

IPUMS Health Data

MATH 301 Data Confidentiality

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```
## read data
data <- read.csv("nhis_00001.csv")
## REMOVE THIS LATER. ONLY TAKING 1000 SAMPLES B/C JAGS TOOK TOO LONG
data <- sample_n(data, 2000, replace = FALSE, prob = NULL)
## log income
data$LOGINC<- log(data$EARNIMPOINT1)
#load("tp.RData")
```

Our goal is to generate synthetic data from the estimated Bayesian synthesizer from the posterior predictive distribution. To produce a good synthesizer, there will be trade-offs between utility and risks.

```
## Remove all NIU (00) values
data <- data[!data$EDUCREC2 == 00, ]
data <- data[!data$HOUSWRK == 00, ]
data <- data[!data$HINOTCOVE == 0, ]
data <- data[!data$HRSLEEP == 00, ]
data <- data[!data$WORFREQ == 0, ]

## Create new column RACE and recode into 6 categories
## 1 = White, 2 = Black, 3 = American Indian, 4 = Asian,
## 5 = Other races, 6 = Two or more races
data <- data %>% mutate(RACE = ifelse(RACEA %in% 100, 1, ifelse(RACEA %in% 200, 2, ifelse(RACEA %in% c(
## Create new column EDUC and recode into 3 categories
## 1 = 4 years of high school or less, 2 = 4 years of college,
## 3 = 5+ years of college
data <- data %>% mutate(EDUC = ifelse(EDUCREC2 %in% c(10,20,30,31,32,40,41,42), 1, ifelse(EDUCREC2 %in%
data <- data %>% mutate(INCOME = ifelse(EARNIMPOINT1 %in% 0, 0, 1))

head(data)
```

```
##   AGE SEX RACEA EDUCREC2 HOUSWRK POORYN EARNIMP1 EARNIMPOINT1 USUALPL
## 1  22  2  100      51      36      1        3      14000      2
## 2  32  2  200      54      35      1       21      37000      2
## 3  19  1  100      42      30      1        2       7000      2
## 4  66  1  200      60      40      1       52      70000      2
## 5  52  2  100      51      47      1       31      47000      2
## 6  20  2  100      42      15      9        0         0      1
##   DELAYCOST HINOTCOVE ALCDAYSWK CIGDAYMO HRSLEEP WORFREQ DEPFREQ RACE EDUC
## 1         2         1        80       22      6        1        2    1    2
## 2         1         1       96       96      7        5        5    2    2
## 3         1         1         0       96      8        5        4    1    1
## 4         1         1       80       96      8        5        5    2    3
## 5         1         1         0       96      6        2        4    1    2
## 6         2         2         0       96      6        2        2    1    1
##   INCOME
```

```
## 1      1
## 2      1
## 3      1
## 4      1
## 5      1
## 6      0
```

```
summary(data)
```

```
##          AGE          SEX          RACEA          EDUCREC2
##  Min.   :18.00  Min.   :1.00  Min.   :100.0  Min.   :10.00
## 1st Qu.:31.00 1st Qu.:1.00 1st Qu.:100.0 1st Qu.:42.00
## Median :42.00 Median :1.00 Median :100.0 Median :51.00
## Mean   :43.78 Mean   :1.49 Mean   :137.1 Mean   :50.67
## 3rd Qu.:56.00 3rd Qu.:2.00 3rd Qu.:100.0 3rd Qu.:54.00
## Max.   :78.00 Max.   :2.00 Max.   :600.0 Max.   :60.00
##  HOURSWRK      POORYN      EARNIMP1      EARNIMPOINT1
##  Min.    : 1.00  Min.    :1.000  Min.    : 0.00  Min.    : 0
## 1st Qu.:35.25 1st Qu.:1.000 1st Qu.: 5.00 1st Qu.: 21451
## Median :40.00 Median :1.000 Median :22.00 Median : 40000
## Mean   :40.36 Mean   :1.315 Mean   :29.07 Mean   : 49986
## 3rd Qu.:50.00 3rd Qu.:1.000 3rd Qu.:52.00 3rd Qu.: 70000
## Max.   :95.00 Max.   :9.000 Max.   :70.00 Max.   :149000
##  USUALPL      DELAYCOST      HINOTCOVE      ALCDAYSWK
##  Min.    :1.000  Min.    :1.000  Min.    :1.000  Min.    : 0.00
## 1st Qu.:2.000 1st Qu.:1.000 1st Qu.:1.000 1st Qu.: 0.00
## Median :2.000 Median :1.000 Median :1.000 Median :10.00
## Mean   :1.859 Mean   :1.126 Mean   :1.113 Mean   :32.85
## 3rd Qu.:2.000 3rd Qu.:1.000 3rd Qu.:1.000 3rd Qu.:70.00
## Max.   :3.000 Max.   :2.000 Max.   :2.000 Max.   :99.00
##  CIGDAYMO      HRSLEEP      WORKFREQ      DEPFREQ
##  Min.    : 4.00  Min.    : 3.000  Min.    :1.000  Min.    :1.000
## 1st Qu.:96.00 1st Qu.: 6.000 1st Qu.:3.000 1st Qu.:4.000
## Median :96.00 Median : 7.000 Median :4.000 Median :5.000
## Mean   :94.16 Mean   : 6.928 Mean   :3.677 Mean   :4.308
## 3rd Qu.:96.00 3rd Qu.: 8.000 3rd Qu.:5.000 3rd Qu.:5.000
## Max.   :96.00 Max.   :12.000 Max.   :5.000 Max.   :5.000
##  RACE          EDUC          INCOME
##  Min.    :1.000  Min.    :1.000  Min.    :0.0000
## 1st Qu.:1.000 1st Qu.:1.000 1st Qu.:1.0000
## Median :1.000 Median :2.000 Median :1.0000
## Mean   :1.351 Mean   :1.905 Mean   :0.9744
## 3rd Qu.:1.000 3rd Qu.:2.000 3rd Qu.:1.0000
## Max.   :5.000 Max.   :3.000 Max.   :1.0000
```

Step 1: Synthetic Logistic Regression Model

```
## JAGS script
modelString <-"
model {
## sampling
for(i in 1:N){
y[i] ~ dbern(p[i])
logit(p[i]) <- beta0 + beta1*x_age[i] +
```

```

beta2*x_sex_male[i] + beta3*x_sex_female[i] +
beta4*x_race_w[i] + beta5*x_race_b[i] +
beta6*x_race_i[i] + beta7*x_race_a[i] +
beta8*x_race_o[i] +
beta10*x_educ_1[i] + beta11*x_educ_2[i] +
beta12*x_educ_3[i] + beta13*x_hourswrk[i] +
beta14*x_health_cov[i] + beta15*x_health_nocov[i] +
beta16*x_hrsleep[i] + beta17*x_wor_daily[i] +
beta18*x_wor_weekly[i] + beta19*x_wor_monthly[i] +
beta20*x_wor_fewtimes[i] + beta21*x_wor_never[i]
}
## priors
beta0 ~ dnorm(mu0, g0)
beta1 ~ dnorm(mu1, g1)
beta2 ~ dnorm(mu2, g2)
beta3 ~ dnorm(mu3, g3)
beta4 ~ dnorm(mu4, g4)
beta5 ~ dnorm(mu5, g5)
beta6 ~ dnorm(mu6, g6)
beta7 ~ dnorm(mu7, g7)
beta8 ~ dnorm(mu8, g8)
beta10 ~ dnorm(mu10, g10)
beta11 ~ dnorm(mu11, g11)
beta12 ~ dnorm(mu12, g12)
beta13 ~ dnorm(mu13, g13)
beta14 ~ dnorm(mu14, g14)
beta15 ~ dnorm(mu15, g15)
beta16 ~ dnorm(mu16, g16)
beta17 ~ dnorm(mu17, g17)
beta18 ~ dnorm(mu18, g18)
beta19 ~ dnorm(mu19, g19)
beta20 ~ dnorm(mu20, g20)
beta21 ~ dnorm(mu21, g21)
}"

