# KU Leuven Summer School Segment 2A First Look at Latents - Missing Data

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## Missing data

```
require(mice) ### just want data ex. from this package
```

#### summary(nhanes2)

```
##
      age
                  bmi
                            hyp
                                        chl
   20-39:12 Min. :20.4 no :13 Min.
##
                                          :113
   40-59: 7 1st Qu.:22.6 yes: 4 1st Qu.:185
##
##
   60-99: 6 Median :26.8 NA's: 8 Median :187
##
             Mean :26.6
                                    Mean : 191
##
             3rd Qu.:28.9
                                    3rd Qu.:212
             Max. :35.3
##
                                    Max. :284
##
             NA's :9
                                    NA's :10
```

Say interested in regressing chl (Y) on age  $(X_1)$ , hyp  $(X_2)$ , and bmi  $(X_3)$ .

# Toward a generative model (1 of 3)

$$f(\theta) \prod_{i=1}^{n} f(x_{1i}|\theta) f(x_{2i}|x_{1i},\theta) f(x_{3i}|x_{1i},x_{2i},\theta) f(y_{i}|x_{1i},x_{2i},x_{3i},\theta)$$

# Toward a generative model (2 of 3)

```
statmod.string <-"
  for (i in 1:n) {
    x2[i] ~ dbern(pr.x2[i])
      logit(pr.x2[i]) <- alpha0 + alpha1a*x1a[i] +</pre>
                           alpha1b*x1b[i]
    x3[i] \sim dnorm(mn.x3[i], prec.x3)
      mn.x3[i] \leftarrow kappa0 + kappa1a*x1a[i] +
                   kappa1b*x1b[i]+kappa2*x2[i]
    y[i] ~ dnorm(mn.y[i], prec.y)
      mn.y[i] \leftarrow beta0 + beta1a*x1a[i] + beta1b*x1b[i] +
                  beta2*x2[i] + beta3*x3[i]
```

# Toward generative model (3 of 3)

```
prior.string <- "</pre>
  alpha0 \sim dnorm(0, 0.1)
  alpha1a ~ dnorm(0, 0.1)
  alpha1b ~ dnorm(0, 0.1)
  kappa0 \sim dnorm(0, 0.01)
  kappa1a ~ dnorm(0, 0.01)
  kappa1b ~ dnorm(0, 0.01)
  kappa2 ~ dnorm(0, 0.01)
  prec.x3 ~ dgamma(0.1, 0.1)
  beta0 ~ dnorm(0, 0.01)
  beta1a ~ dnorm(0, 0.01)
  beta1b ~ dnorm(0, 0.01)
  beta2 \sim dnorm(0, 0.01)
  beta3 ~ dnorm(0, 0.01)
  prec.y ~ dgamma(0.5, 0.5)
  sig.y <- sqrt(1/prec.y)</pre>
```

## Housekeeping

```
genmod.string <- paste(
"model {",prior.string, statmod.string,"}")</pre>
```

# Pause to comment on this prior and stat model specification

Almost have supplied a joint distribution of everything

#### Turn the JAGS crank

```
### generative model, data go in
mod <- jags.model(textConnection(genmod.string),</pre>
         data=list(x1a=as.numeric(nhanes2$age=="40-59"),
                   x1b=as.numeric(nhanes2$age=="60-99"),
                    x2=as.numeric(nhanes2$hyp)-1,
                    x3=nhanes2$bmi,
                     y=nhanes2$ch1,
                     n=dim(nhanes2)[1]),
         n.chains=4)
update(mod, 2000) ### burn-in
### MC output comes out
opt1.JAGS <- coda.samples(mod, n.iter=10000,
  variable.names=c("beta1a","beta1b","beta2","beta3","sig.y",
    "x2[6]","x3[6]","y[6]"))
```

#### JAGS, continued

#### summary(opt1.JAGS)

```
##
## Iterations = 3001:13000
## Thinning interval = 1
## Number of chains = 4
## Sample size per chain = 10000
##
## 1. Empirical mean and standard deviation for each variable,
     plus standard error of the mean:
##
##
##
                    SD Naive SE Time-series SE
            Mean
## beta1a 5.427 9.354 0.04677
                                     0.05238
## beta1b 7.789 9.838 0.04919
                                     0.05583
## beta2 4.614 9.455 0.04728
                                     0.05084
## beta3 6.886 0.586 0.00293
                                     0.00486
## sig.y 43.158 9.252 0.04626
                                     0.05684
## x2[6] 0.431 0.495 0.00248
                                     0.00339
## x3[6] 24.807 3.992 0.01996
                                     0.02557
## y[6] 184.000 0.000 0.00000
                                      0.00000
##
## 2 Quantiles for each variable.
```

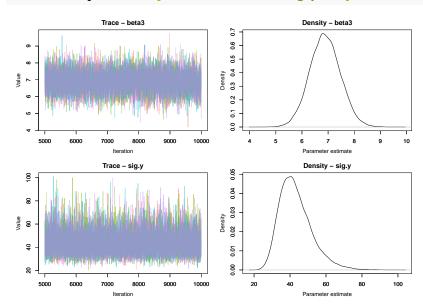
#### Or

```
require(MCMCvis)
MCMCsummary(opt1.JAGS)
```

```
##
                  sd
                      2.5% 50% 97.5% Rhat n.eff
           mean
        5.427 9.354 -13.00
                            5.43
## beta1a
                                  23.67
                                          1 31926
## beta1b 7.789 9.838 -11.54 7.87
                                  27.06
                                          1 31076
## beta2 4.614 9.455 -13.96 4.65
                                  23.04
                                          1 34592
## beta3 6.886 0.586 5.76 6.88 8.05
                                          1 14580
## sig.y 43.158 9.252 29.12 41.77
                                  65.05
                                          1 26513
## x2[6] 0.431 0.495 0.00 0.00 1.00
                                          1 21329
## x3[6] 24.807 3.992 17.01 24.78 32.77
                                          1 24376
## y[6]
        184.000 0.000 184.00 184.00 184.00 NaN
```

### Some due diligence on our computational work

MCMCtrace(opt1.JAGS, params=c("beta3", "sig.y"), pdf=F)



Thoughts: Under-the-hood, exactly what distribution are the Monte Carlo draws (approximately) coming from?

Thoughts: Hall-pass that freed me from having a model for  $X_1$ ?

More space for thoughts?

# Thoughts: In concept at least could I have done the computing in the "collapsed" frame of reference?

$$f(\theta) \prod_{i=i}^{n} f(observed_i | \theta)$$

## Collapsed, for instance:

#### nhanes2[c(3,6),]

```
## age bmi hyp chl
## 3 20-39 NA no 187
## 6 60-99 NA <NA> 184
```

# Collapsed versus Augmented: Two different strategies for computing the same thing

Collapsed:

$$f(\theta|\text{observed}) \propto f(\text{observed}|\theta)f(\theta)$$

#### Augmented:

$$f(\theta|\text{observed}) = \int f(\theta, \text{latent}|\text{observed})d\text{latent}$$

Any more thoughts?