Probit regression for ordinal data (Asymmetric): MAR

Setting:

- For each observations, we have 3 associated variables

X1: Nomial variable with 3 possible outcomes {1,2,3} which we will generate from $Mult(1, [0.2, 0.3, 0.5])$ X2: Nomial variable with 3 possible outcomes {1,2,3} which we will generate from $Mult(1, [0.3, 0.5, 0.2])$ Y: Ordinal variable with 5 levels, {1,2,3,4,5} generated using the following process

The proportion of members in each ordered category will be asymmetric. Specifically, the percent of each group will be 10%, 20%, 40%, 15%, and 15% respectively.

$\epsilon_i \sim N(0, 1)$ $z_i = \beta^T X_i + \epsilon$ where $X = [X1 == 2, X1 == 3, X2 == 2, X2 == 3]$ i.e. we drop category (1,1) as the baseline $g(z_i) = Y_i$.

Here $\beta = [-3, 2, 2, -4]$ and function g will be the binning function which will bin data into 5 different bins corresponding to 5 possible ordinal outcome.

- There will be data missing at random (MAR) in Y. The probability of missingness is govern by $logit(w^T x_i - 0.75)$ where $w = [0.4, -0.3, -0.8, 0.3]$. This results in 25% of missing data in the last feature.
- We will try to model Y conditioned on other variables (X1, and X2) using probit regression with latent variable Z with rank likelihood on parameter Z.
- We have two unknown parameters β and z_i which will be sampled from the full conditional posterior distribution using blocked gibbs sampling.

Summary on modelling process

$\epsilon_i \sim N(0, 1)$ $z_i = \beta^T X_i + \epsilon$ $z_i \in R(Y)$ where R(Y) = {z_i: $z_i > z_j$ if $Y_i > Y_j$ and $z_i < z_j$ if $Y_i < Y_j$}

```r
# Data generating process
set.seed(0)
n = 600
beta = c(-3, 2, 2, -4)

# noise term
epsilon = rnorm(n, mean = 0, sd = 1)

# X1
X1 = t(rmultinom(n, size = 1, prob = c(0.2, 0.3, 0.5)))

# X2
X2 = t(rmultinom(n, size = 1, prob = c(0.3, 0.5, 0.2)))

# X
X = cbind(X1[,2:3], X2[,2:3])
colnames(X) <- c('X1_cat2', 'X1_cat3', 'X2_cat2', 'X2_cat3')

# Z
Z = X%*%beta + epsilon

# Cut-off points and Y
g = quantile(Z, probs = c(0.1, 0.3, 0.7, 0.85))
Y = rep(NA, n)
```

```
Y[Z<g[1]] = 1
Y[Z>=g[1] & Z<g[2]] = 2
Y[Z>=g[2] & Z<g[3]] = 3
Y[Z>=g[3] & Z<g[4]] = 4
Y[Z>=g[4]] = 5
Z_original = Z
Y_original = Y
```

Generate missingness in data

```
# Define parameter of logistic function
w= c(0.4, -0.3, -0.8, 0.3)

# Calculate probability of missingness of features 3
prob = apply(t(w*t(X)), MARGIN = 1, FUN = sum)-0.75
prob = 1/(exp(-prob)+1)

# Indicator for X3miss
indicator = rbernoulli(n = n, p = prob)
Y[indicator] = NA
Z[indicator] = NA
```

Prior specifications:

$\beta \sim multiN(0, n(X^T X)^{-1})$

Blocked Gibbs Sampling here consists of two major steps

1. Sample new β from its full conditional

$\beta \mid z, X, Y, z \in R(Y) \sim multiN(\frac{n}{n+1}(X^T X)^{-1} X^T z, \frac{n}{n+1}(X^T X)^{-1})$

2. for each i, using inverse cdf method, sample new z_i from its full conditional which is a truncated normal distribution:

$z_i \mid \beta, X, Y, z_i \in R(Y) \sim N(\beta^T x_i, 1) * I\{z_i \in (a, b)\}$

where a = max(z_j for $Y_j < Y_i$) b = min(z_j for $Y_j > Y_i$)

For observations where the target is missing, we need not condition on $z_i \in R(Y)$ and the resulting full conditional distribution becomes unconstrained normal distribution.

