# framingham health data

```r
library(runjags)
library(coda)
library(ggplot2)
data2<- read.csv("frmgham2.csv")
data2$sexd= fastDummies::dummy_cols(data2$SEX)[,names(fastDummies::dummy_cols(data2$SEX))== ".data_1"]
data2$educhs= fastDummies::dummy_cols(data2$educ)[,names(fastDummies::dummy_cols(data2$educ))== ".data_2
data2$educsc= fastDummies::dummy_cols(data2$educ)[,names(fastDummies::dummy_cols(data2$educ))== ".data_3
data2$educc= fastDummies::dummy_cols(data2$educ)[,names(fastDummies::dummy_cols(data2$educ))== ".data_4
data2<- na.omit(data2)
```

```r
modelString2 <-"
model {
for (i in 1:N){
y[i] ~ dnorm(beta0 + beta1*x_age[i] + beta2*x_sexd[i] +
beta3*x_educhs[i] + beta4*x_educsc[i] +
beta5*x_educc[i], invsigma2)
}
beta0 ~ dnorm(mu0, g0)
beta1 ~ dnorm(mu1, g1)
beta2 ~ dnorm(mu2, g2)
beta3 ~ dnorm(mu3, g3)
beta4 ~ dnorm(mu4, g4)
beta5 ~ dnorm(mu5, g5)
invsigma2 ~ dgamma(a, b)
sigma <- sqrt(pow(invsigma2, -1))
}
"
y= as.vector(data2$BMI)
x_age= as.vector(data2$AGE)
x_sexd= as.vector(data2$sexd)
x_educhs= as.vector(data2$educhs)
x_educsc= as.vector(data2$educsc)
x_educc= as.vector(data2$educc)
N= length(y)
```

```r
the_data<- list("y" = y, "x_age"= x_age,
                 "x_sexd"= x_sexd, "x_educhs"= x_educhs,
                 "x_educsc"= x_educsc, "x_educc"= x_educc,
                 "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,
                 "a" = 1, "b" = 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))
}
```

```
posterior<- run.jags(modelString2,
                      n.chains = 1,
                      data = the_data,
                      monitor = c("beta0", "beta1", "beta2",
                                  "beta3", "beta4", "beta5",
                                  "sigma"),
                      adapt = 1000,
                      burnin = 5000,
                      sample = 5000,
