Bayesian Spatio-temporal Small Area Modeling: A Case Study of Estimating Late-Stage Melanoma Incidence in Texas

Simulation Example

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12/10/2024

This is an R Markdown document for the paper **Bayesian Spatio-temporal Small Area Modeling: A Case Study of Estimating Late-Stage Melanoma Incidence in Texas**, where we demonstrate how to fit the proposed Bayesian Heterogeneous Spatio-Temporal Logistic Regression with Nonlinear Demographic Effect (BHSTLR-NDE) using a simulated dataset. The simulated data is based on the geography of 254 counties in Texas, over 10 time points.

Let $t \in [T]$ denote the discrete time of interest, and let $i \in [M]$ represent the geographical units (e.g., counties). For each diagnosed case $j \in [n_{it}]$ within area i at time t, let y_{itj} denote the stage of melanoma. Specifically, $Y_{itj} = 1$ if the case is in late-stage melanoma, and $Y_{itj} = 0$ if the case is in the early stage. At each time t, for each case j in area i let $\mathbf{z}_{it} \in \mathbb{R}^q$ denote the county-level covariates. Additionally, the population is categorized into different strata $\{1, 2, \ldots, H\}$ based on cross-tabulated demographic variables such as sex and race/ethnicity. We use $h_{itj} \in [H]$ and g_{itj} to represent the stratum and the age, respectively, of the case j in area i at time t.

The proposed model takes the following form:

$$y_{itj} \mid p_{itj} \sim \text{Bernoulli}(p_{itj}),$$

$$\theta_{itj} := \text{logit}(p_{itj}) = \mathbf{z}_{it}^\top \boldsymbol{\alpha} + G_{itj} + \delta_i + \epsilon_{it},$$

where ϵ_{it} is a latent spatiotemporal process, δ_i is a latent county-level effect, and G_{itj} represents the effect of an case's age g_{itj}, given the corresponding stratum h_{ij} at time t. Our focus is on estimating the regression coefficients $\boldsymbol{\beta} = (\beta_1, \ldots, \beta_p)^\top$, $\boldsymbol{\alpha} = (\alpha_1, \ldots, \alpha_q)^\top$, as well as the age effect G across different times and strata.

We generate data according to the above model where the spatial domain contains $M = 254$ Texas counties, and $T = 10$ years are considered. Given each county $i \in [M]$ and year $t \in [T]$, $n_{it} = 30$ observations are collected, with the population equally assigned into $H = 3$ strata. Overall, we obtain $76,200$ observations. We generate $q = 20$ county-level covariates independently from a standard normal distribution. The regression coefficients are set to $\alpha_i = 1$ if $i \leq 2$ and $\alpha_i = 0$ otherwise, mimicking a sparse regression scenario. For the basis functions, we select $J = L = 8$.

1. Data generation

```r
library(sp)
library(nimble)
library(splines2)
# Read Texas county data
load('Data/polygons_list_bycounty.RData')  # county_list, polygons_list_bycounty
```

```r
load('Data/Adj_mat.RData')
Adj_mat = as.matrix(Adj_mat) # 254*254
source('Functions/Basis_functions.R')


n_it = 30  # number of samples in each county at each time
T = 10
num_group = 3
M = dim(Adj_mat)[1]
n = n_it*M*T
q = 20
q0 = 2


L = 8
degree = 3
J = 8


# Generete covariates
set.seed(0)
Z = array(rnorm(T*M*q), dim = c(T, M, q))
DATA = expand.grid(stage = rep(1, n_it/num_group), group = seq(num_group), county = seq(M), dxyear = se
DATA$age = runif(n)

county_design = DATA$county
h_design = DATA$group
t_design = DATA$dxyear
H = length(unique(h_design))

# Basis function
internal_nodes = as.vector(quantile(DATA$age,
                           probs = seq(0,1,length.out=J-degree+1)[-c(1,J-degree+1)]))
Phi = Bspline.Basis(DATA$age, r = J, knots = internal_nodes, degree = degree)
MI = array(0, dim = c(T, M, L))
for(t in 1:T){
    MI[t,,] = MoransI.Basis(cbind(matrix(1, M, 1), Z[t,,]), r = L, A = Adj_mat)
}


# Generate coefficients
alpha = c(rep(1,q0),rep(0,q-q0))

xi = array(1, dim = c(H, T, J))
for (h in 1:H) {  xi[h,,] = h  }
B = 0.8*diag(J)
sigmasq_xi = 0.001
for (h in 1:H) { for (t in 2:T){ for(i_J in 1:J){
    xi[h, t, i_J] = rnorm(1,  inprod(B[i_J, 1:J], xi[h, t - 1, 1:J]), sd = sqrt(sigmasq_xi))
}}}

eta = matrix(1, T, L)
A = 0.8*diag(L)
sigmasq_eta = 0.001
for (t in 2:T){for(i_L in 1:L){
    eta[t, i_L] = rnorm(1, inprod(A[i_L, 1:L], eta[t - 1, 1:L]), sd = sqrt(sigmasq_eta) )
```

```r
}}

delta = rep(0, M)

# Generate response
DATA$prob = rep(0, n)
for(i in 1:n){
    DATA$prob[i] = ilogit(inprod(Z[t_design[i],county_design[i],1:q], alpha[1:q]) +
                   inprod(Phi[i,1:J], xi[h_design[i], t_design[i], 1:J]) +
                   inprod(MI[t_design[i],county_design[i],1:L], eta[t_design[i], 1:L]) +
                   delta[county_design[i]])
    DATA$stage[i] = rbinom(1, 1, p = DATA$prob[i])
}
y = DATA$stage

#save(DATA, Z, alpha, Phi, xi, MI, eta, delta, file = 'Data/data.RData')
```