Note that in the gibbs sampling process, we force the first threshold (g1) to be at the true value in the data generating process otherwise the parameters will be unidentifiable (we can definitely fine infinite combinations of weights parameter to order the outcome according to their target Y: scaling, shifting, etc.)

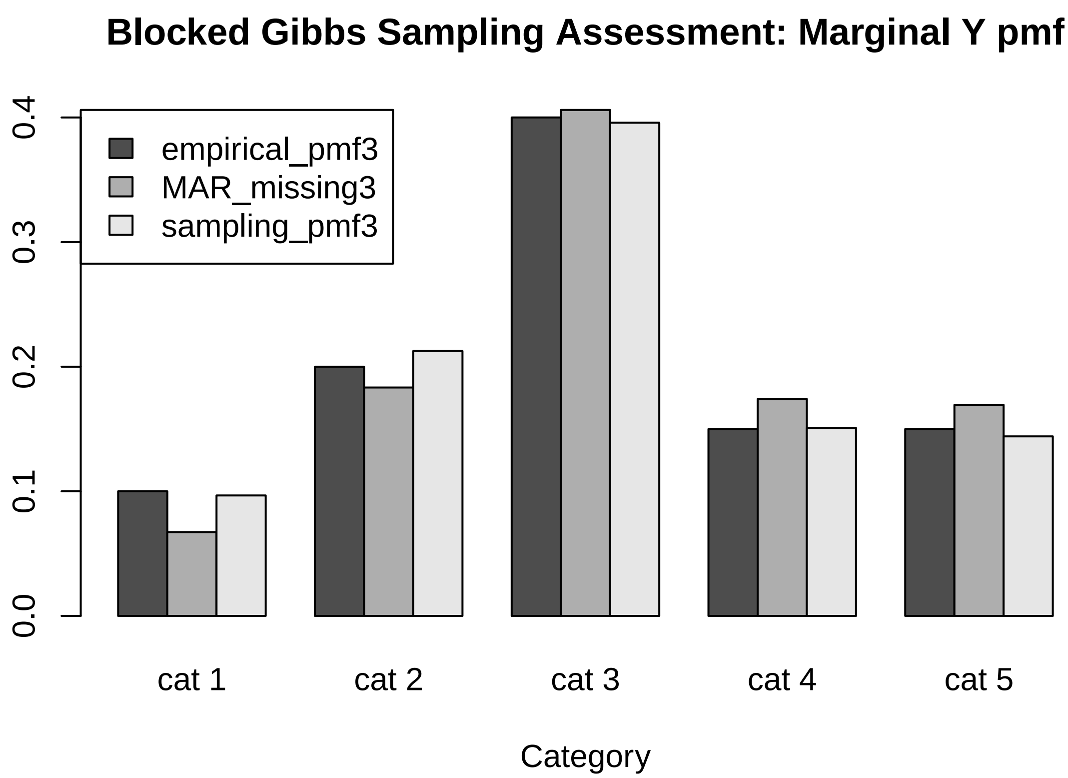
```
# Blocked Gibbs Sampling
set.seed(2)

# Prior Parameter
g1 = g[1] #Fix g1 the first cutoff

# Imputation for first trial
df <- data.frame(cbind(apply(t(t(X1)*c(1,2,3)),1,sum),
                       apply(t(t(X2)*c(1,2,3)),1,sum), Y))
colnames(df) <- c('X1', 'X2', 'Y')
df$Y <- as.factor(df$Y)
df$X1 <- as.factor(df$X1)
df$X2 <- as.factor(df$X2)
mod <- multinom(Y~., data=df[!is.na(df$Y),])
```

```
## # weights:  30 (20 variable)
## initial  value 693.667740
## iter  10 value 388.320469
## iter  20 value 306.713265
## iter  30 value 303.025802
## iter  40 value 302.895636
## final  value 302.895211
## converged
```