#invsigma2 ~ dgamma(a, b)
#sigma <- sqrt(pow(invsigma2, -1))

y = as.vector(data$INCOME)
x_age = as.vector(data$AGE) ## age
x_sex_male = as.vector(data$SEX$.data_1) ## male
x_sex_female = as.vector(data$SEX$.data_2) ## female
x_race_w = as.vector(data$RACE$.data_1) ## white
x_race_b = as.vector(data$RACE$.data_2) ## black/african-american
x_race_i = as.vector(data$RACE$.data_3) ## american indian
x_race_a = as.vector(data$RACE$.data_4) ## asian
x_race_o = as.vector(data$RACE$.data_5) ## other races
x_educ_1 = as.vector(data$EDUC$.data_3) ## 4 years of high school or less
x_educ_2 = as.vector(data$EDUC$.data_1) ## 4 years of college
x_educ_3 = as.vector(data$EDUC$.data_2) ## 5+ years of college
x_hourswrk = as.vector(data$HOURS WRK) ## hours of work
x_health_cov = as.vector(data$HEALTH$.data_1) ## has health coverage
x_health_nocov = as.vector(data$HEALTH$.data_2) ## has no health coverage
x_hrsleep = as.vector(data$HRSLEEP) ## hours of sleep

```

```

x_wor_daily = as.vector(data$WORRY$.data_2) ## worry daily
x_wor_weekly = as.vector(data$WORRY$.data_5) ## worry weekly
x_wor_monthly = as.vector(data$WORRY$.data_4) ## worry monthly
x_wor_fewtimes = as.vector(data$WORRY$.data_3) ## worry few times a year
x_wor_never = as.vector(data$WORRY$.data_1) ## worry never

```

```

N = length(y) # Compute the number of observations

```

```

## Pass the data and hyperparameter values to JAGS

```

```

the_data <- list("y" = y,
"x_age" = x_age, "x_sex_male" = x_sex_male,
"x_sex_female" = x_sex_female, "x_race_w" = x_race_w,
"x_race_b" = x_race_b, "x_race_i" = x_race_i,
"x_race_a" = x_race_a, "x_race_o" = x_race_o,
"x_educ_1" = x_educ_1,
"x_educ_2" = x_educ_2, "x_educ_3" = x_educ_3,
"x_hourswrk" = x_hourswrk, "x_health_cov" = x_health_cov,
"x_health_nocov" = x_health_nocov, "x_hrsleep" = x_hrsleep,
"x_wor_daily" = x_wor_daily, "x_wor_weekly" = x_wor_weekly,
"x_wor_monthly" = x_wor_monthly, "x_wor_fewtimes" = x_wor_fewtimes,
"x_wor_never" = x_wor_never,
"N" = N,
"mu0" = 0, "g0" = 1, "mu1" = 0, "g1" = 1,
"mu2" = 0, "g2" = 1, "mu3" = 0, "g3" = 1,
"mu4" = 0, "g4" = 1, "mu5" = 0, "g5" = 1,
"mu6" = 0, "g6" = 1, "mu7" = 0, "g7" = 1,
"mu8" = 0, "g8" = 1,
"mu10" = 0, "g10" = 1, "mu11" = 0, "g11" = 1,
"mu12" = 0, "g12" = 1, "mu13" = 0, "g13" = 1,
"mu14" = 0, "g14" = 1, "mu15" = 0, "g15" = 1,
"mu16" = 0, "g16" = 1, "mu17" = 0, "g17" = 1,
"mu18" = 0, "g18" = 1, "mu19" = 0, "g19" = 1,
"mu20" = 0, "g20" = 1, "mu21" = 0, "g21" = 1)

```

```

initsfunction <- function(chain){
.RNG.seed <- c(1,2)[chain]
.RNG.name <- c("base:Super-Duper",
"base:Wichmann-Hill")[chain]
return(list(.RNG.seed=.RNG.seed,
.RNG.name=.RNG.name))
}

```

```

## Run the JAGS code for this model:

```

```

posterior_MLR <- run.jags(modelString,
n.chains = 1,
data = the_data,
monitor = c("beta0", "beta1", "beta2",
"beta3", "beta4", "beta5",
"beta6", "beta7", "beta8", "beta10",
"beta11", "beta12", "beta13", "beta14", "beta15", "beta16", "beta17",
"beta18", "beta19", "beta20", "beta21"),
adapt = 1000,
burnin = 5000,
sample = 5000,

```

```
thin = 1,
inits = initsfunction)
```

```
## Loading required namespace: rjags

## Compiling rjags model...
## Calling the simulation using the rjags method...
## Adapting the model for 1000 iterations...
## Burning in the model for 5000 iterations...
## Running the model for 5000 iterations...
## Simulation complete
## Calculating summary statistics...