2. Model Fitting

```r
nimbleOptions(MCMCusePredictiveDependenciesInCalculations = TRUE)

code <- nimbleCode({
  for(i in 1:n){
      y[i] ~ dbern(prob[i])
      prob[i] <- ilogit(inprod(Z[t_design[i],county_design[i],1:q], alpha[1:q]) +
                   inprod(Phi[i,1:J], xi[h_design[i], t_design[i], 1:J]) +
                   inprod(MI[t_design[i],county_design[i],1:L], eta[t_design[i], 1:L]) +
                   delta[county_design[i]])
  }


  # Age AR
  for (h in 1:H) {
    for(i_J in 1:J)  xi[h, 1, i_J] ~ dnorm(mu_xi[i_J], var = kappasq_1)
    for (t in 2:T){ for(i_J in 1:J){
        xi[h, t, i_J] ~ dnorm( inprod(B[i_J, 1:J], xi[h, t - 1, 1:J]), var = sigmasq_xi)
    }}
  }
  for(i_J in 1:J) mu_xi[i_J] ~ dnorm(0, var = kappasq_0)
  for(i_J in 1:J){
      B[i_J, i_J] ~ dnorm(1, var = kappasq_B)
      for(ii_J in (seq(from = 1, to = J)[-i_J])){  B[i_J, ii_J] ~ dnorm(0, var = kappasq_B) }
  }
  sigmasq_xi ~ dinvgamma(a_xi, b_xi)


  # Spatial AR
  for (t in 2:T){for(i_L in 1:L){
    eta[t, i_L] ~ dnorm( inprod(A[i_L, 1:L], eta[t - 1, 1:L]), var = sigmasq_eta)
  }}
  for(i_L in 1:L) eta[1, i_L] ~ dnorm(0, var = kappasq_2)
```

```r
    for(i_L in 1:L){
        A[i_L, i_L] ~ dnorm(1, var = kappasq_A)
        for(ii_L in (seq(from = 1, to = L)[-i_L])){  A[i_L, ii_L] ~ dnorm(0, var = kappasq_A) }
    }
    sigmasq_eta ~ dinvgamma(a_eta, b_eta)

    # alpha S-and-S
    for (i_q in 1:q) {
      include[i_q] ~ dbern(0.5)  # Spike-and-slab prior
      alpha_latent[i_q] ~ dnorm(0, var = kappasq_alpha)
      alpha[i_q] <- alpha_latent[i_q] * include[i_q]
    }

    # prior for delta
    for(i in 1:M){
        delta[i] ~ dnorm(mu_delta, var = sigmasq_delta)
    }
    mu_delta ~ dnorm(0, var = 100)
    sigmasq_delta ~ dinvgamma(1, 1)


})

kappasq_alpha = 100
kappasq_0 = 100
kappasq_1 = 100
kappasq_B = 100
a_xi = 1
b_xi = 1
kappasq_2 = 100
kappasq_A = 100
a_eta = 1
b_eta = 1

constants <- list(
    n = n,
    T = T,
    M = M,
    q = q,
    J = J,
    L = L,
    H = H,
    h_design = h_design,
    t_design = t_design,
    county_design = county_design,
    Z = Z,
    Phi = Phi,
    MI = MI,
    kappasq_alpha = kappasq_alpha, # regression coeff
    kappasq_0 = kappasq_0, kappasq_1 = kappasq_1, kappasq_B = kappasq_B, a_xi = a_xi, b_xi = b_xi,
    kappasq_2 = kappasq_2, kappasq_A = kappasq_A, a_eta = a_eta, b_eta = b_eta
)
```

```r
inits <- list(
    alpha_latent = rep(0, q), include = rep(1,q),
    xi = array(0, dim = c(H, T, J)), mu_xi = rep(0, J), sigmasq_xi = 1, B = diag(J),
    eta = matrix(0, T, L), sigmasq_eta = 1,  A = diag(L),
    mu_delta = 0, sigmasq_delta = 1, delta = rep(0, M)
)
data = list(
    y = y
)