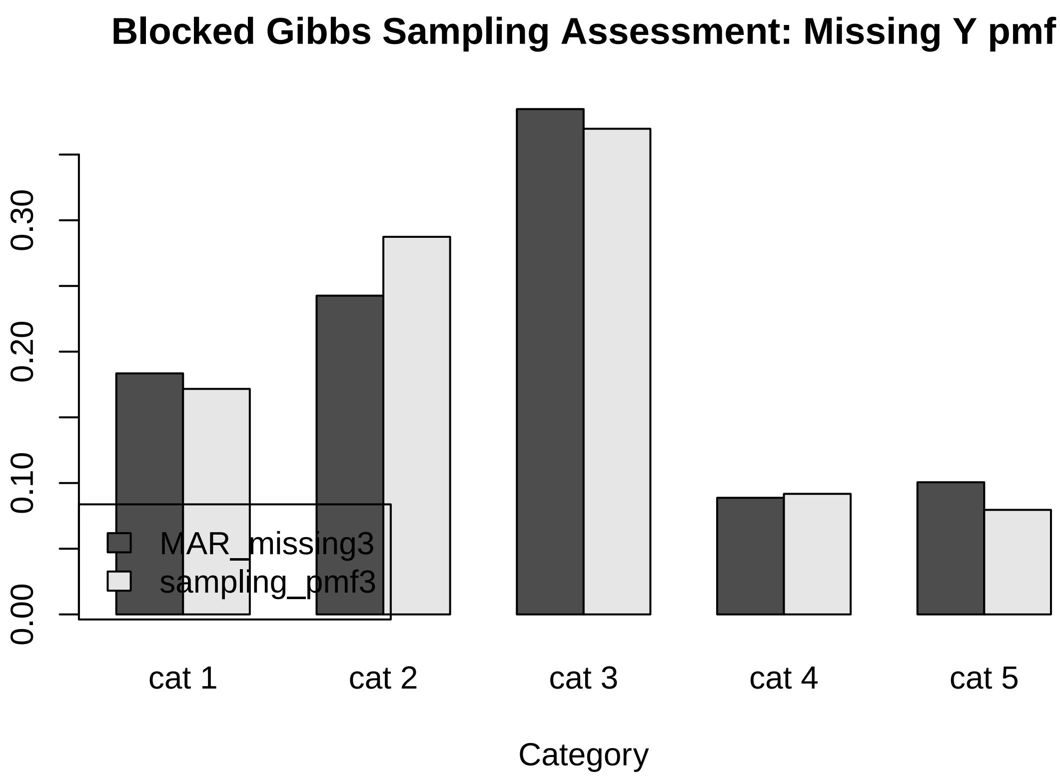
```
Y_i = Y
Y_i[indicator] = predict(mod, newdata = df[is.na(df$Y),], 'class')
#Y_i[indicator] = 3
Z_i = g1 + Y_i - 1.5
variance_beta = (n/(n+1))*solve(t(X)%*%X)
mean_beta_hat = (n/(n+1))*solve(t(X)%*%X)%*%t(X)

# Initialize the sampling matrix
S = 30000
SAMPLED_Z = matrix(nrow=S,ncol=n)
SAMPLED_Y = matrix(nrow = S, ncol = n)
BETA = matrix(nrow=S,ncol=4)

for (round in 1:S) {
  # Step 1: Sample Beta
  mean_beta = mean_beta_hat%*%Z_i
  beta_sampled = dae::rmvnorm(mean = mean_beta,
                              V = variance_beta, method = 'choleski')
  BETA[round,] <- beta_sampled

  # Step 2: Sample Z using inverse cdf appraoch
  for (i in 1:n) {
    # Get the lower and upper bound (a, b) of truncated normal
    a = max(-Inf, Z_i[Y_i<Y[i]], na.rm = TRUE)
    b = min(Z_i[Y_i>Y[i]], Inf, na.rm = TRUE)

    # Force the lowest cutoff to be at g1
    if(indicator[i] == FALSE){
      if (Y_i[i] == 1) {
        b = g1
      }else if (Y_i[i] == 2) {
        a = g1
      }
    }
    # Sample using inverse cdf
    ez = t(beta_sampled)%*%X[i,]
    u = runif(1, pnorm(a - ez), pnorm(b-ez))
    Z_i[i] = ez + qnorm(u)
    if (indicator[i]==TRUE) {
      # Impute Y for missing values
      Y_i[i] = -1
      if (Z_i[i] < g1) {
        Y_i[i] = 1
      }else if (Z_i[i] < min(Z_i[Y_i==3],na.rm = TRUE)) {
```

```
        Y_i[i] = 2
      }else if (Z_i[i] < min(Z_i[Y_i==4],na.rm = TRUE)){
        Y_i[i] = 3
      }else if (Z_i[i] < min(Z_i[Y_i==5],na.rm = TRUE)){
        Y_i[i] = 4
      }else{
        Y_i[i] = 5
      }
    }
  }
  SAMPLED_Z[round,] <-  Z_i
  SAMPLED_Y[round,] <-  Y_i
}
```

```
burnin = 5000
thining = 100
# Imputation accuracy
empirical_pmf3 = table(Y_original)/n
MAR_missing3 = table(Y[!indicator])/(n-sum(indicator))
sampling_pmf3 = table(SAMPLED_Y[seq(burnin, dim(BETA)[1], thining),])/
  sum(table(SAMPLED_Y[seq(burnin, dim(BETA)[1], thining),]))

df3 = rbind(empirical_pmf3, MAR_missing3, sampling_pmf3)
colnames(df3)<- c('cat 1', 'cat 2', 'cat 3', 'cat 4', 'cat 5')
barplot(df3, xlab = 'Category', beside = TRUE,
        legend = TRUE, args.legend=list(x='topleft'),
        main = 'Blocked Gibbs Sampling Assessment: Marginal Y pmf')
```



```r
# Imputation accuracy
MAR_missing3 = table(Y_original[indicator])/sum(indicator)
sampling_pmf3 = table(SAMPLED_Y[seq(burnin, dim(BETA)[1], thining),indicator])/
  sum(table(SAMPLED_Y[seq(burnin, dim(BETA)[1], thining), indicator]))

df3 = rbind(MAR_missing3, sampling_pmf3)
colnames(df3)<- c('cat 1', 'cat 2', 'cat 3', 'cat 4', 'cat 5')
barplot(df3, xlab = 'Category', beside = TRUE,
        legend = TRUE, args.legend=list(x='bottomleft'),
        main = 'Blocked Gibbs Sampling Assessment: Missing Y pmf')
```

