE MODEL    ###############

bc_modelstring<-"model
  {
    for(i in 1:n){
        bcarot[i] ~ dnorm( mu[i], tau_bc )
          mu[i] <- inprod( x[i,], beta[] ) + gamma[ ptid[i] ]
    }
      for(j in 1:n_patients){
        gamma[j] ~ dnorm( 0, tau_g )
      }
    for(k in 1:n_covariates){
        beta[k] ~ dnorm( 0, tau_b )
      }
    tau_bc ~ dgamma(0.001, 0.001)
      tau_g ~ dgamma(0.001, 0.001)
    sigma_bc <- pow(tau_bc,-0.5)
      sigma_g <- pow(tau_g,-0.5)
  }"

beta_carotene.m <- jags.model( data=data,
                               inits=inits,
                               file=textConnection(bc_modelstring),
                               n.chains=chains )
```

```
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 689
##    Unobserved stochastic nodes: 56
##    Total graph size: 9713
##
```

Initializing model

```r
beta_carotene.sim <- coda.samples(beta_carotene.m,
                                  parameters,
                                  n.iter=iterations,
                                  thin=thin,
                                  n.burn=burn_in)

## Assign variable names to posterior samples.
beta_carotene.iterates <- as.matrix(beta_carotene.sim)
beta_carotene.iterates <- as.data.frame(beta_carotene.iterates)