model <- nimbleModel(code, constants = constants, data = data, inits = inits)


initInfo <- model$initializeInfo()
uninitializedNodes <- initInfo$uninitializedNodes
warnings <- initInfo$warnings
errors <- initInfo$errors
cat("\nWarnings:\n")
print(warnings)
cat("\nErrors:\n")
print(errors)


# Set up the MCMC configuration
mcmcConf <- configureMCMC(model)
mcmcConf$setMonitors('alpha_latent', 'alpha', 'xi', 'eta',
                     'include', 'delta', 'mu_delta', 'sigmasq_delta')
# Build and compile the MCMC
mcmc <- buildMCMC(mcmcConf)
Cmodel <- compileNimble(model)
Cmcmc <- compileNimble(mcmc, project = model)

n_batches <- 200
batch_size <- 200
n_batches_save = 40
num_thin <- 20
mcmc.out = runMCMC(Cmcmc, niter=batch_size*n_batches,
        nburnin=batch_size*(n_batches - n_batches_save),
        thin=num_thin, nchains=1, setSeed = TRUE, progressBar = TRUE)
# ===== Samplers =====
# RW sampler (594)
#   - eta[]   (80 elements)
#   - alpha_latent[]   (20 elements)
#   - xi[]   (240 elements)
#   - delta[]   (254 elements)
# conjugate sampler (140)
#   - mu_xi[]   (8 elements)
#   - B[]   (64 elements)
#   - sigmasq_xi
#   - A[]   (64 elements)
#   - sigmasq_eta
#   - mu_delta
#   - sigmasq_delta
# binary sampler (20)
```

```r
#   - include[]   (20 elements)
# thin = 1: alpha, alpha_latent, delta, eta, include, mu_delta, sigmasq_delta, xi

samples_save = as.matrix(mcmc.out)
# Calculate WAIC
waic_results = calculateWAIC(Cmcmc)
save(samples_save, waic_results, file = 'Data/MCMCsamples.RData')



## Prediction
## ----------##  ----------##  ----------##  ----------##  ----------##  ----------
load(file = 'Data/MCMCsamples.RData')
num_save = batch_size * n_batches_save / num_thin
age_range = c(10,100)

# Designs for prediction
age_grid = seq(from = 20, to = 90, by = 5)
age_grid = (age_grid - age_range[1]) / (diff(age_range))
num_G = length(age_grid)
phi_grid = Bspline.Basis(age_grid, r = J, knots = internal_nodes, degree = degree)

# Posterior prediction
posterior_params = as.data.frame(samples_save)

# Extracting alpha vector
alpha <- as.matrix(posterior_params[,grep("^alpha", colnames(posterior_params))])

# Extracting 3-d array xi
xi <- array(0, dim = c(num_save, H, T, J))
for(h in 1:H) {
  for(t in 1:T) {
    for(j in 1:J) {
      xi[, h, t, j] <- as.matrix(posterior_params[,paste0("xi[", h,", ", t, ", ", j, "]")])
    }
  }
}

# Extracting matrix eta
eta <- array(0, dim = c(num_save, T, L))
for(t in 1:T) {
  for(l in 1:L) {
    eta[, t, l] <- as.matrix(posterior_params[,paste0("eta[", t, ", ", l, "]")])
  }
}

# Extracting delta
delta <- as.matrix(posterior_params[,grep("^delta", colnames(posterior_params))])