## Warning: Convergence cannot be assessed with only 1 chain

## Finished running the simulation
```

```
## JAGS output
```

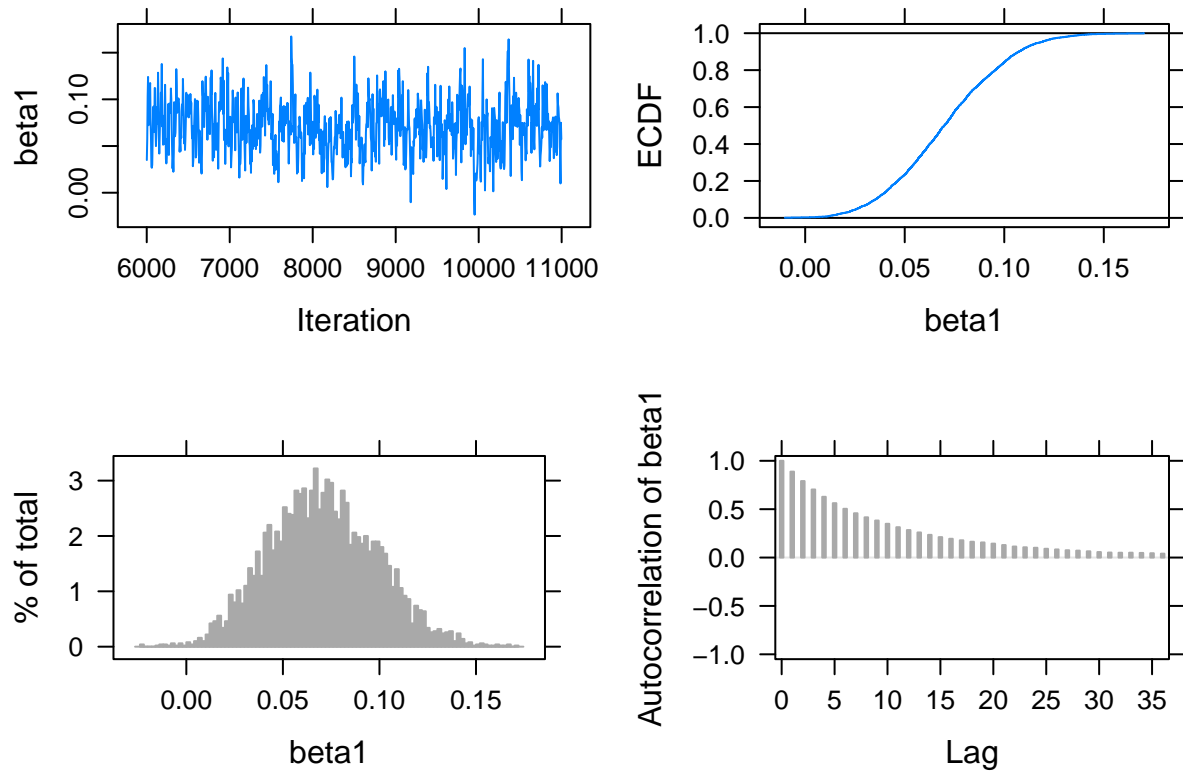
```
summary(posterior_MLR)
```

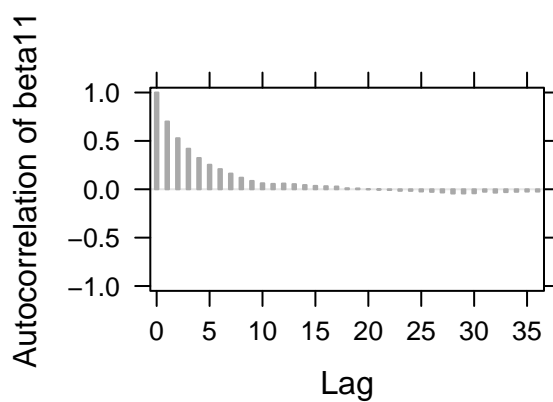
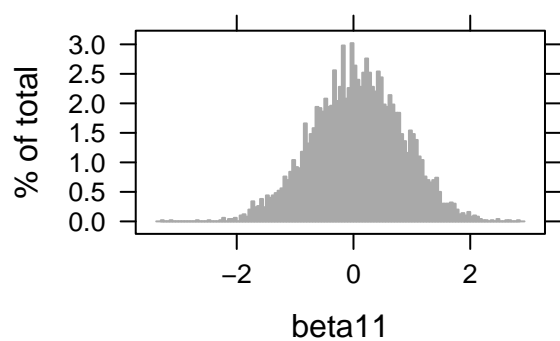
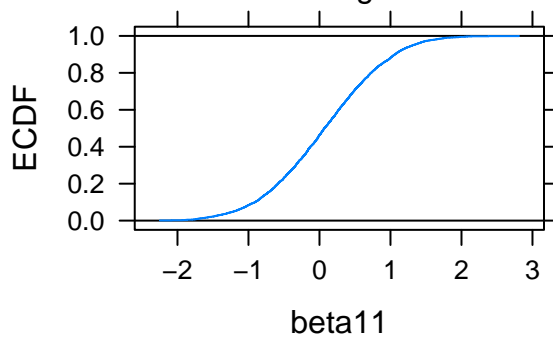
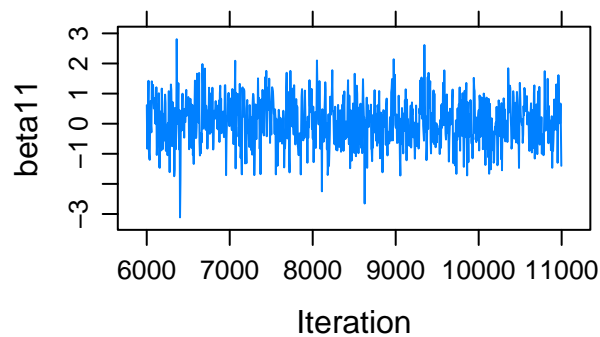
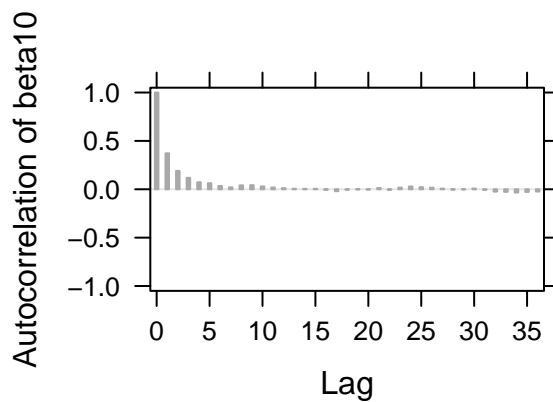
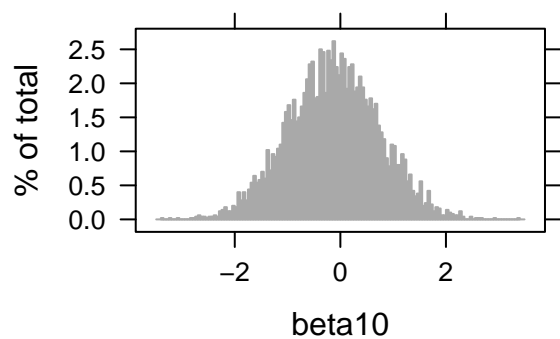
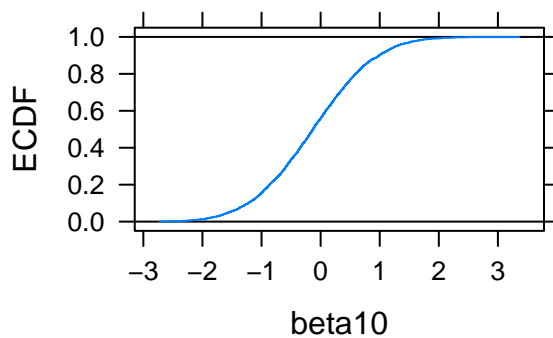
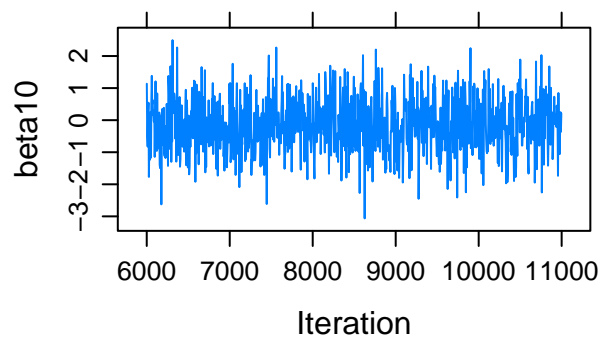
##	Lower95	Median	Upper95	Mean	SD	Mode
## beta0	-1.94216286	-0.064370798	1.7087691	-0.059244782	0.95755888	NA
## beta1	0.01703532	0.069855437	0.1243447	0.070712076	0.02800400	NA
## beta2	-1.52081205	-0.010785325	1.5617397	-0.001100925	0.78853927	NA
## beta3	-1.42833200	-0.030058490	1.6036287	-0.037891187	0.76633484	NA
## beta4	-1.70854020	-0.238894845	1.2627460	-0.261122309	0.77038375	NA
## beta5	-1.90242561	-0.266598173	1.3632391	-0.247070020	0.83764811	NA
## beta6	-1.80407664	0.125012061	1.9626125	0.118639226	0.98157860	NA
## beta7	-1.46997316	0.258248644	2.0954143	0.279991684	0.91151560	NA
## beta8	-1.82410712	