posterior_betas <- beta_carotene.iterates[,(1:n_covariates)]
names(posterior_betas) <- c("intercept", "dose", "vite", "month", "age", "bmi", "chol", "cauc", "vauc")
posterior_gammas <- beta_carotene.iterates[,((n_covariates+1):(n_covariates+n_patients))]
posterior_sigmas <- beta_carotene.iterates[,((n_covariates+n_patients+1):(n_covariates+n_patients+2))]
```
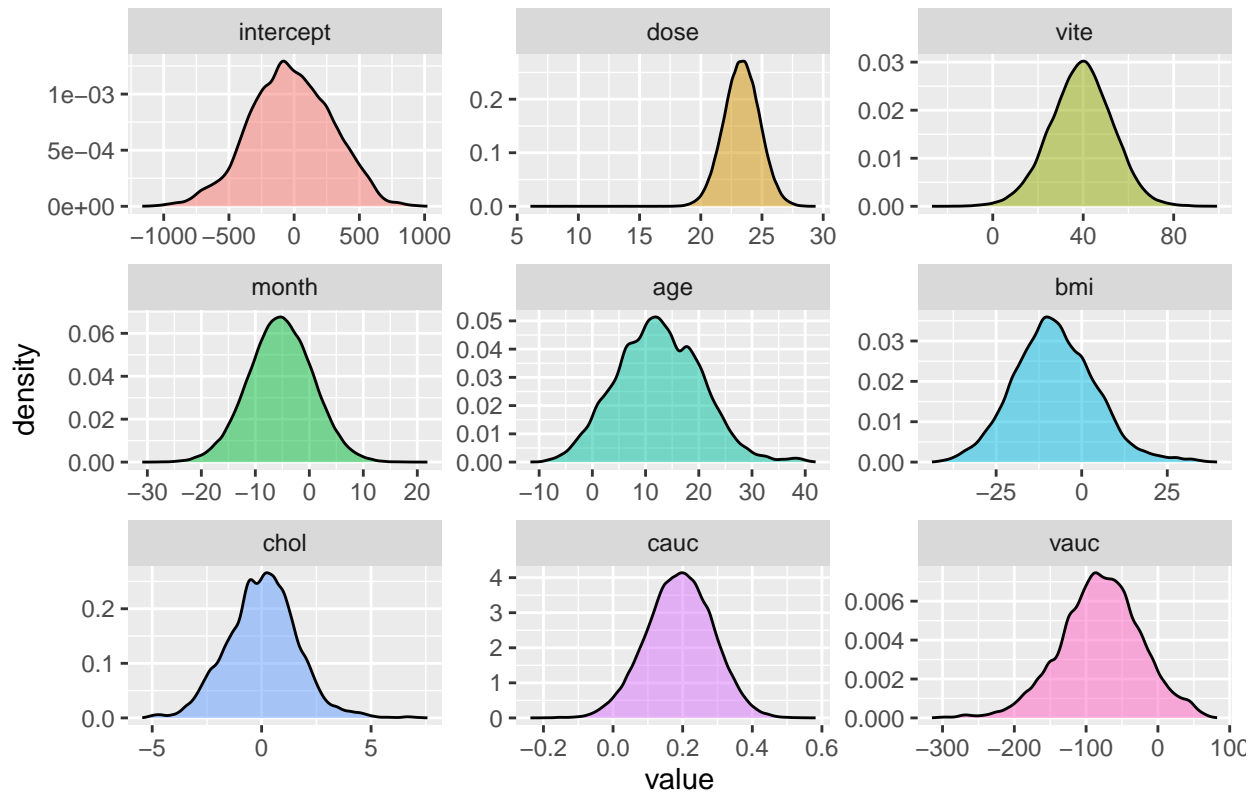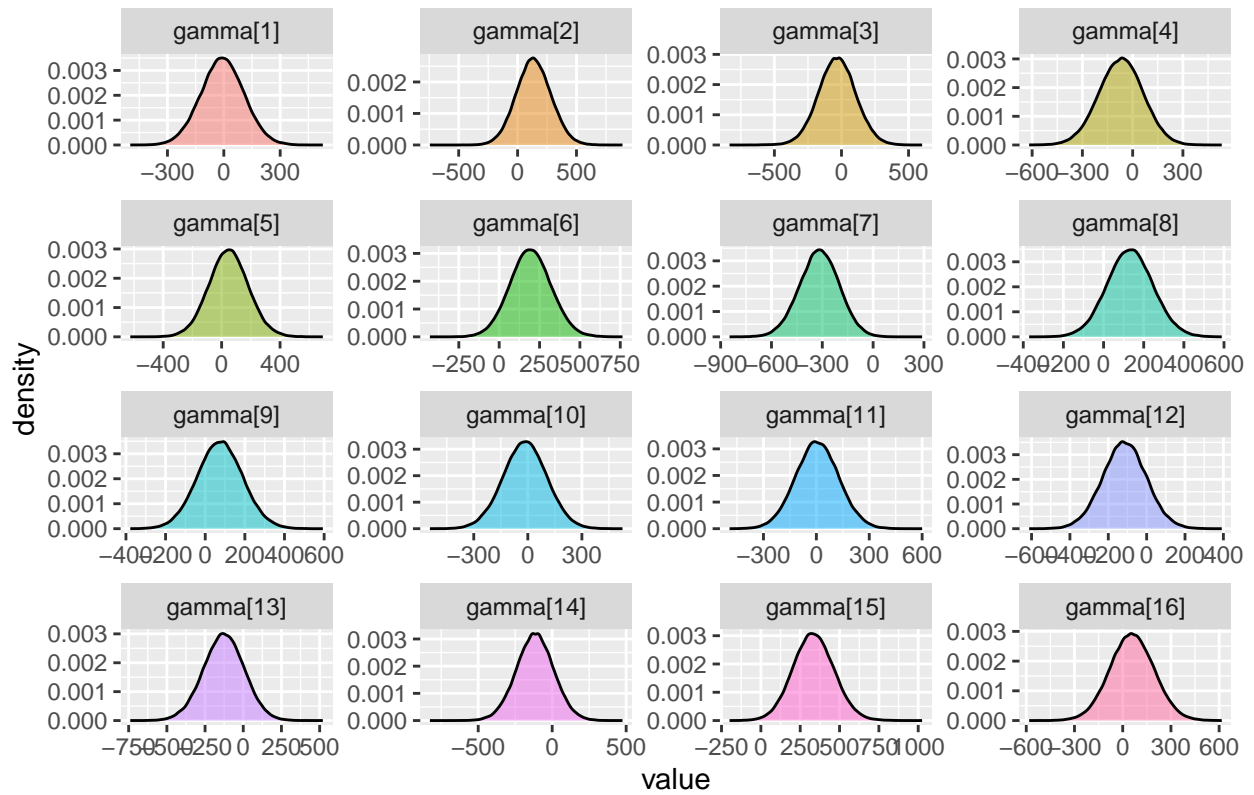
No id variables; using all as measure variables
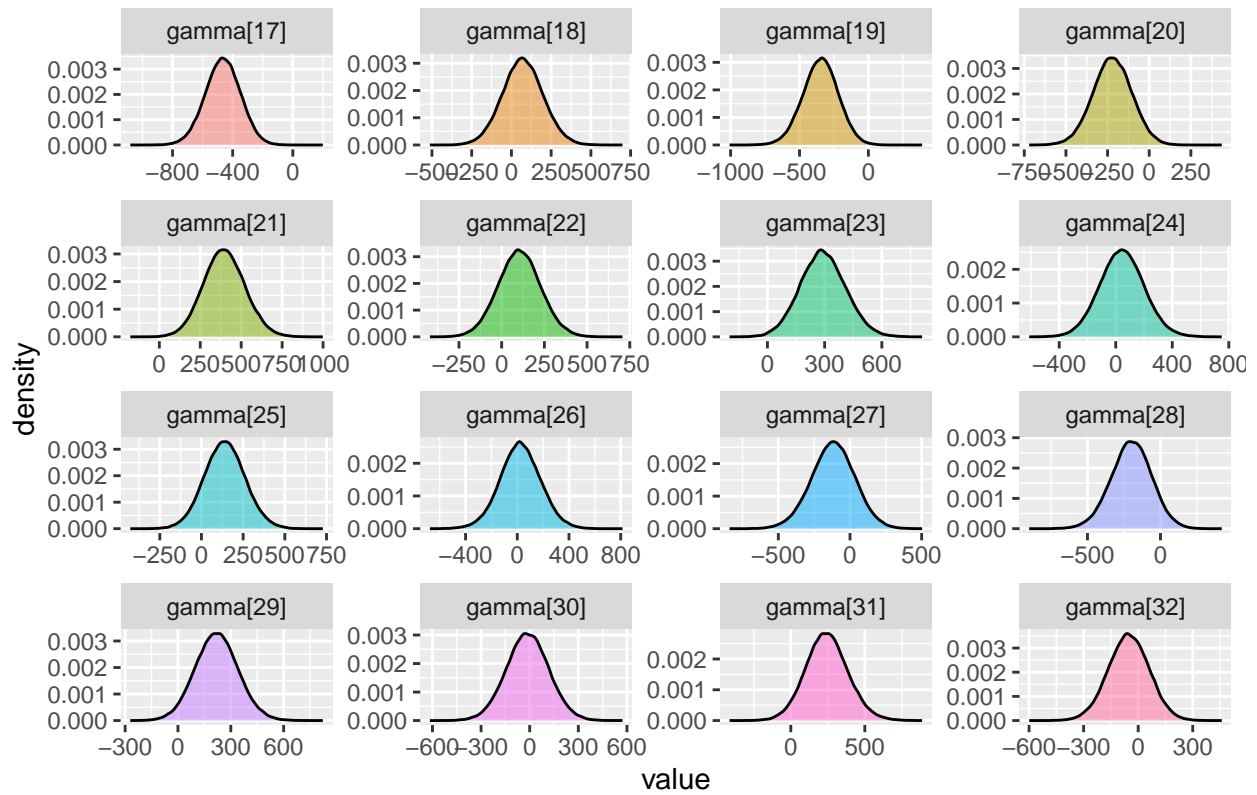

Density Plots of Posterior Betas

No id variables; using all as measure variables

Density Plots of Posterior Betas


