WEB APPENDIX

R Code and Results:

```
mydir='Q:\\ DataAnalysis\\NORM'
setwd(mydir)
set.seed(9252)
m=100 # number of imputations
###########################################################
Data1
###########################################################
data1<- read.csv("Q:/Data/ dataset1.csv")
##############################################################################

data1<-as.matrix(data1)
s <- prelim.norm(data1)
thetahat <- em.norm(s)
rngseed(1234567)
mylogit<-NULL

theta<-da.norm(s,thetahat,steps=20,showits=TRUE)
getparam.norm(s,theta) # look at result

##Data augmentation
da.list<-list()
 #out<-da.norm(pre,theta.hat,steps=20,return.ymis=TRUE)
 for (i in 1:1000){print(i)
          out<-da.norm(s,thetahat,steps=1)
          theta.hat<-out
          da.list[[i]]<-getparam.norm(s,out)
          }

temp<-list()
for (i in 1:1000){temp[[i]]<-da.list[[i]][[1]][[2]]}
 pdf("DA_acf.pdf")
 par(mfrow=c(2,1))
 acf(unlist(temp),main="All Draws - No Burn-in")
 acf(unlist(temp[-c(1:100)]),main="Burn-in 100 Draws")
 dev.off()

pdf("TS_plot.pdf")
plot(unlist(temp),type="l",xlab="Iteration", ylab="Parameter Estimate")
 dev.off()
```

```
for(i in 1:m){

a<-imp.norm(s, thetahat, data1)
a<-as.data.frame(a)
a$abort[a$abort<=0.5]<-0
a$abort[a$abort>0.5]<-1
a$abort<-as.factor(a$abort)

a$smoke[a$smoke<=0.5]<-0
a$smoke[a$smoke>0.5]<-1
a$smoke<-as.factor(a$smoke)

mylogit[[i]] <- glm(abort ~ smoke + black + other + age + bmi, data = a, family =
"binomial")
                }

mylogit<-as.mira(mylogit)
analysis1<-summary(pool(mylogit, method="small sample"))
write.table(analysis1, file="Data1NORMResults.csv", sep=",", col.names=T,
row.names=T)

###########
# Plots
#######################################################################

aggr(data1, delimiter = NULL, plot = TRUE, numbers=T, prop=t)

par(mfrow=c(3,2))
matrixplot(data1, sortby='abort', interactive=F)
matrixplot(data1, sortby='smoke', interactive=F)
matrixplot(data1, sortby='black', interactive=F)
matrixplot(data1, sortby='other', interactive=F)
matrixplot(data1, sortby='age', interactive=F)
matrixplot(data1, sortby='bmi', interactive=F)
```

SAS Example Code

###

```
data missing;
set missing.mnar;  /* change dataset */
run;
proc freq data=missing;
tables abort;
where bmi~=. and smoke~=.;
run;
proc logistic data=missing desc ;
model abort=smoke bmi age black other/rl;
ods output ParameterEstimates=parm CLoddsWald=or;
run;
proc mi data = missing nimpute = 20 seed = 11 out=data_imp
  minimum = . 0 0 . . . .
  maximum = . 1 1 . . . .
;
  var site  abort  smoke  black  other  age  bmi;
run;
data data_imp;
  set data_imp;
  if abort < 0.5 then abort = 0;
  else abort = 1;
if smoke < 0.5 then smoke = 0;
  else smoke = 1;
run;
proc logistic data=data_imp desc ;
model abort=smoke bmi age black other/rl;
by _imputation_;
ods output parameterestimates=logparms;
run;
proc mianalyze parms=logparms;
  modeleffects intercept smoke bmi age black other;
  ods output parameterestimates = parmimp;
run;
```