# county-level prediction
prob_summary_M_H_T_Age_MCMC = array(0, dim = c(num_save, M,H,T,num_G))
prob_summary_M_H_T_Age = array(0, dim = c(M,H,T,num_G))
prob_summary_M_H_T_Age_upper = array(0, dim = c(M,H,T,num_G))
prob_summary_M_H_T_Age_lower = array(0, dim = c(M,H,T,num_G))
```

```r
# Make prediction
for(i in 1:M){
    temp_i = delta[, i, drop = FALSE]
    for (t in 1:T){
        temp_it =  temp_i + alpha[, 1:q]%*% as.vector(Z[t,i,1:q]) +
                              eta[, t, 1:L]%*%as.vector(MI[t,i,1:L])
        for(h in 1:H){for(i_age in 1:num_G){
            prob_summary_M_H_T_Age_MCMC[,i,h,t,i_age] =
                        as.vector(temp_it + xi[, h, t, 1:J]%*% as.vector(phi_grid[i_age, 1:J]))
        }}
    }
}
prob_summary_M_H_T_Age_MCMC = ilogit( prob_summary_M_H_T_Age_MCMC )
prob_summary_M_H_T_Age <- apply(prob_summary_M_H_T_Age_MCMC, c(2, 3, 4, 5), mean)
prob_summary_M_H_T_Age_upper <- apply(prob_summary_M_H_T_Age_MCMC,
                                        c(2, 3, 4, 5), quantile, probs = c(0.95))
prob_summary_M_H_T_Age_lower <- apply(prob_summary_M_H_T_Age_MCMC,
                                        c(2, 3, 4, 5), quantile, probs = c(0.05))
prob_summary_M_H_T_Age_average_mcmc <- apply(prob_summary_M_H_T_Age_MCMC, 1, mean)

# Make prediction to all cases
Phi_Data = Bspline.Basis(DATA$age, r = J, knots = internal_nodes, degree = degree)
prob_summary_individuals_MCMC = matrix(0, num_save, n)
prob_summary_individuals = rep(0, n)
prob_summary_individuals_upper = rep(0, n)
prob_summary_individuals_lower = rep(0, n)
for(i_individual in 1:n){
    i = county_design[i_individual]
    t = t_design[i_individual]
    h = h_design[i_individual]
    prob_summary_individuals_MCMC[,i_individual] = delta[, i, drop = FALSE] +
                    alpha[, 1:q]%*% as.vector(Z[t,i,1:q]) + eta[, t, 1:L]%*%as.vector(MI[t,i,1:L])
                    as.vector(xi[, h, t, 1:J]%*% as.vector(Phi_Data[i_individual, 1:J]))
}

prob_summary_individuals_MCMC = ilogit( prob_summary_individuals_MCMC )
prob_summary_individuals <- apply(prob_summary_individuals_MCMC, 2, mean)
prob_summary_individuals_upper <- apply(prob_summary_individuals_MCMC, 2, quantile, probs = c(0.95))
prob_summary_individuals_lower <- apply(prob_summary_individuals_MCMC, 2, quantile, probs = c(0.05))
prob_summary_individuals_average_mcmc = apply(prob_summary_individuals_MCMC, 1, mean)

save(prob_summary_M_H_T_Age, prob_summary_M_H_T_Age_upper,
    prob_summary_M_H_T_Age_lower, prob_summary_M_H_T_Age_average_mcmc,
    prob_summary_individuals, prob_summary_individuals_upper,
    prob_summary_individuals_lower, prob_summary_individuals_average_mcmc,
    file = 'Data/Posterior_summary_ALL.RData')
```