0.082366429	1.9653833	0.082791730	0.96465078	NA
## beta10	-1.80561893	-0.127869671	1.5390520	-0.129151490	0.86019312	NA
## beta11	-1.47775601	0.068138162	1.5119147	0.069102320	0.76951951	NA
## beta12	-1.46719304	0.042431748	1.5549516	0.024320356	0.77475482	NA
## beta13	0.04660710	0.100308705	0.1553877	0.101392498	0.02817009	NA
## beta14	-0.91600088	0.532118514	2.0267029	0.551548048	0.77527016	NA
## beta15	-2.20148535	-0.584046364	0.9382540	-0.598551876	0.79961200	NA
## beta16	-0.67530542	-0.231626161	0.2103327	-0.229364201	0.23163627	NA
## beta17	-1.74548598	-0.333244751	1.0957288	-0.331396086	0.72269332	NA
## beta18	-1.65502601	-0.169343372	1.1056249	-0.169482359	0.70711899	NA
## beta19	-0.56718725	0.987889468	2.5936241	0.994046300	0.81821663	NA
## beta20	-1.62605643	0.004998299	1.5255489	0.013384858	0.80716359	NA
## beta21	-1.99993607	-0.575112387	1.0555822	-0.548693811	0.77444022	NA
##	MCerr	MC%ofSD	SSeff	AC.10	psrf	
## beta0	0.056190074	5.9	290	2.982882e-01	NA	
## beta1	0.001626187	5.8	297	3.489078e-01	NA	
## beta2	0.030278286	3.8	678	6.002516e-02	NA	
## beta3	0.031597559	4.1	588	1.017022e-01	NA	
## beta4	0.034138273	4.4	