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

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September 15, 2022

Missing data

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

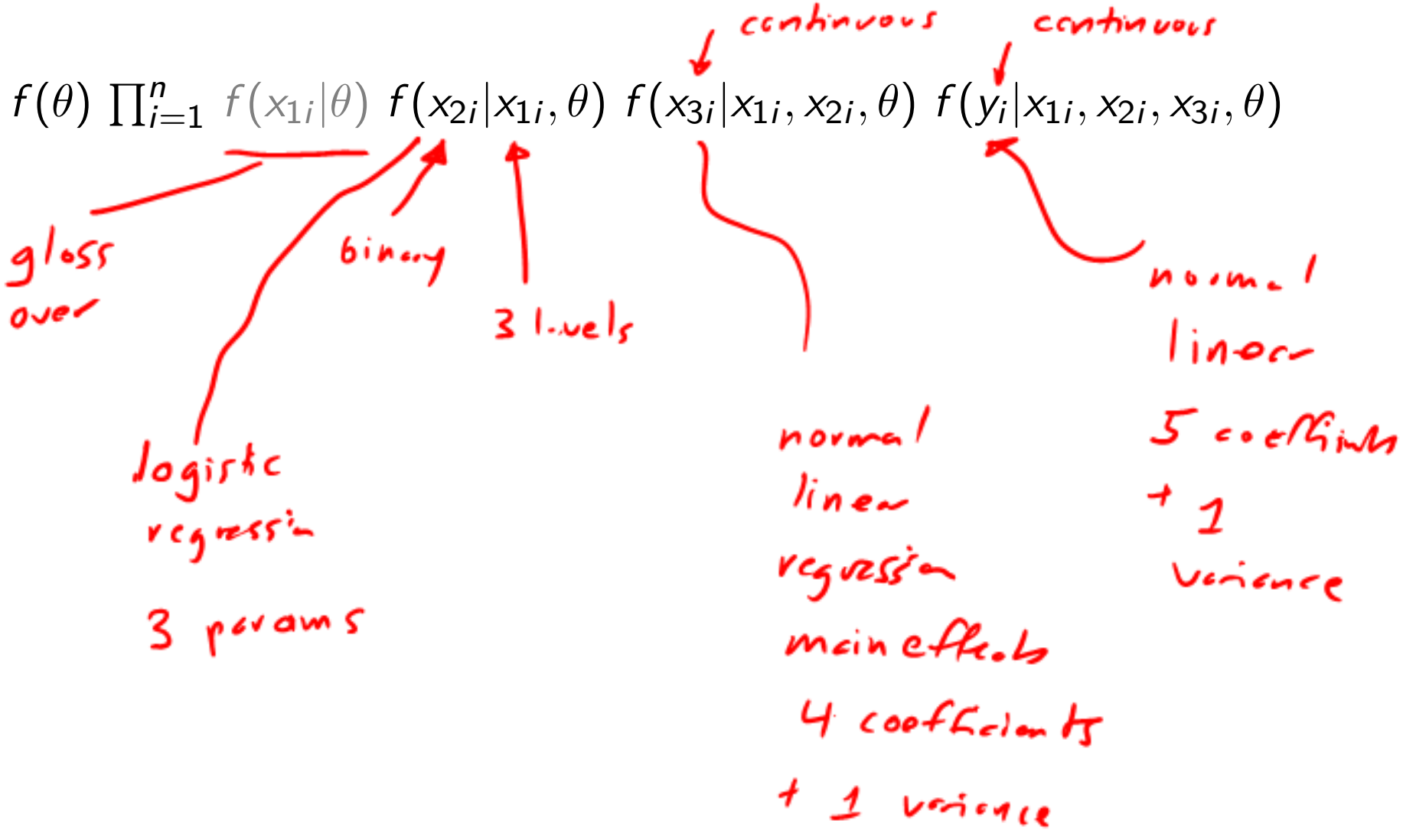
```
summary(nhanes2)
```

```
##     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] +
                         alpha1b*x1b[i]

    x3[i] ~ dnorm(mn.x3[i], prec.x3)
      mn.x3[i] <- kappa0 + kappa1a*x1a[i] +
                  kappa1b*x1b[i]+kappa2*x2[i]

    y[i] ~ dnorm(mn.y[i], prec.y)
      mn.y[i] <- beta0 + beta1a*x1a[i] + beta1b*x1b[i] +
                 beta2*x2[i] + beta3*x3[i]
  }
"
```