Estimated Late-Stage Probability

To investigate the estimation performance of the proposed model, we calculate the true average late-stage probabilities averaged over each cross-classification of county, year, and stratum, and compare them with their corresponding predictive values based on posterior mean estimates. The simulation results show that

the predictions match the true values very well, indicating that BHSTLR-NDE can accurately estimate the unobserved true late-stage probabilities.

```r
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----------------------------------------------------
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.1     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.1
## v purrr     1.0.2
## -- Conflicts ----------------------------------------------------------------------------
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become error
```

```r
load(file = 'Data/data.RData')
load(file = 'Data/Posterior_summary_ALL.RData')
DATA_temp = DATA
DATA_temp$stage_pred = prob_summary_individuals
DATA_summary = DATA_temp %>% group_by(county, dxyear, group) %>%
          summarize(prob_truth = mean(prob, na.rm = TRUE), prob_pred= mean(stage_pred, na.rm = TRUE))
```

```
## 'summarise()' has grouped output by 'county', 'dxyear'. You can override using
## the '.groups' argument.
```

```r
ggplot(DATA_summary, aes(x = prob_truth, y = prob_pred)) +
  geom_point(size = 2, color = 'orange') +
  geom_abline(intercept = 0, slope = 1, color = "blue", linetype = "dashed") +
  labs(x = "True Late-stage Probability", y = "Predicted Late-stage Probability") +
  xlim(0, 1) + ylim(0, 1) +
  theme_minimal() +
  theme(axis.title = element_text(size = 15), axis.text = element_text(size = 20),
        legend.position = NULL
        )
```
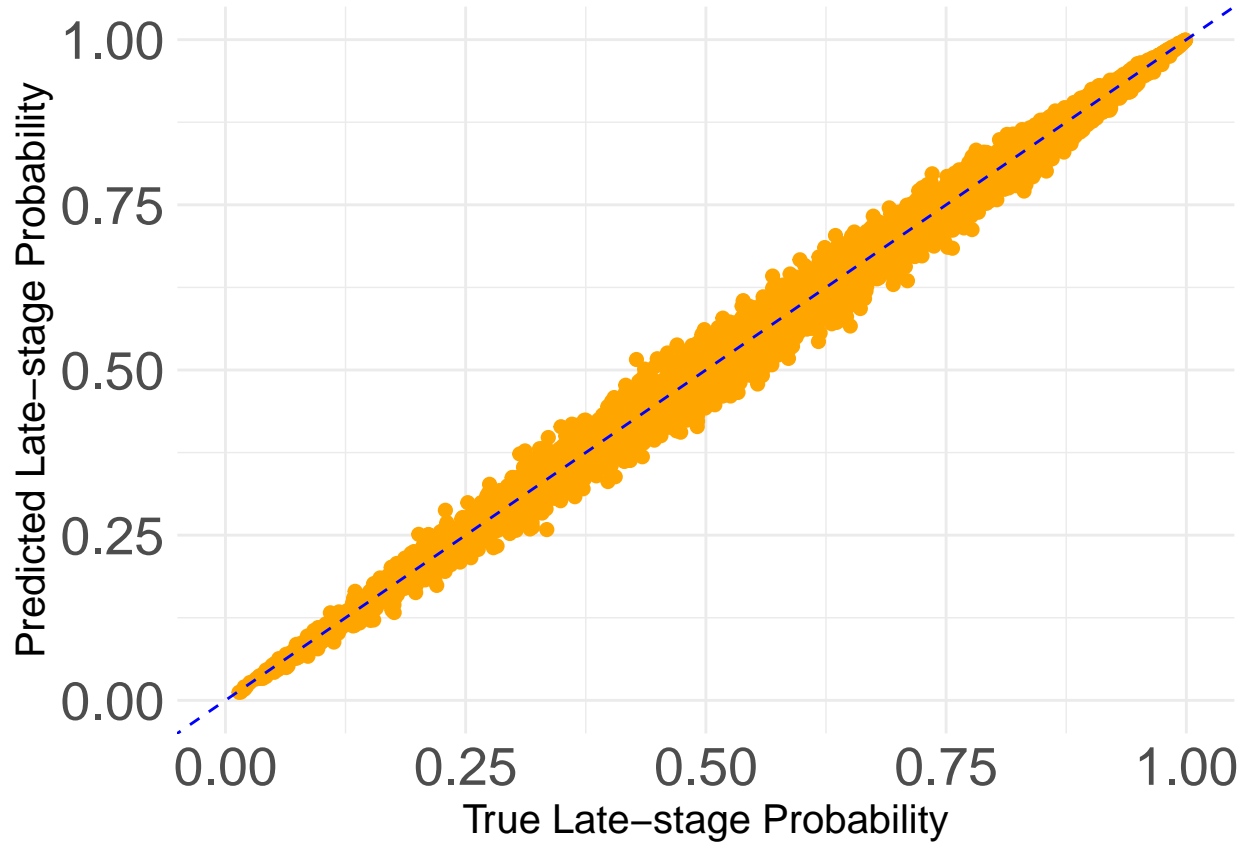
```
ggsave(file = 'Data/Prob_Overall_compare.pdf', width = 8, height = 6)
```