509	1.546571e-01	NA	
## beta5	0.026542528	3.2	996	8.377229e-02	NA	
## beta6	0.017770571	1.8	3051	2.837257e-02	NA	
## beta7	0.018196566	2.0	2509	4.529739e-05	NA	
## beta8	0.017802231	1.8	2936	6.935257e-03	NA	
## beta10	0.019769596	2.3	1893	2.958121e-02	NA	
## beta11	0.029331843	3.8	688	6.214165e-02	NA	
## beta12	0.027965868	3.6	767	4.804411e-02	NA	
## beta13	0.001304828	4.6	466	1.538657e-01	NA	

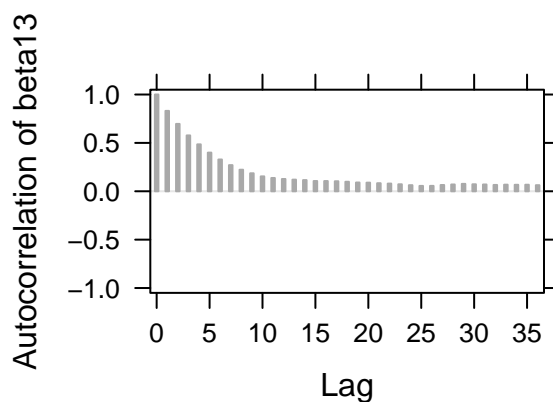
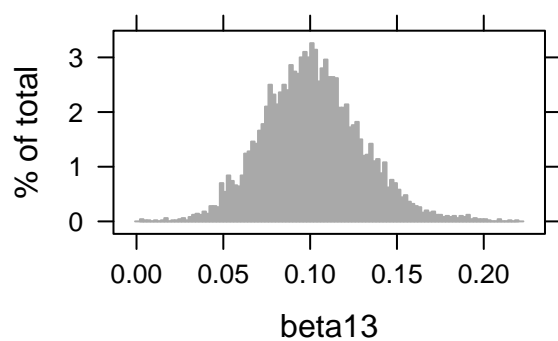
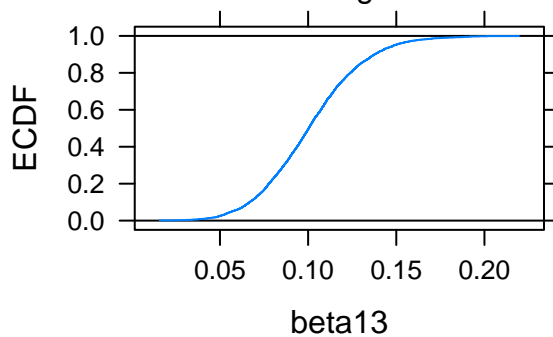
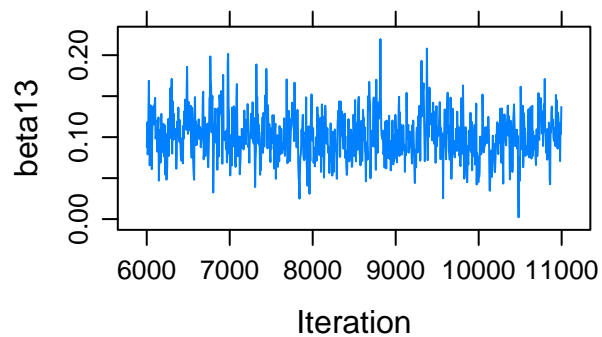
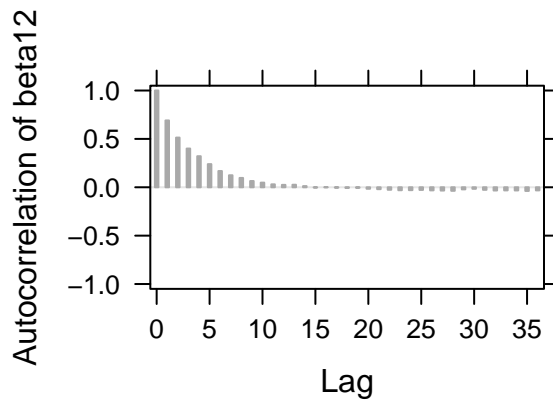
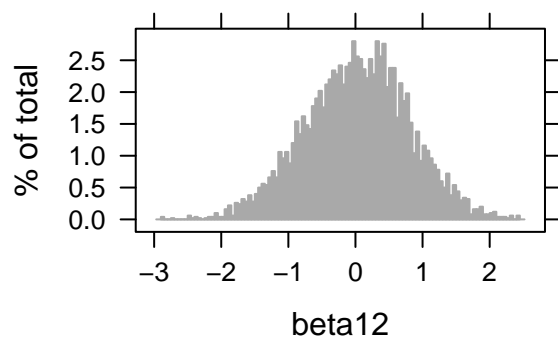
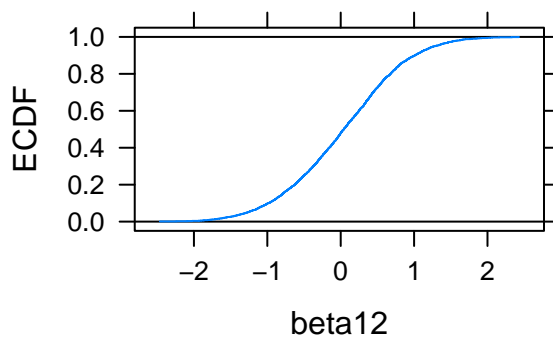
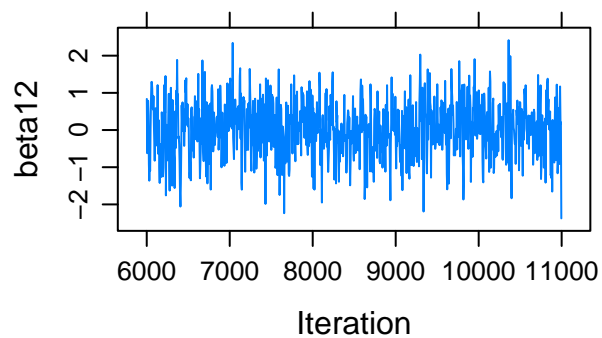
```
## beta14 0.033415330      4.3   538  1.097408e-01  NA
## beta15 0.028190107      3.5   805  5.718940e-02  NA
## beta16 0.022056978      9.5   110  6.568611e-01  NA
## beta17 0.018092380      2.5  1596  9.121764e-03  NA
## beta18 0.020274399      2.9  1216  1.647437e-02  NA
## beta19 0.016687399      2.0  2404 -2.150645e-02  NA
## beta20 0.016393582      2.0  2424 -4.418488e-02  NA
## beta21 0.019459208      2.5  1584  3.691483e-02  NA
```

