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

Simulation Example

Jiahao Cao

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 Mixed-effect Spatial-temporal Logistic Regression Model (BMSTLM) 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 individual $j \in [n_{it}]$ within area i at time t, let y_{itj} denote the stage of melanoma. Specifically, $Y_{itj} = 1$ if the individual is in late-stage melanoma, and $Y_{itj} = 0$ if the individual is in the early stage. At each time t, for each individual j in area i, let $\mathbf{x}_{itj} \in \mathbb{R}^{p+1}$ denote the corresponding unit-level covariates, and let $\mathbf{z}_{it} \in \mathbb{R}^q$ denote the area-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 individual j in area i at time t.

The proposed model takes the following form:

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

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

where ϵ_{it} is a latent spatiotemporal process, δ_i is a latent area-level effect, and G_{itj} represents the effect of an individual'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
```

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

```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*num_group
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) )
}}

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

```
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)
  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
)
```

```
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 individuals
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 BMSTLM can accurately estimate the unobserved true late-stage probabilities.

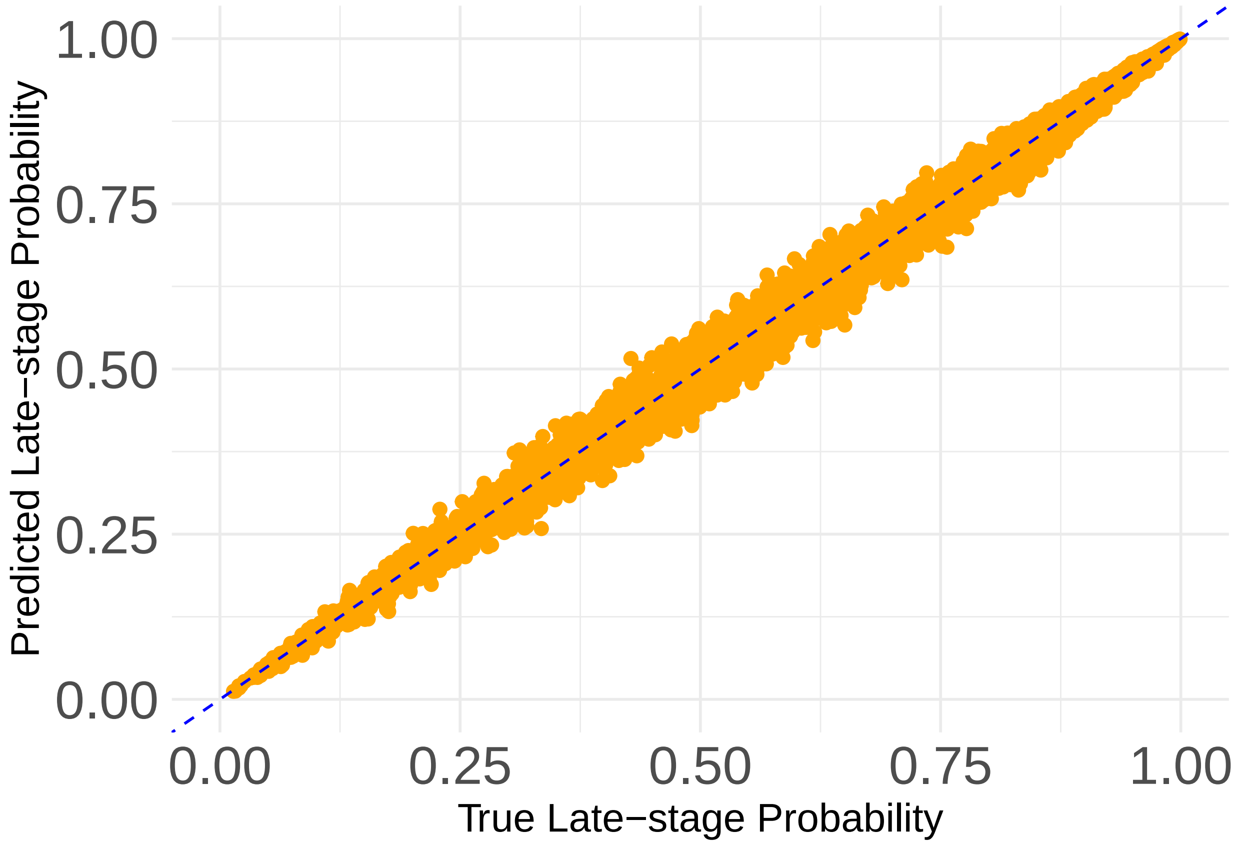
```r
library(tidyverse)
```

```
## -- 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 $(\xi_{1(1)}(1), \xi_{2(1)}(1), \xi_{3(1)}(1))$. The respective true values are represented by orange horizontal lines. The trace plots indicate that BMSTLM accurately estimates both the county-level regression coefficients and the basis coefficient vector values, and successfully identifies non-zero county-level regression coefficients.