Toward generative model (3 of 3)

```
prior.string <- "
  alpha0 ~ dnorm(0, 0.1)
  alpha1a ~ dnorm(0, 0.1)
  alpha1b ~ dnorm(0, 0.1)

  kappa0 ~ 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 ~ dnorm(0, 0.01)
  beta3 ~ dnorm(0, 0.01)
  prec.y ~ dgamma(0.5, 0.5)
  sig.y <- sqrt(1/prec.y)
"
```

bit of a rabbit hole

prior SDs

$= \sqrt{\frac{1}{.1}} \sim 3$

quite wide for log odds or log odd ratios

prior SD's

$\sqrt{\frac{1}{.01}} = 10$

wide in present context?

Housekeeping

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

Pause to comment on this prior and stat model specification

Almost have supplied a joint distribution of everything

could / should have added something like

$x_1 \sim \text{Mult}(p_1, p_2, 1-p_1-p_2)$

$p \sim \text{prior}$

come back to this

Turn the JAGS crank

runs - even though some NA elements

```
### generative model, data go in
mod <- jags.model(textConnection(genmod.string),
         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$chl,
                     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]"))
```

keep output for these ones

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:
##
##             Mean     SD Naive SE Time-series SE
## 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:
```

posterior uncertainty about these LATENT variables but not about this OBSERVED value

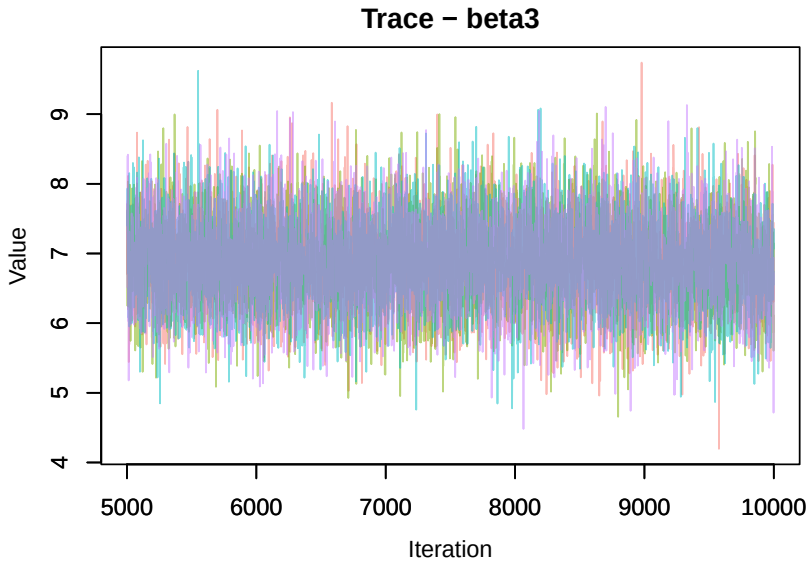
Or

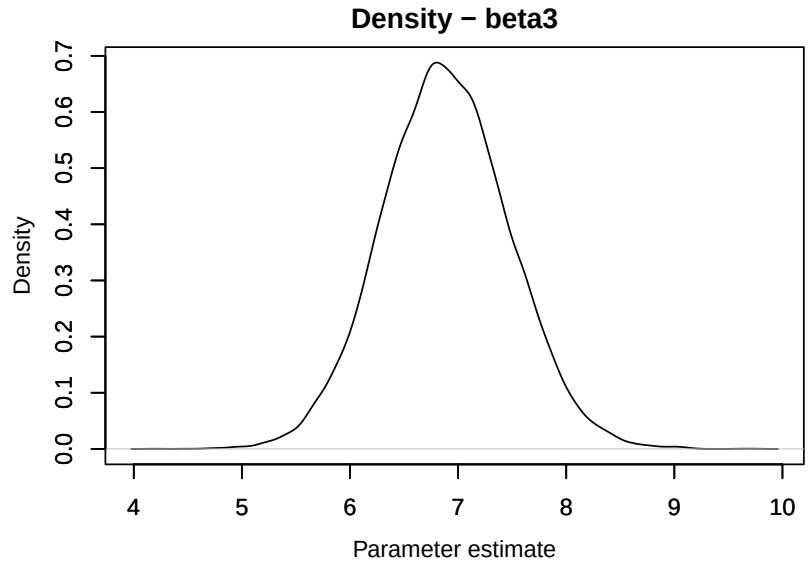
```
require(MCMCvis)
MCMCsummary(opt1.JAGS)