Finally, we present the trace plots for the estimates of the regression coefficients $(\alpha_1, \alpha_2, \alpha_3, \alpha_4)$, as well as the initial basis coefficient vector values $(\xi_{11}(1), \xi_{21}(1), \xi_{31}(1))$. The respective true values are represented by orange horizontal lines. The trace plots indicate that BHSTLR-NDE accurately estimates both the county-level regression coefficients and the basis coefficient vector values, and successfully identifies non-zero county-level regression coefficients.

```
load(file = 'Data/MCMCsamples.RData')
posterior_params = as.data.frame(samples_save)

mcmc_samples = as.matrix(posterior_params[,c( paste("alpha", "[", c(1,2,3,4), "]", sep = "") , paste("x:
df = data.frame(iter = seq(dim(mcmc_samples)[1]), value = as.vector(as.matrix(mcmc_samples)),
                variable = rep( c('alpha[1]','alpha[2]','alpha[3]','alpha[4]',"xi[\"11\"](1)", "xi[\"21'
                    each = dim(mcmc_samples)[1]),
                truth = rep( c(1,1,0,0,1,2,3), each = dim(mcmc_samples)[1]) )


figure = ggplot(df) + geom_path(aes(x = iter, y = value), color = 'red') +
        facet_grid(variable ~ ., scales = 'free_y', labeller = label_parsed) +
        labs(x = 'Sampling Iteration', y =  "Posterior Samples")+
        geom_hline(aes(yintercept = truth), color = 'orange') +
        theme(legend.key.size = unit(1, 'cm'),
            legend.title = element_text(size=20),legend.text = element_text(size=15)) +
        theme(axis.text=element_text(size=20),axis.title=element_text(size=25)) +
```

```
            theme(strip.text=element_text(size=20)) +
            theme(panel.spacing = unit(1, 'lines'))
ggsave(figure, filename = 'Data/Traceplot.pdf', width = 10, height = 20)
```
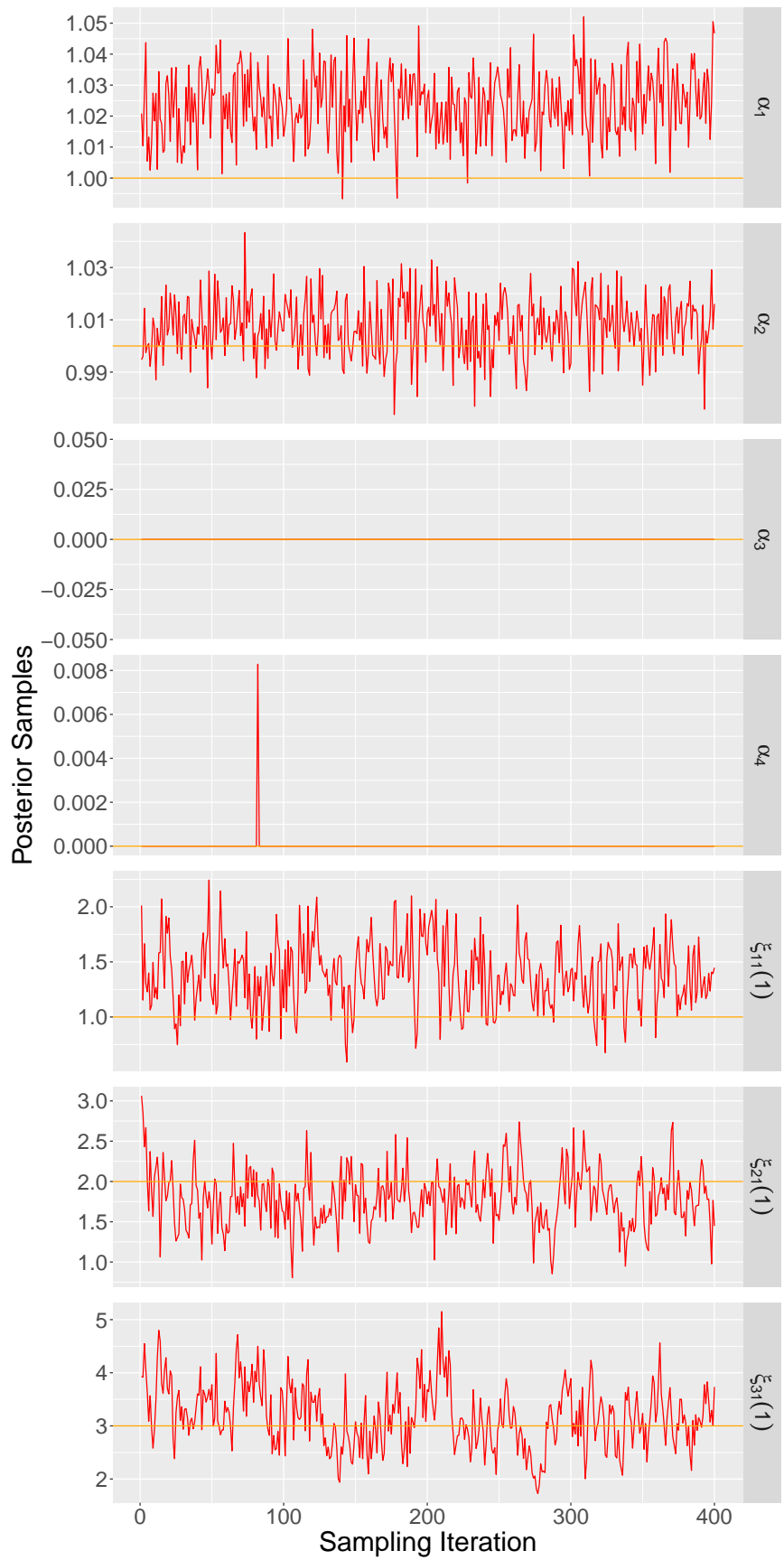
Model Comparison

