# Missing Data and Imputation

Hoff Chapter 7, GH Chapter 25

April 21, 2017

#### Bednets and Malaria

- Y:presence or absence of parasites in a blood smear
- AGE: age of child
- ▶ BEDNET: bed net use (exposure)
- GREEN:greenness of the surrounding vegetation based on satellite photography
- ▶ PHC: whether a village is part of a primary health-care system

#### Bednets and Malaria

```
malaria = read.csv("gambia.dat", header=TRUE)
summary(malaria)
                    AGE
                                  BEDNET
                                                 GREEN
       :0.0000 Min.
Min.
                      :1.000
                             Min.
                                    :0.0000 Min.
                                                    :28.85
                                                            Min.
1st Qu.:0.0000 1st Qu.:1.000 1st Qu.:0.0000
                                             1st Qu.:40.85
                                                            1st
Median :0.0000 Median :2.000
                             Median :1.0000 Median :40.85
                                                            Medi
Mean :0.3093 Mean :2.399
                             Mean :0.7049 Mean :39.84
                                                            Mean
3rd Qu.:1.0000 3rd Qu.:3.000 3rd Qu.:1.0000 3rd Qu.:40.85
                                                            3rd
Max. :1.0000
               Max.
                      :4.000
                             Max. :1.0000 Max. :47.65
                                                            Max.
                              NA's :317
```

39% missing

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- Analysis depends on assumptions about missingness

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Cannot tell from data

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- Model Based Methods

- $(Y_{i,1}, Y_{i,2}, Y_{i,3}, Y_{i,4}, Y_{i,5})$
- $(O_{i,1}, O_{i,2}, O_{i,3}, O_{i,4}, O_{i,5})$

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Marginal Model for observed data

$$\begin{aligned} p(o_i, y[o_i = 1] \mid \theta) &= p(o_i) p(y[o_i = 1] \mid \theta) \\ &= p(o_i) \int \left\{ p(y_{i,1}, y_{i,2}, y_{i,3}, y_{i,4}, y_{i,5} \mid \theta) \prod_{y_{i,j} \ni o_{i,j} = 0} dy_{i,j} \right] \end{aligned}$$

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Integrate over the missing variables to obtain the likelihood



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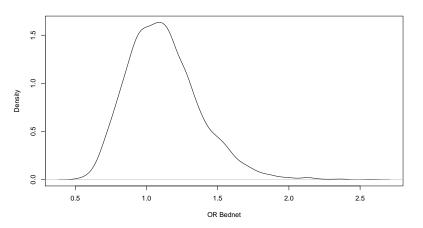
Averaging over the draws of  $Y_{miss}$  "integrates" marginalizes over the missing dimensions

#### **JAGS Model**

```
model = function() {
 for (i in 1:N) {
 Y[i] ~ dbern(p[i])
  logit(p[i]) <- alpha + beta.age*AGE[i] + beta.bednet*BEDNET[i]</pre>
                 +beta.green*GREEN[i] + beta.phc*PHC[i]
   # model for missing exposure variable
for (i in 1:N) {
  BEDNET[i] ~ dbern(q) #prior model for whether or not child
                       # sleeps under treated bednet
  #uniform prior (uniform) on prob of sleeping under bednet
  q ~ dbeta (1,1)
 #vaque priors on regression coefficients
   alpha ~ dnorm(0,0.00000001)
   beta.age ~ dnorm(0,0.00000001)
   beta.bednet ~ dnorm(0,0.00000001)
   beta.green ~ dnorm(0,0.00000001)
  beta.phc ~ dnorm(0,0.00000001)
  # calculate odds ratios of interest
  OR. bednet <- exp(beta.bednet) #OR of malaria for children using bedne
```

## Posterior Density

```
theta = as.data.frame(sim$BUGSoutput$sims.matrix)
plot(density(theta[,1]), xlab="OR Bednet", main="")
```

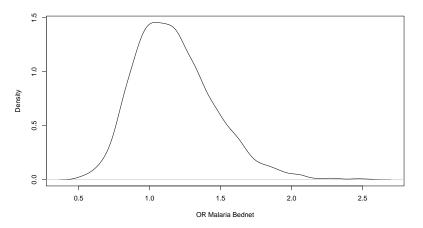


#### JAGS Model

```
model2 = function() {
 for (i in 1:N) {
 Y[i] ~ dbern(p[i])
  logit(p[i]) <- alpha + beta.age*AGE[i] + beta.bednet*BEDNET[i]</pre>
                 +beta.green*GREEN[i] + beta.phc*PHC[i]
   # model for missing exposure variable
for (i in 1:N) {
  BEDNET[i] ~ dbern(q[i]) #prior model for bednet use
  logit(q[i]) <- gamma[1] + gamma[2]*PHC[i] #allow prob depend on PHC
 #vaque priors on regression coefficients
   gamma[1] ~ dnorm(0,0.00000001)
   gamma[2] ~ dnorm(0,0.00000001)
   alpha ~ dnorm(0,0.00000001)
   beta.age ~ dnorm(0,0.00000001)
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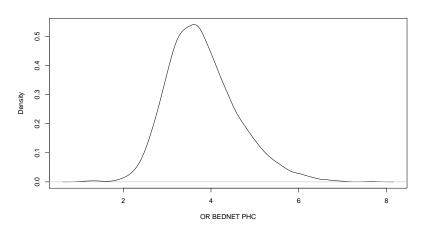
### Posterior Density

```
theta.phc = as.data.frame(sim.phc$BUGSoutput$sims.matrix)
plot(density(theta.phc[,1]), xlab="OR Malaria Bednet", main="")
```



#### Posterior Density

plot(density(theta.phc[,"OR.bednet.PHC"]), xlab="OR BEDNET PHC", main="



#### intervals

```
exp(confint(glm(Y ~ . , data=malaria, family=binomial), parm="BEDNET"))
   2.5 % 97.5 %
0.7104643 1.7646674
HPDinterval(as.mcmc(theta))
                 lower upper
OR.bednet 0.6730938 1.6168561
beta.bednet -0.3414251 0.5189801
deviance 1564.7933630 1579.4668447
attr(,"Probability")
[1] 0.95
HPDinterval(as.mcmc(theta.phc))
                   lower
                             upper
OR.bednet 0.6752977 1.742158
OR.bednet.PHC 2.4186453 5.499151
deviance 1524.1955374 1539.457613
attr(,"Probability")
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