```

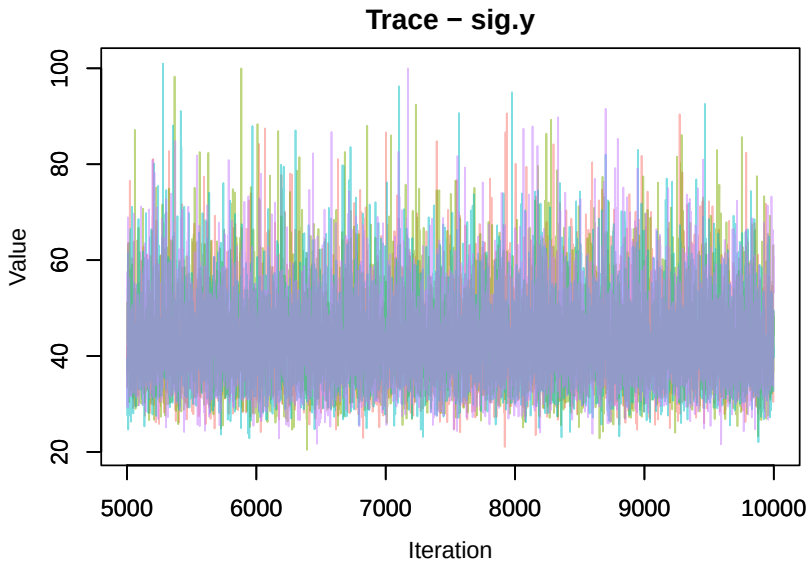
```
##              mean    sd   2.5%    50%  97.5% Rhat n.eff
## beta1a      5.427 9.354 -13.00   5.43  23.67    1 31926
## beta1b      7.789 9.838 -11.54   7.87  27.06    1 31076
## beta2       4.614 9.455 -13.96   4.65  23.04    1 34592
## beta3       6.886 0.586   5.76   6.88   8.05    1 14580
## 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     0
```

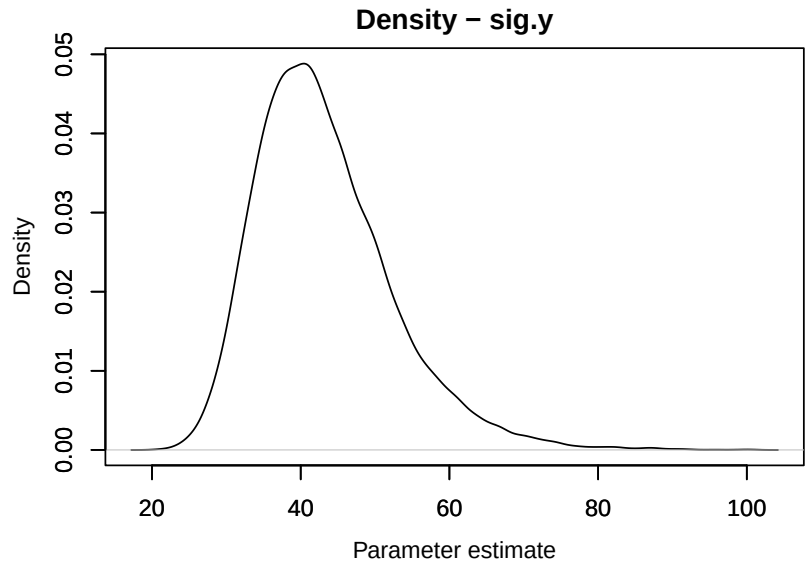
Some due diligence on our computational work

```
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?

$$f\left(\text{parms}, x_2^{(mis)}, x_3^{(mis)}, y^{(mis)} \,\middle|\, x_1, x_2^{(obs)}, x_3^{(obs)}, y^{(obs)}\right)$$

proportional to the expression on slide 3

as a function of stuff on left,

for fixed vals of stuff on right

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

X_1 is observed for everyone

- an X_1 model would have no downstream impact

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),]
```

x_1 x_3 x_2 Y

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

for patient 3

$$f_{Y,X_2|X_1}(187,0|0) =$$

$$\int f_{X_2|X_1}(0,0)\, f_{X_3|X_1,X_2}(z|0,0)\, f_{Y|X_3,X_2,X_1}(187|z,0,0)\, dz$$

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

foreshadowing

Collapsed:

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

if feasible, make this the JAGS input

we've seen this as the JAGS output

Augmented:

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

Any more thoughts?