```
## No id variables; using all as measure variables
```
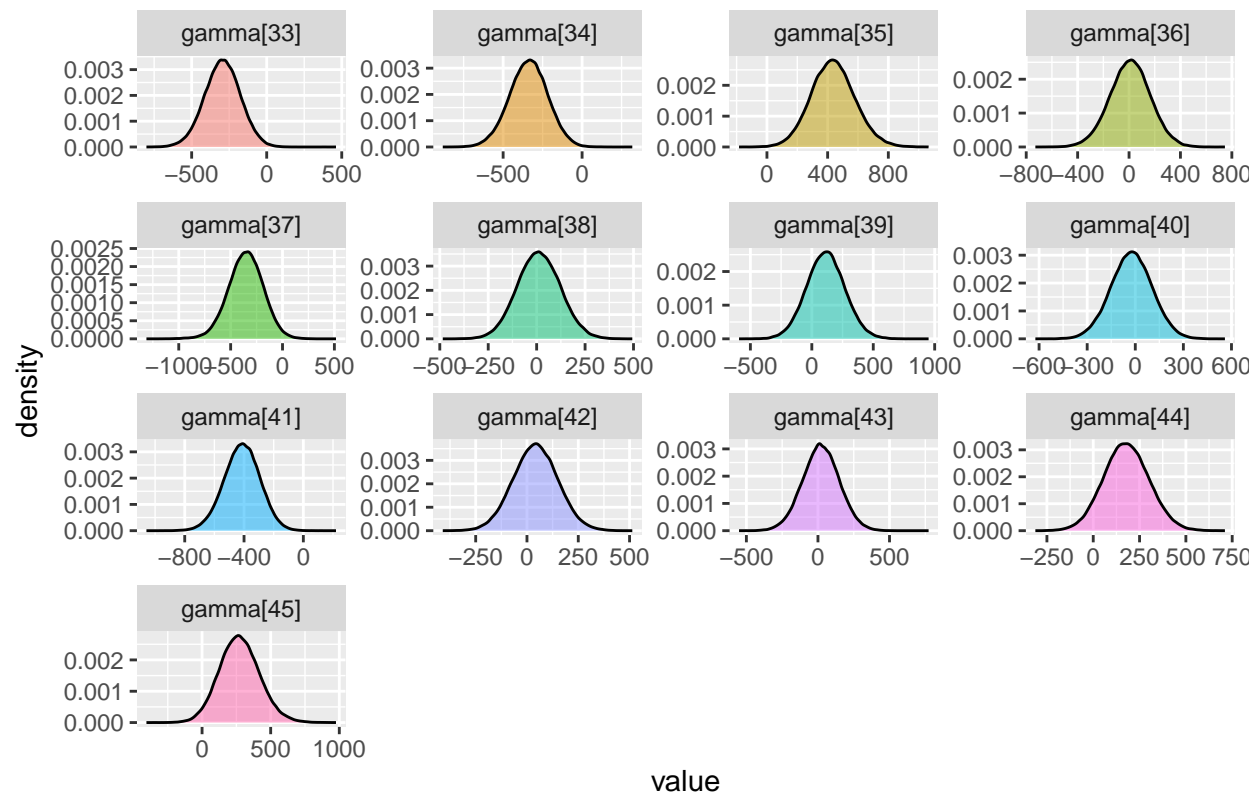
Density Plots of Posterior Betas


```
## No id variables; using all as measure variables
```

Density Plots of Posterior Betas


```
## No id variables; using all as measure variables
```

Density Plots of Posterior Betas