At last, we implement "Area Linear", which is the Bayesian Binomial linear regression model using county-level covariates as predictors, and "BHSTLR Linear", where the demographic effect G_{itj} of BHSTLR-NDE is modeled through a linear model based on the case's age and stratum.

```
source('Functions/BMSTLMLinear.R')
save(samples_save, waic_results, file ='Data/BMSTLMLinear_MCMCsamples.RData')
save(prob_summary_M_H_T_Age, prob_summary_M_H_T_Age_upper,
     prob_summary_M_H_T_Age_lower, prob_summary_M_H_T_Age_average_mcmc,
     prob_summary_individuals, prob_summary_individuals_upper,
     prob_summary_individuals_lower, prob_summary_individuals_average_mcmc,
     file = 'Data/BMSTLMLinear_Posterior_summary_ALL.RData')

source('Functions/GLMM.R')
save(fit_bayes, log_lik, waic_result, file  = 'Data/GLMM_MCMCsamples.RData')
```

We compare these models using the Watanabe-Akaike Information Criterion (WAIC). The results indicate that BHSTLR-NDE achieves the best performance with the lowest WAIC of 74715.38, while the competitive models "Area Linear" and "BHSTLR Linear" achieve WAIC values of 79238.85 and 77940.32, respectively.

```
load(file ='Data/MCMCsamples.RData')
WAIC_BMSTLM = waic_results$WAIC
load(file ='Data/BMSTLMLinear_MCMCsamples.RData')
WAIC_BMSTLM_linear = waic_results$WAIC
load(file ='Data/GLMM_MCMCsamples.RData')
WAIC_GLMM = waic_result$estimates['waic','Estimate']
cat(sprintf('The WAIC values of Area Linear, BHSTLR Linear, and BHSTLR-NDE are \n
        %.2f, %.2f, %.2f, respectively', WAIC_GLMM, WAIC_BMSTLM_linear, WAIC_BMSTLM ))
```

```
## The WAIC values of Area Linear, BHSTLR Linear, and BHSTLR-NDE are
##
##          79238.85, 77940.32, 74715.38, respectively
```