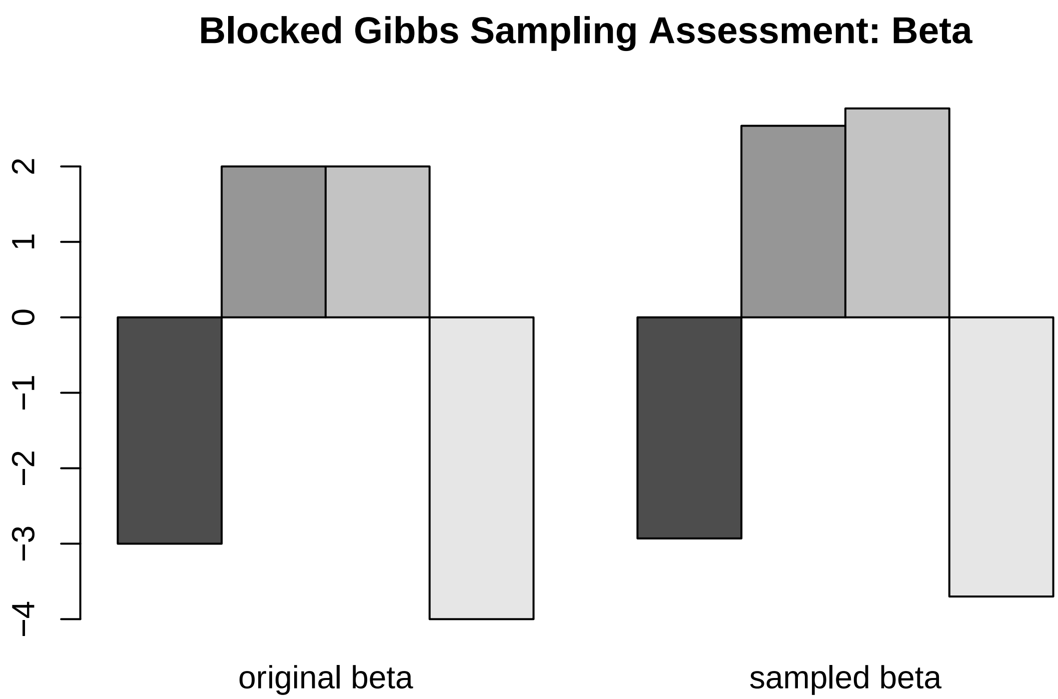



```r
# Imputation accuracy
true_label = Y_original[indicator]
sampled_label = SAMPLED_Y[seq(burnin, dim(BETA)[1], thining),indicator]
mean(t(sampled_label) == true_label)
```