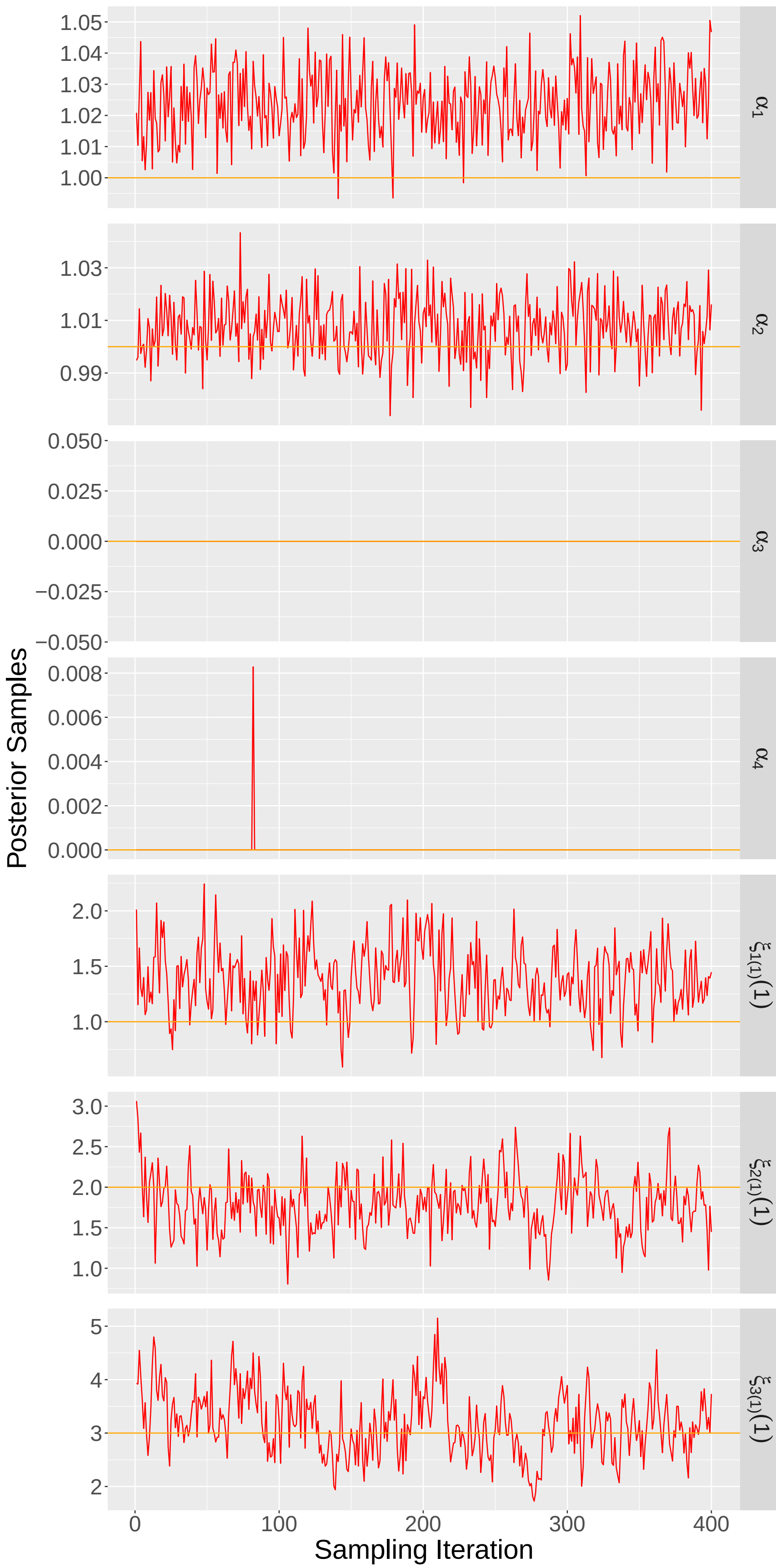
```
load(file = 'Data/MCMCsamples.RData')
posterior_params = as.data.frame(samples_save)

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[\"1(1)\"](1)", "xi[\"
                    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)) +
```

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

knitr::include_graphics('Data/Traceplot.pdf')
```


Posterior Samples
Sampling Iteration
α_1
α_2
α_3
α_4
$\xi_{1(1)}(1)$
$\xi_{2(1)}(1)$
$\xi_{3(1)}(1)$
0
100
200
300
400