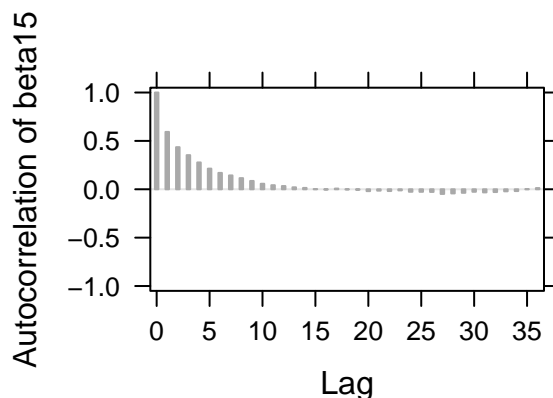
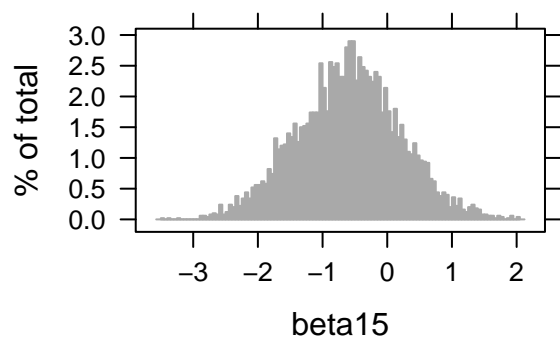
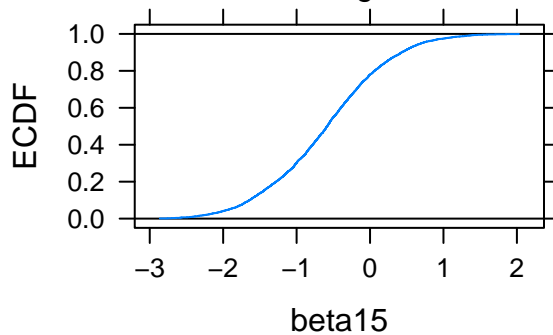
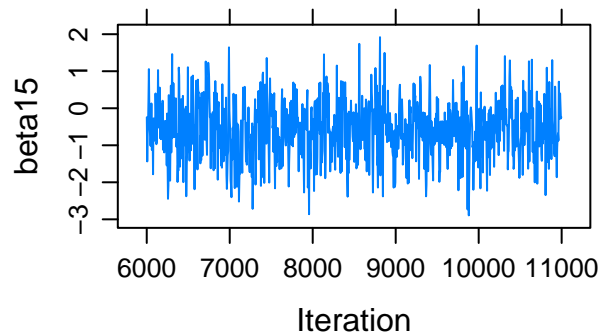
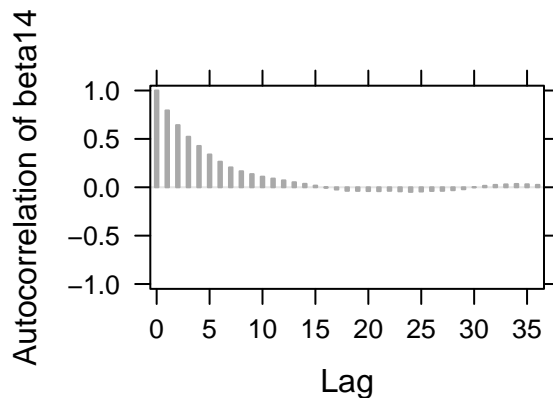
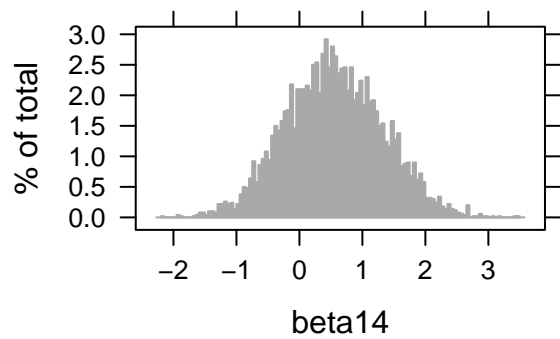
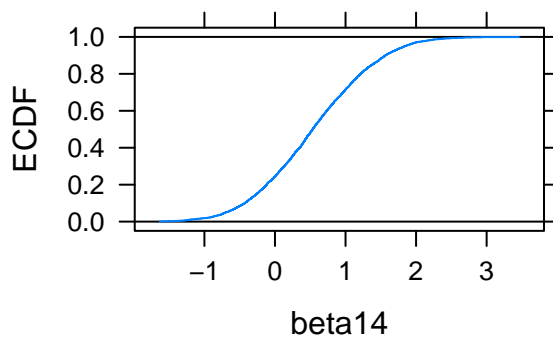
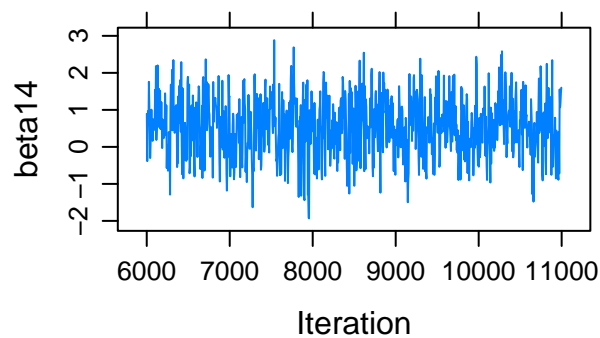
```
plot(posterior_MLR, vars = "beta1")
```

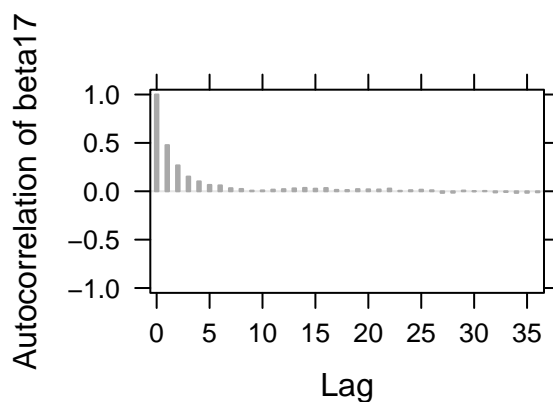
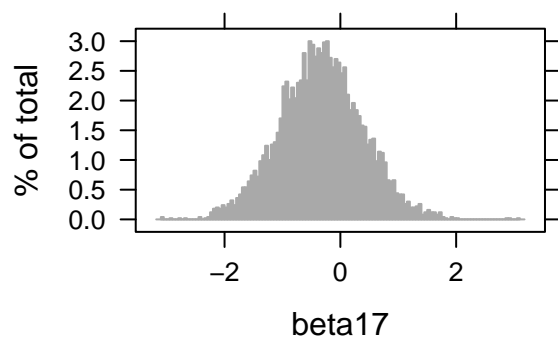
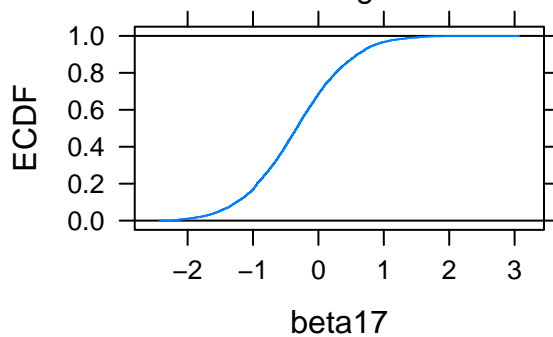
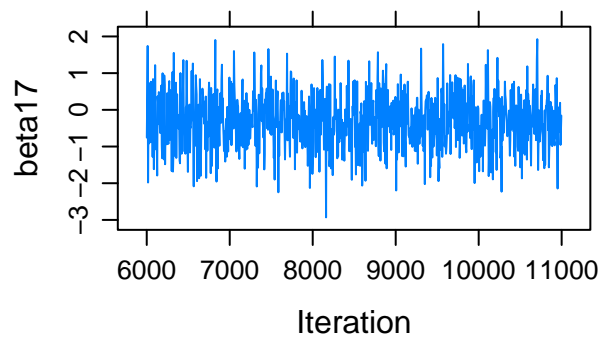
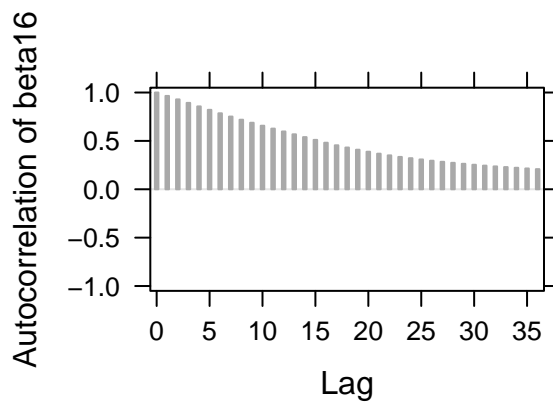
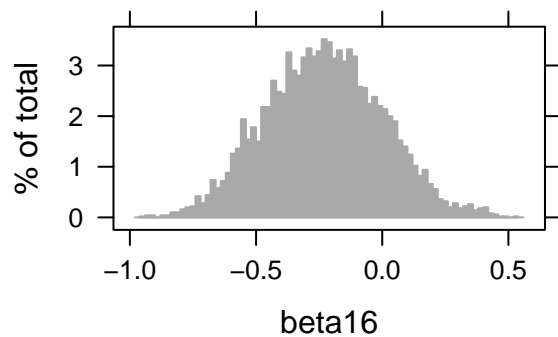
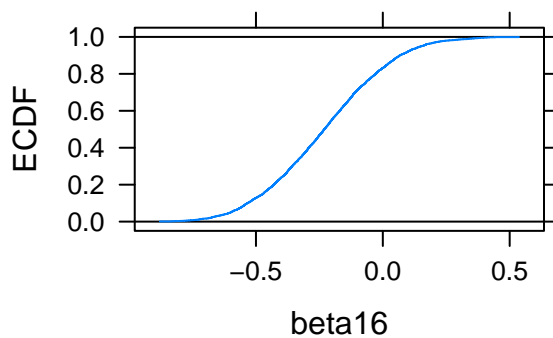
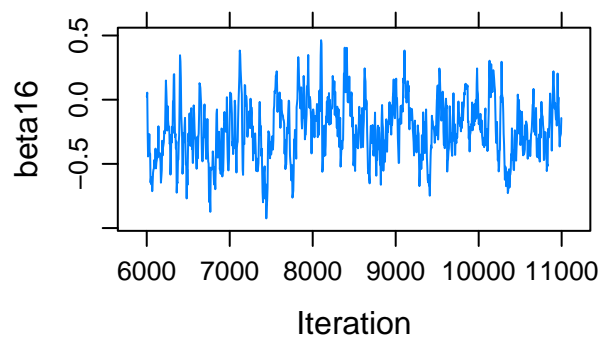
```
## Generating plots...
```

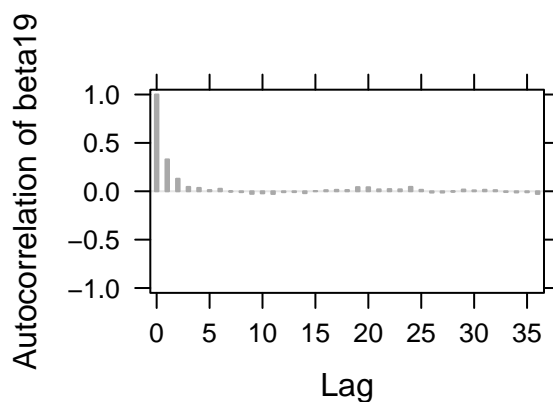
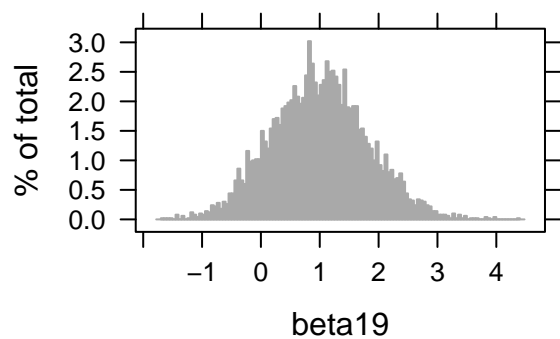
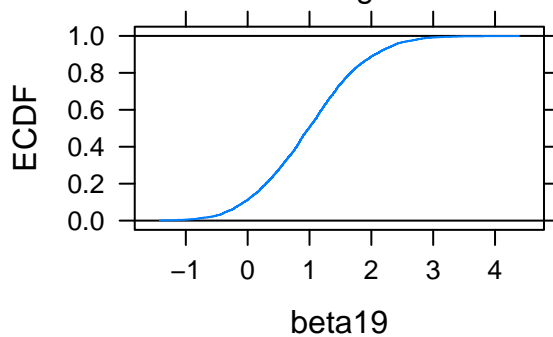
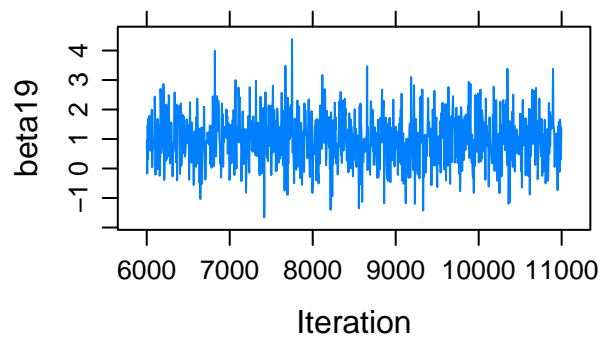
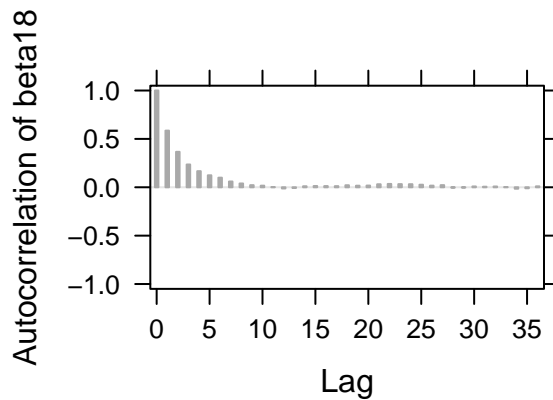
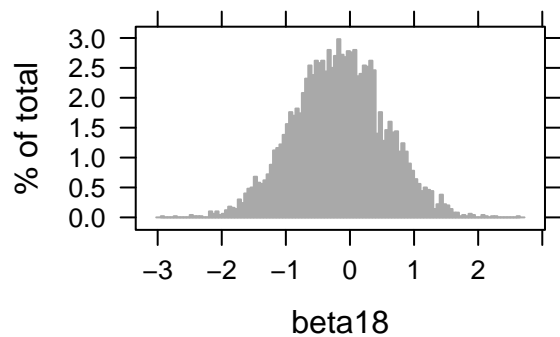
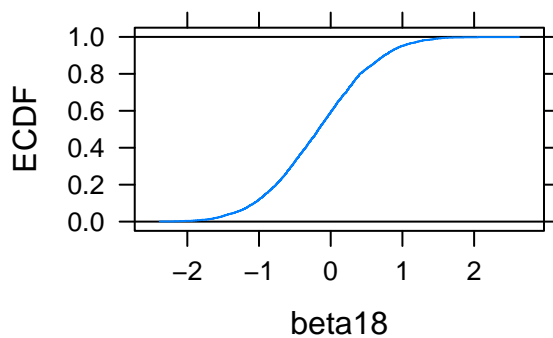
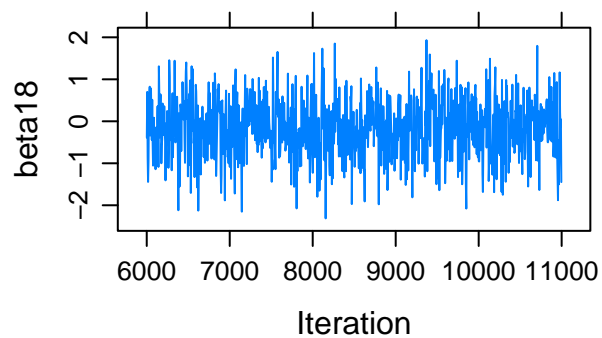


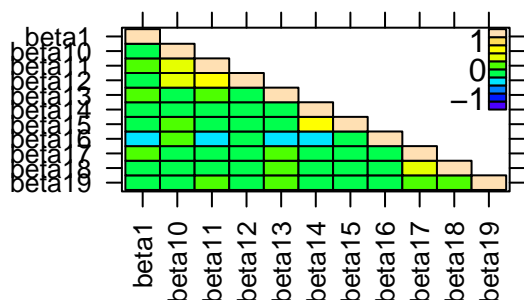