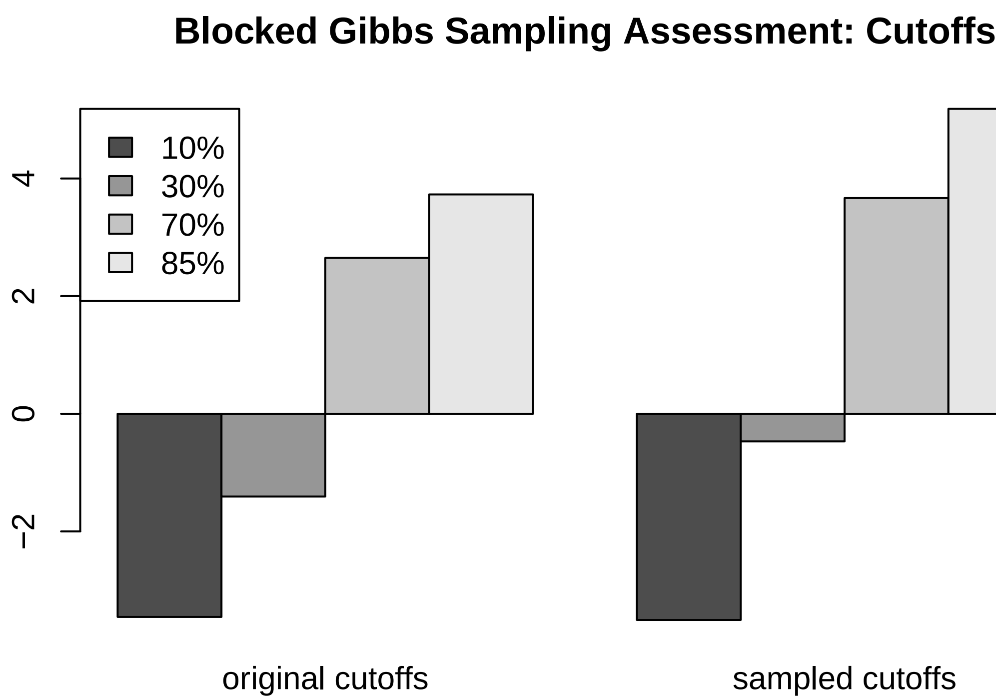
```
## [1] 0.5908909
```

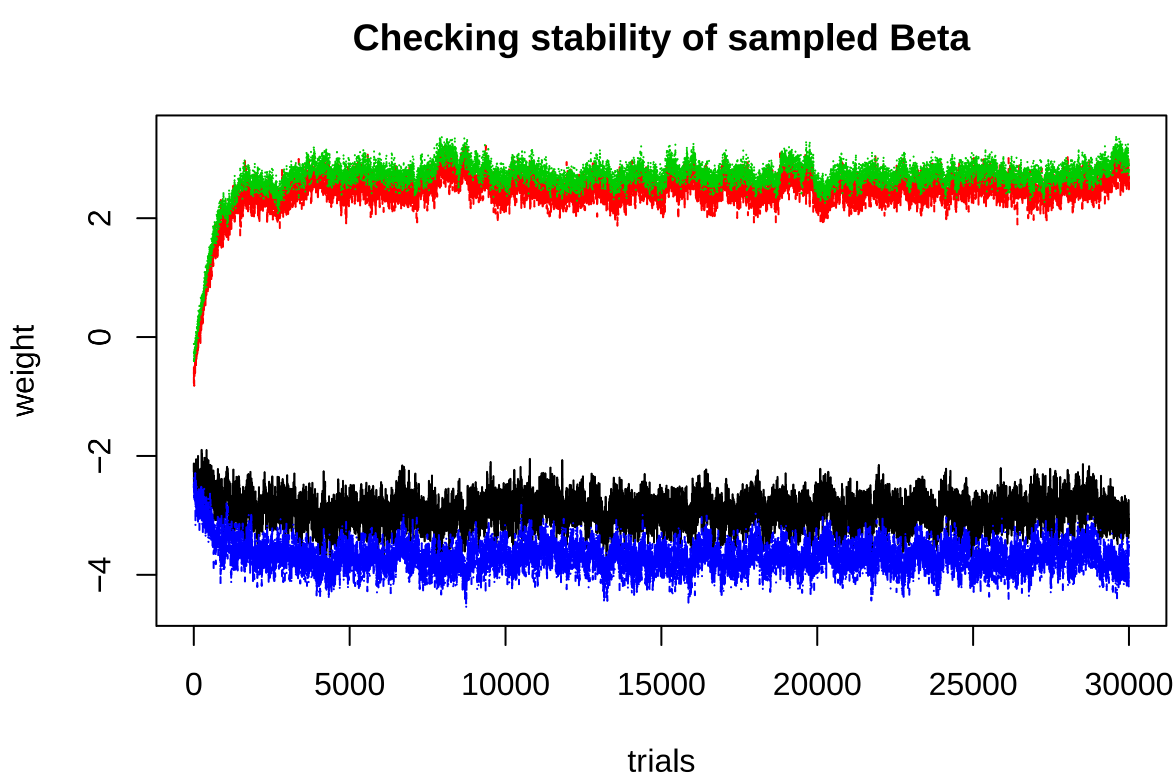
```r
# Check posterior expectation of beta
sampling_beta = apply(BETA[seq(burnin, dim(BETA)[1], thining),], MARGIN = 2, mean)
df_beta= cbind(beta, sampling_beta)
colnames(df_beta)<- c('original beta', 'sampled beta')
barplot(df_beta, beside = TRUE,
