KU Leuven Summer School Segment 2C Missing (Perhaps?) Not at Random

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September 15, 2022

Minimal Working Example

Creating the problem

```
r <- rbinom(n, size=1,
    prob=expit(0.1 + 0.3*x - 0.6*x*y))

x.obs <- rep(NA, n); x.obs[r==1] <- x[r==1]
dat <- data.frame(x=x.obs, y=y)</pre>
```

MAR analysis (i)

```
genmod.mar.string <- "</pre>
model {
  alpha ~ dnorm(0, 0.1)
  beta0 \sim dnorm(0, 0.1)
  beta1 \sim dnorm(0, 0.1)
  for (i in 1:n) {
    x[i] ~ dbern(pr.x)
    y[i] ~ dbern(pr.y[i])
    logit(pr.y[i]) <- beta0 + beta1*x[i]</pre>
  logit(pr.x) <- alpha</pre>
}"
```

MAR analysis (ii)

```
### generative model, data go in
mod <- jags.model(</pre>
  textConnection(genmod.mar.string),
  data=list(x=dat$x, y=dat$y,
            n=dim(dat)[1]).
         n.chains=3)
update(mod, 2000) # burn-in
### MC output comes out
opt.mar.JAGS <- coda.samples(mod, n.iter=15000,
  variable.names=c("alpha","beta0","beta1"))
```

MAR Analysis (iii)

MCMCsummary(opt.mar.JAGS)

```
## mean sd 2.5% 50% 97.5% Rhat n.eff
## alpha -0.382 0.0626 -0.505 -0.382 -0.2590 1 11722
## beta0 -0.843 0.0744 -0.991 -0.843 -0.6988 1 6559
## beta1 -0.217 0.1446 -0.500 -0.216 0.0629 1 5586
```

Now explictly model the missingness

```
statmod.mnar.string <- "
for (i in 1:n) {
  x[i] ~ dbern(pr.x)
  y[i] ~ dbern(pr.y[i])
  logit(pr.y[i]) <- beta0 + beta1*x[i]</pre>
  r[i] ~ dbern(pr.r[i])
  logit(pr.r[i]) <- gamma0 + gamma1*y[i] +</pre>
    gamma2*x[i] + (gamma3-gamma2)*x[i]*v[i]
logit(pr.x) <- alpha"</pre>
```

With this prior specification

```
prior.mnarA.string <- "
    alpha ~ dnorm(0, 0.1)
    beta0 ~ dnorm(0, 0.1)
    beta1 ~ dnorm(0, 0.1)
    gamma0 ~ dnorm(0, 0.1)
    gamma1 ~ dnorm(0, 0.1)
    gamma2 ~ dnorm(0, 100)
    gamma3 ~ dnorm(0, 100)"</pre>
```

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

Any pertinent remarks about our generative model?

Turn the crank

```
### generative model, data go in
mod <- jags.model(</pre>
  textConnection(genmod.mnarA.string),
  data=list(x=dat$x, y=dat$y,
            r=as.vector(!is.na(dat$x)),
            n=dim(dat)[1]),
           n.chains=3)
update(mod,2000) # burn-in
### MC output comes out
opt.mnarA.JAGS <- coda.samples(</pre>
 mod,
 n.iter=15000,
  variable.names=c("alpha","beta0","beta1",
  "gamma0", "gamma1", "gamma2", "gamma3"))
```

And report posterior quantities

MCMCsummary(opt.mnarA.JAGS)

```
##
                      sd
                           2.5% 50% 97.5% Rhat n.eff
              mean
## alpha -0.381089 0.0719 -0.5211 -0.38133 -0.2394
                                                     6076
## beta0 -0.844381 0.0793 -1.0003 -0.84397 -0.6912
                                                   1 4669
## beta1 -0.214351 0.1606 -0.5323 -0.21375 0.0977
                                                   1 4050
                                                   1 6141
## gamma0 0.172698 0.0681 0.0415 0.17162
                                         0.3076
## gamma1 -0.236507 0.1144 -0.4625 -0.23676 -0.0136
                                                   1 8084
## gamma2 0.000243 0.0993 -0.1935 0.00073 0.1917
                                                     5126
## gamma3 -0.001862 0.0995 -0.1971 -0.00177 0.1926
                                                   1 10451
```

And now the same with this prior specification

```
prior.mnarB.string <- "
    alpha ~ dnorm(0, 0.1)
    beta0 ~ dnorm(0, 0.1)
    beta1 ~ dnorm(0, 0.1)
    gamma0 ~ dnorm(0, 0.1)
    gamma1 ~ dnorm(0, 0.1)
    gamma2 ~ dnorm(0, 25)
    gamma3 ~ dnorm(0, 25)"</pre>
```

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

Crank

```
### generative model, data go in
mod <- jags.model(</pre>
  textConnection(genmod.mnarB.string),
  data=list(x=dat$x, y=dat$y,
    r=as.vector(!is.na(dat$x)),
    n=dim(dat)[1]),
  n.chains=3)
update(mod, 2000) # burn-in
### MC output comes out
opt.mnarB.JAGS <- coda.samples(</pre>
 mod,
 n.iter=15000,
  variable.names=c("alpha","beta0","beta1","gamma0",
    "gamma1", "gamma2", "gamma3"))
```

Answer

MCMCsummary(opt.mnarB.JAGS)

```
##
                     sd
                           2.5% 50% 97.5% Rhat n.eff
            mean
## alpha -0.37978 0.0951 -0.56618 -0.37993 -0.1932
                                                  1 2213
## beta0 -0.84465 0.0917 -1.02539 -0.84368 -0.6687
                                                  1 2496
## beta1 -0.21456 0.1987 -0.60383 -0.21329 0.1720
                                                  1 2152
                                                  1 1835
## gamma0 0.17851 0.1002 -0.00844 0.17576 0.3863
## gamma1 -0.23858 0.1501 -0.53573 -0.23850 0.0576
                                                  1 2548
## gamma2 -0.00209 0.2014 -0.39610 -0.00159 0.3953
                                                  1 1579
## gamma3 -0.00483 0.2019 -0.40203 -0.00533 0.3888
                                                     3619
```

Take a bit of stock

Recall γ_2 , γ_3 describe $\log OR(R, X|Y=y)$

quality of prior SDs posterior SDs numerical approximation

Adjective soup

 $\begin{array}{ccc} {\rm MAR} & {\rm MNAR} \\ \gamma_2=\gamma_3=0 \ {\rm known} & \gamma_2,\gamma_3 \ {\rm unknown} \\ {\rm (and \ don't \ need \ to \ model} \ R) \end{array}$

Folk theorem

Important distinction related to folk theorem