```
## Saving posterior parameter draws
```

```
post <- as.mcmc(posterior_MLR)
```

```
post[1, "beta0"]
```

```
## [1] 0.2047922
```

```
## Generating one set of sythetic data
```

```
synthesize <- function(X, index, n){
```

```
  synthetic_Y <- c()
```

```
  for(i in 1:n){
```

```
    p <- plogis(post[index, "beta0"] + X$x_age[i] * post[index, "beta1"] + X$x_sex_male[i] * post[in
```

```
    synthetic_Y[i] <- rbinom(1,1,p)
```

```
  }
```

```
  data.frame(X$y, synthetic_Y)
```

```
}
```

```
n <- dim(data)[1]
```

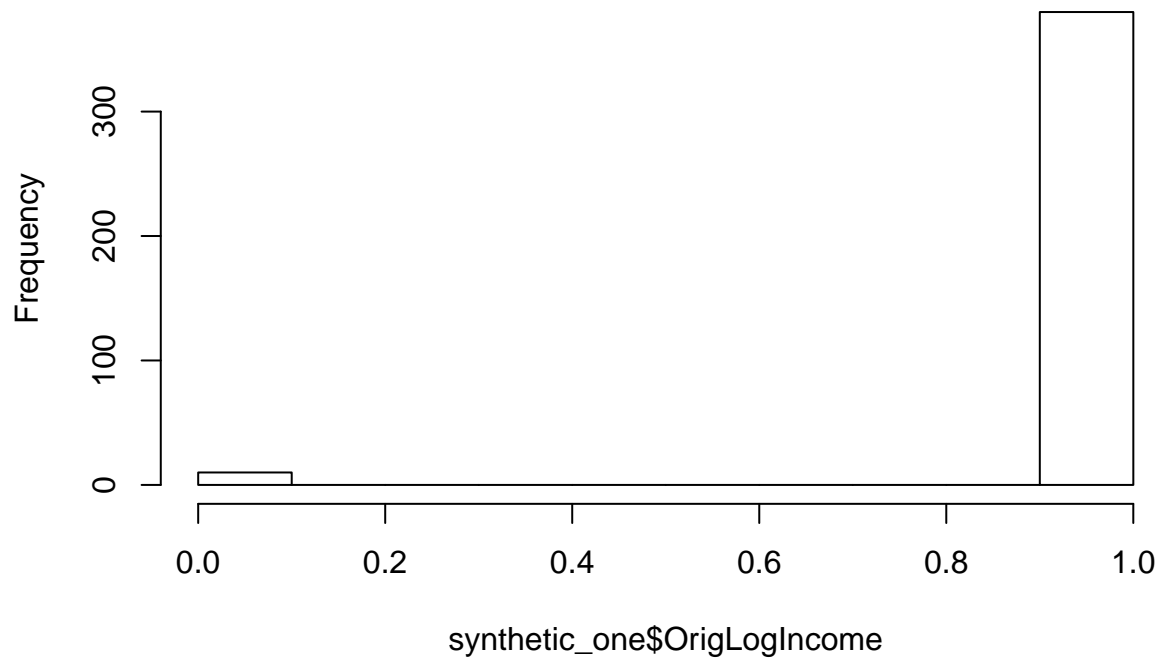
```
params <- data.frame(y, x_age, x_sex_male, x_sex_female, x_race_w, x_race_b, x_race_i, x_race_a, x_race
```

```
synthetic_one <- synthesize(params, 1, n)
```

```
names(synthetic_one) <- c("OrigLogIncome", "SynLogIncome")
```

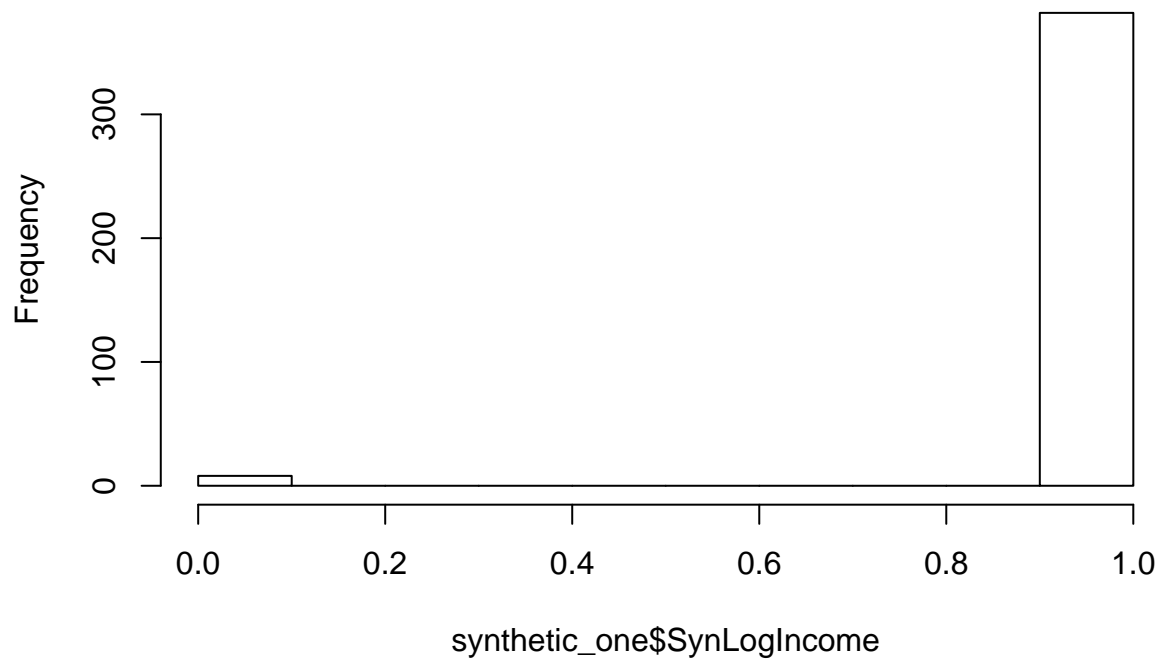
```
hist(synthetic_one$OrigLogIncome)
```

Histogram of synthetic_one\$OrigLogIncome



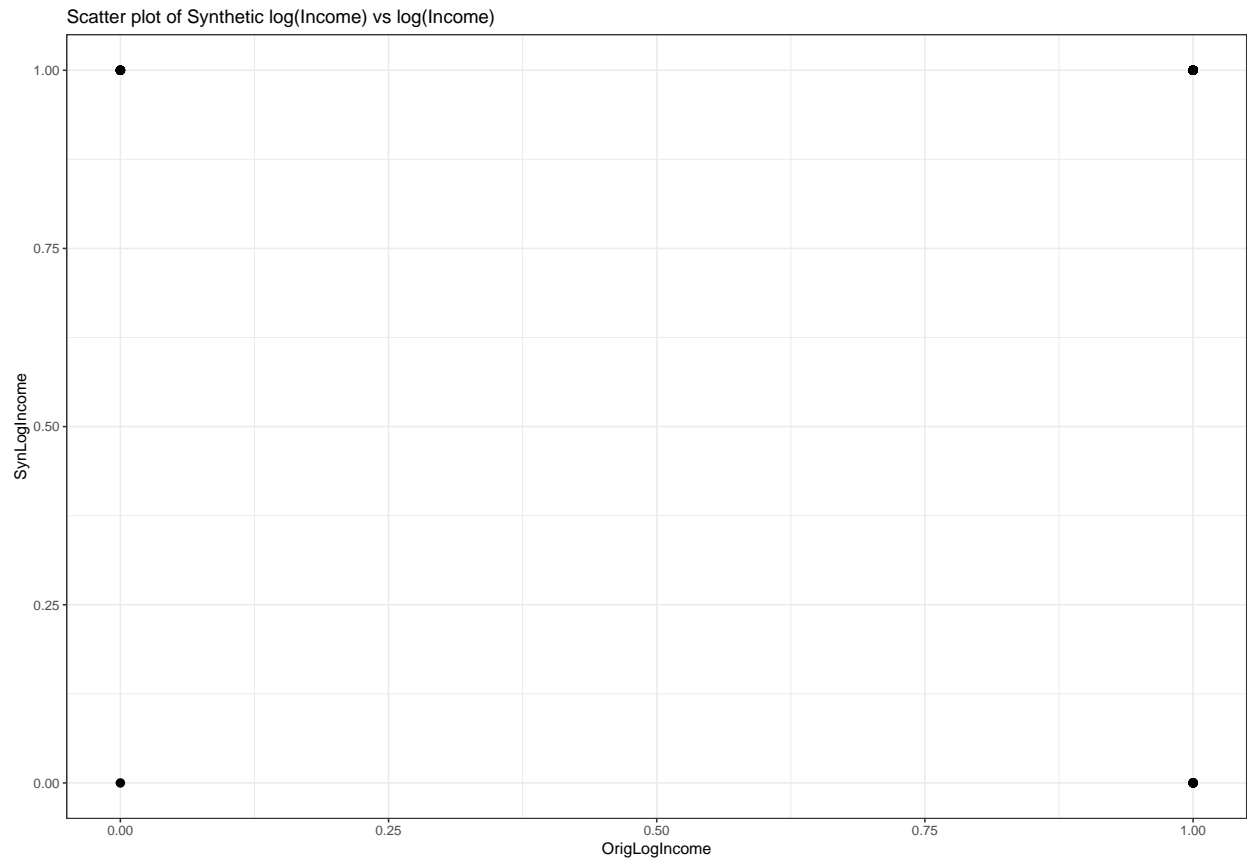
```
hist(synthetic_one$SynLogIncome)
```

Histogram of synthetic_one\$SynLogIncome