        legend = TRUE, main = 'Blocked Gibbs Sampling Assessment: Beta')
```

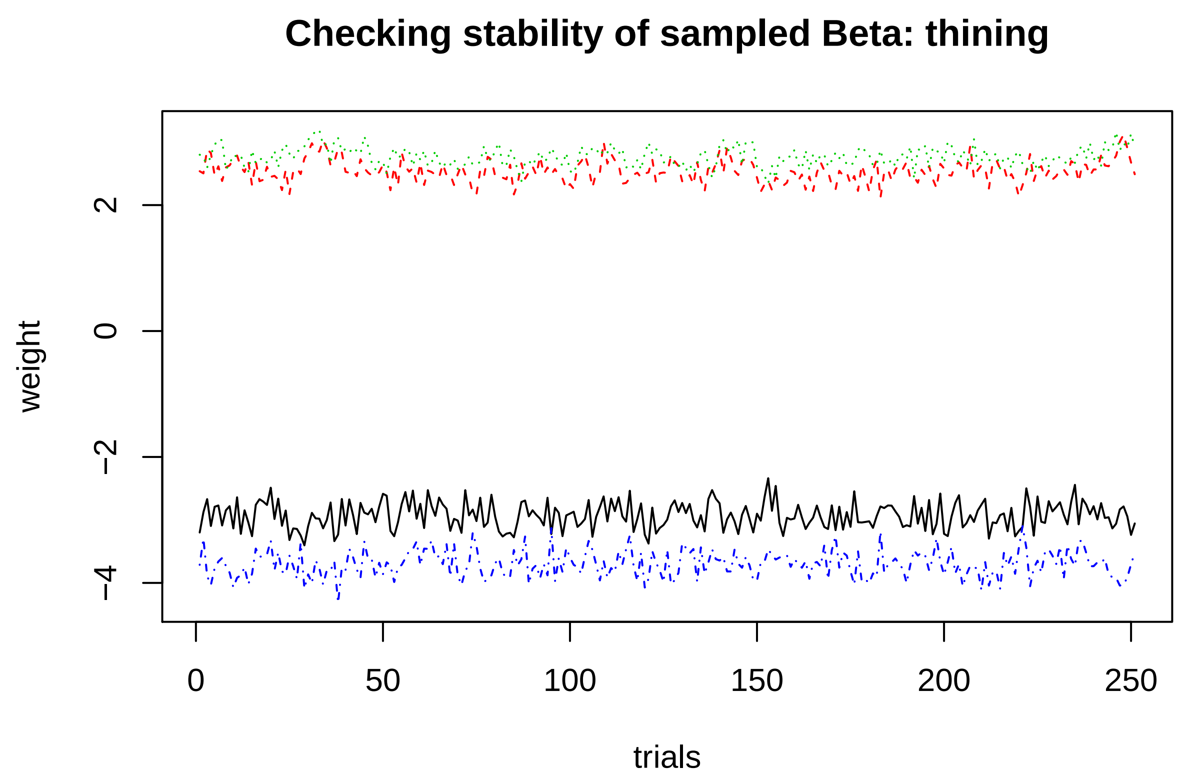
```r
# Check cut off points
g1 = apply(SAMPLED_Z[, Y == 1], MARGIN = 1, max, na.rm = TRUE)
g2 = apply(SAMPLED_Z[, Y == 2], MARGIN = 1, max, na.rm = TRUE)
g3 = apply(SAMPLED_Z[, Y == 3], MARGIN = 1, max, na.rm = TRUE)
g4 = apply(SAMPLED_Z[, Y == 4], MARGIN = 1, max, na.rm = TRUE)
```