                      thin = 1,
                      inits = initsfunction)
```

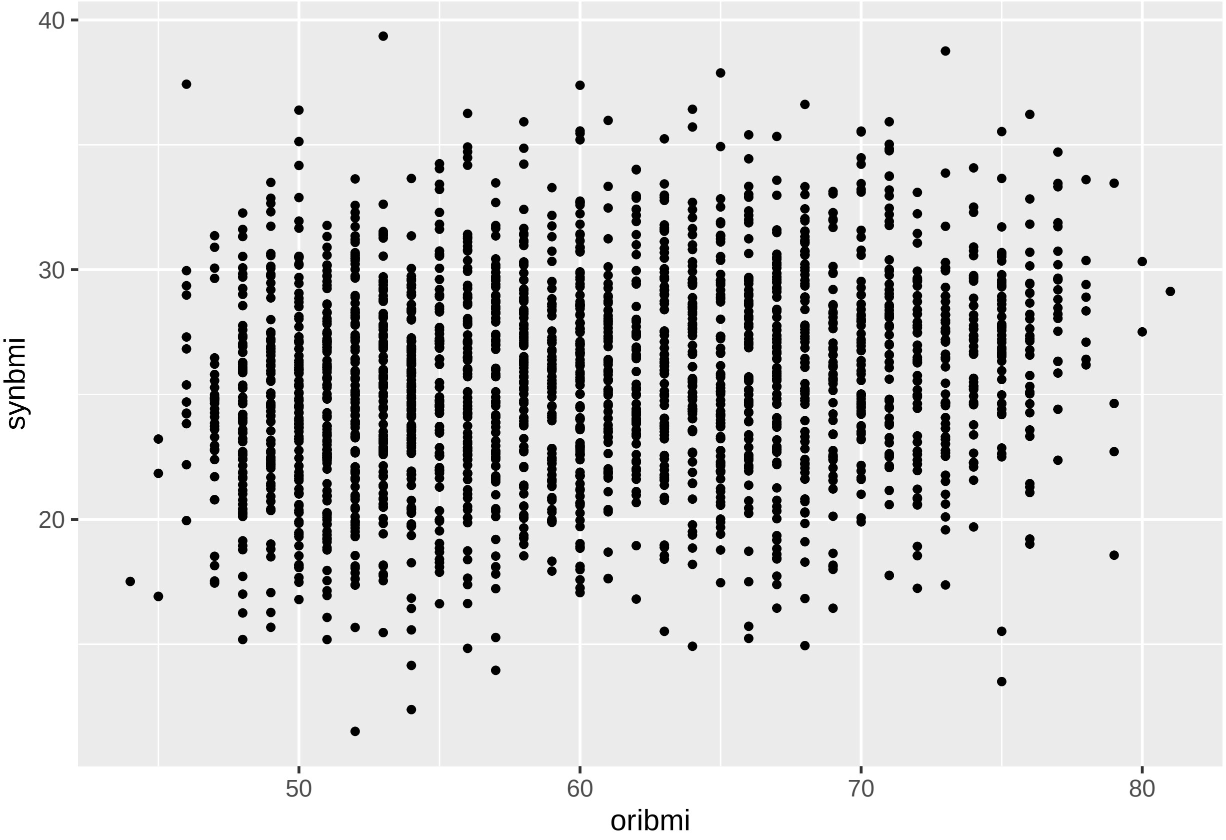
```
## Loading required namespace: rjags

## Compiling rjags model...
## Calling the simulation using the rjags method...
## Note: the model did not require adaptation
## 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
```

```
posterior
```

```
##
## JAGS model summary statistics from 5000 samples (adapt+burnin = 6000):
##
##        Lower95   Median  Upper95     Mean        SD Mode     MCerr MC%ofSD
## beta0   17.904   19.145   20.382   19.152   0.63679   --  0.088165    13.8
## beta1 0.082442  0.10161  0.12175  0.10176 0.0099933   -- 0.0014264    14.3
## beta2  0.69838    1.008   1.3397   1.0091   0.16627   -- 0.0037247     2.2
## beta3 -0.16589  0.21878  0.60871  0.22017   0.19887   -- 0.0070986     3.6
## beta4  -1.0781 -0.62646 -0.17261 -0.62898   0.23253   -- 0.0052512     2.3
## beta5 -0.90959 -0.40818  0.08918 -0.41333   0.25698   -- 0.0052736     2.1
## sigma   3.8519   3.9798   4.1022   3.9817  0.064504   -- 0.0027398     4.2
##
##       SSeff       AC.10 psrf
## beta0    52     0.80953   --
## beta1    49     0.80366   --
## beta2  1993  -0.0085434   --
## beta3   785    0.016964   --
## beta4  1961 -0.00021548   --
## beta5  2375  -0.0061096   --
## sigma   554    0.094295   --
##
## Total time taken: 5.9 seconds
```

```
post<- as.mcmc(posterior)
syn<- function(X, index, n){
  mean_Y<- post[index, "beta0"] + X$x_age * post[index, "beta1"] + X$x_sexd * post[index, "beta2"] + X$
  syny<- rnorm(n,mean_Y, post[index,"sigma"])
  data.frame(X$x_age, syny)
}
n<- dim(data2)[1]
frame<- data.frame(y, x_age, x_sexd, x_educhs, x_educsc, x_educc)
syndata<- syn(frame, 1, n)
names(syndata)<- c("oribmi", "synbmi")
```

```
ggplot(syndata, aes(x= oribmi, y= synbmi)) + geom_point(size = 1)
```


synbmi
oribmi