```
ggplot(synthetic_one, aes(x = OrigLogIncome, y = SynLogIncome)) +  
  geom_point(size = 1) +  
  labs(title = "Scatter plot of Synthetic log(Income) vs log(Income)") +
```

```
theme_bw(base_size = 6, base_family = "")
```



Utility Evaluation

Analysis-specific measures

Synthetic IPUMS sample: step 1

```
n <- dim(data)[1]
m <- 20
synthetic_m <- vector("list",m)

for(i in 1:m){
  seed <- round(runif(1, 1, 1000))
  synthetic_new <- synthesize(params, 2000 + i, n)
  names(synthetic_new) <- c("params", "LogIncome")
  synthetic_m[[i]] <- synthetic_new
}

q <- rep(NA, m)
v <- rep(NA, m)
for (i in 1:m){
  synthetic_new <- synthetic_m[[i]]
  q[i] <- mean(synthetic_new$LogIncome)
  v[i] <- var(synthetic_new$LogIncome)/n
}
```

Synthetic IPUMS sample: step 2

```
q_bar_m <- mean(q)
b_m <- var(q)
v_bar_m <- mean(v)
```

Synthetic IPUMS sample: step 3

```
T_p <- b_m / m + v_bar_m
v_p <- (m - 1) * (1 + v_bar_m / (b_m / m))^2
```

Synthetic CE sample: step 4

- Obtain the point estimate for mean estimand Q , and the 95% confidence interval

```
set.seed(123)
q_bar_m

## [1] 0.9725641
t_score_syn <- qt(p = 0.975, df = v_p)
c(q_bar_m - t_score_syn * sqrt(T_p), q_bar_m + t_score_syn * sqrt(T_p))
```

```
## [1] 0.9557478 0.9893804
```

Synthetic mean estimand: 0.974 Synthetic 95% CI: [0.957, 0.990]

Synthetic CE sample: step 4-extra

```
## Obtain the point estimate for mean estimand Q, and the 95%
## confidence interval from the original data
set.seed(123)
mean_org <- mean(data$INCOME)
sd_org <- sd(data$INCOME)
t_score_org <- qt(p = 0.975, df = n-1)
mean_org

## [1] 0.974359
set.seed(123)
c(mean_org - t_score_org * sd_org / sqrt(n), mean_org + t_score_org * sd_org / sqrt(n))
```

```
## [1] 0.9586027 0.9901153
```

Original mean estimand: 0.970 Original 95% CI: [0.952, 0.987]

Interval overlap utility measure

Combining rules provide point estimate and confidence interval estimates. We can also obtain point estimate and confidence interval estimate from the original, confidential data.

```
L_s = quantile(synthetic_new$params, 0.025)
U_s = quantile(synthetic_new$params, 0.975)
L_o = quantile(data$INCOME, 0.025)
U_o = quantile(data$INCOME, 0.975)
L_i = max(L_s, L_o)
U_i = min(U_s, U_o)
I = (U_i - L_i) / (2 * (U_o - L_o)) + (U_i - L_i) / (2 * (U_s - L_s))
I
```

```
## 97.5%
##      1
```

It seems like the interval overlap measure is 1 so we have high utility. We can potentially try to calculate multiple estimands and then take the average values of I over all estimands to obtain a summary.

Identification Risk Evaluation

First, we look into identification disclosure through expected match risk, true match rate, and false match rate. Then attribute disclosure will be examined.

Higher expected match risk, higher true match rate, and lower false match rate indicate higher identification disclosure risk for the sample. Since we are doing a two-part synthesis model, we could potentially calculate three summaries on each synthetic dataset, and take the average.

Step 1: calculate key quantities

```
CalculateKeyQuantities <- function(data, params, known.vars, syn.vars, n){ data <- data params
<- params n <- n c_vector <- rep(NA, n) T_vector <- rep(NA, n) for (i in 1:n){ match <-
(eval(parse(text=paste("data", syn.vars, "[i] == params", syn.vars, sep=" ", collapse="&"))) & eval(parse(text=paste("data", kn
params", known.vars, sep=" ", collapse="&")))) match.prob <- ifelse(match, 1/sum(match), 0)

if (max(match.prob) > 0){
  c_vector[i] <- length(match.prob[match.prob == max(match.prob)])
}
else
  c_vector[i] <- 0
  T_vector[i] <- is.element(i, rownames(data)[match.prob == max(match.prob)])
}

K_vector <- (c_vector * T_vector == 1) F_vector <- (c_vector * (1 - T_vector) == 1) s <-
length(c_vector[c_vector == 1 & is.na(c_vector) == FALSE])

res_r <- list(c_vector = c_vector, T_vector = T_vector, K_vector = K_vector, F_vector = F_vector, s
= s ) return(res_r) }
```

Step 1: calculate key quantities cont'd

```
known.vars <- c("SEX", "RACE", "AGE", "EDUC", "HOUSWRK", "HEALTH", "HRSLEEP", "WORRY")
syn.vars <- c("INCOME") n <- dim(data)[1] KeyQuantities <- CalculateKeyQuantities(data, param,
known.vars, syn.vars, n)
```

Step 2: calculate 3 summary measures

```
IdentificationRisk <- function(c_vector, T_vector, K_vector, F_vector, s, N){
nonzero_c_index <- which(c_vector > 0) exp_match_risk <- sum(1/c_vector[nonzero_c_index]*T_vector[nonzero_c_index])
true_match_rate <- sum(na.omit(K_vector))/N false_match_rate <- sum(na.omit(F_vector))/s res_r
<- list(exp_match_risk = exp_match_risk, true_match_rate = true_match_rate, false_match_rate =
false_match_rate ) return(res_r) }
```

Step 2: calculate 3 summary measures cont'd

- each record is a target, therefore $N = n$

```
c_vector <- KeyQuantities[["c_vector"]] T_vector <- KeyQuantities[["T_vector"]] K_vector <- KeyQuanti-
ties[["K_vector"]] F_vector <- KeyQuantities[["F_vector"]] s <- KeyQuantities[["s"]] N <- n ThreeSummaries
<- IdentificationRisk(c_vector, T_vector, K_vector, F_vector, s, N)
```


Step 2: calculate 3 summary measures cont'd

ThreeSummaries[["exp_match_risk"]] ThreeSummaries[["true_match_rate"]] ThreeSummaries[["false_match_rate"]]