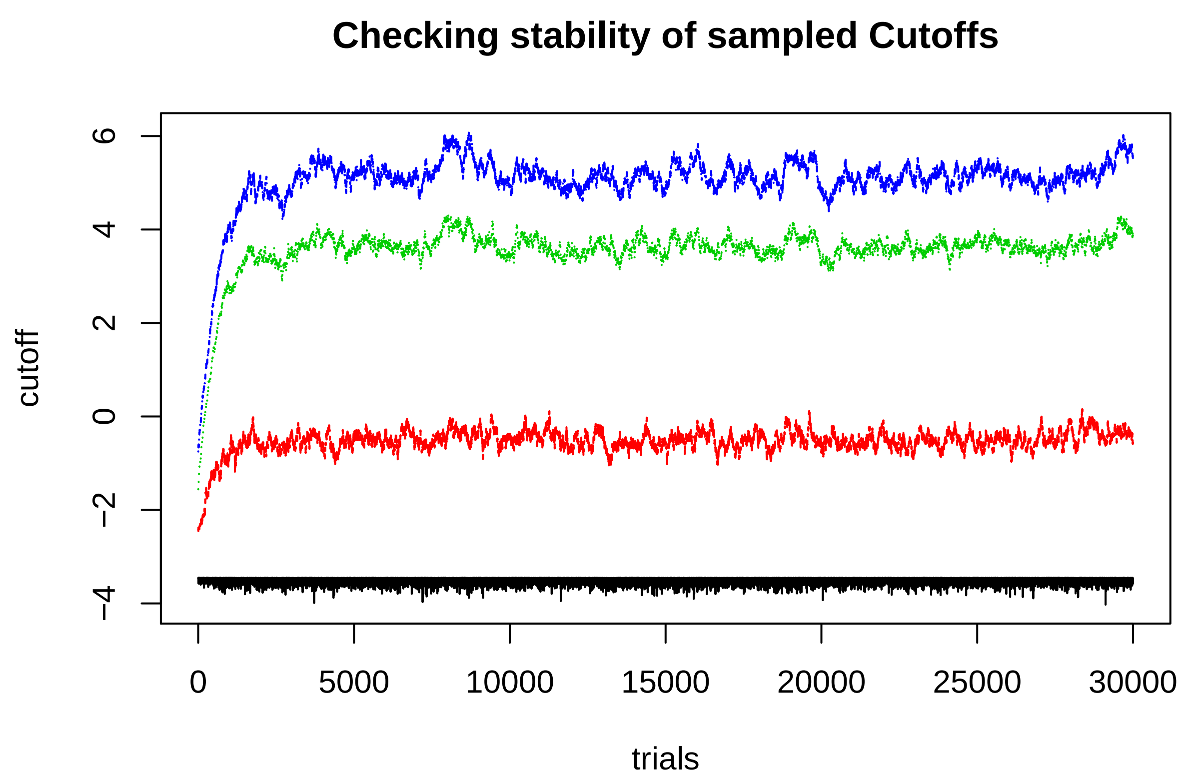


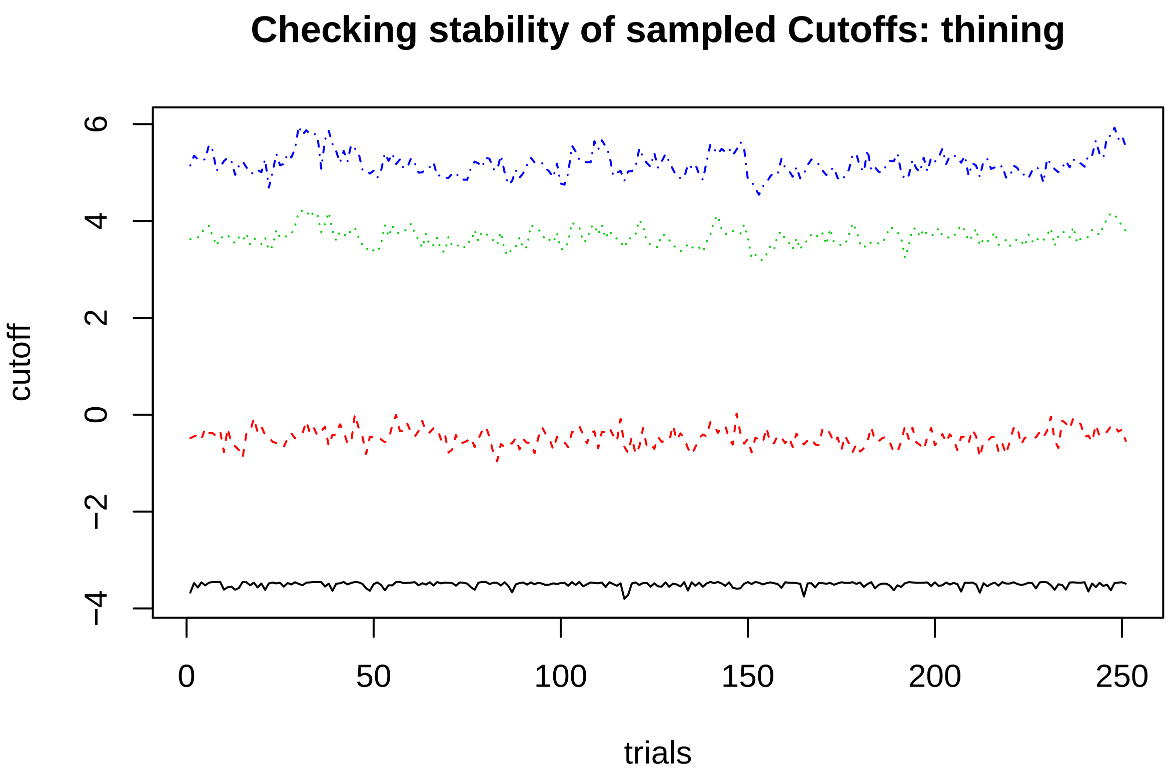

```
df_g= cbind(g, c(mean(g1[seq(burnin, dim(BETA)[1], thining)]),
                 mean(g2[seq(burnin, dim(BETA)[1], thining)]),
                 mean(g3[seq(burnin, dim(BETA)[1], thining)]),
                 mean(g4[seq(burnin, dim(BETA)[1], thining)])))
colnames(df_g)<- c('original cutoffs', 'sampled cutoffs')
barplot(df_g, beside = TRUE,
        legend = TRUE, main = 'Blocked Gibbs Sampling Assessment: Cutoffs',
        args.legend=list(x='topleft'))
```


Blocked Gibbs Sampling Assessment: Cutoffs
10%
30%
70%
85%
4
2
0
−2
original cutoffs
sampled cutoffs


Checking stability of sampled Beta
weight
2
0
−2
−4
0
5000
10000
15000
20000
25000
30000
trials


Checking stability of sampled Beta: thining
weight
2
0
−2
−4
0
50
100
150
200
250
trials


Checking stability of sampled Cutoffs
cutoff
6
4
2
0
−2
−4
0
5000
10000
15000
20000
25000
30000
trials


Checking stability of sampled Cutoffs: thining
cutoff
trials
6
4
2
0
−2
−4
0
50
100
150
200
250