Assignment 1 - Incomplete Data Analysis

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Note:*The R code for Question 3 and Question 4 are available via the link (https://github.com/ZheWANG331/IDA-Assignment-1.git) to the repository of Github.*

1.

(a) The probability of ALQ being missing for those with ALQ=No is **(ii) 0.3**.

Reason: ALQ is MCAR,which means the missing of ALQ is completely at random and is unrelated to the value Yes/No

(b) ALQ being MAR given gender means so **(ii) The probability of ALQ being missing is independent of the Yes/No value of ALQ after adjusting for gender**.

Reason: ALQ is MAR given gender, which means the missing of ALQ depends only on gender information but it is further unrelated to the specific missing values Yes/No. Therefore, after adjusting for gender, the probability of ALQ being missing is independent of the value.

(c) What is the probability of ALQ being missing for women? **(iii) It is impossible to conclude from the information given**.

Reason: As mentioned in (b), ALQ is MAR given gender, which means the missing of ALQ depends only on gender, but by the given information, we cannot get the certain probability of missing in each gender.

2. The largest possible subsample under a complete case analysis is **90**, the smallest is **0**.

Reason: Complete case analysis is to exclude the data for any case/indivisual that has one or more missing values and get a subsample.

The largest possible subsample is the case that all the missing values of 10 variales occur in the same 10 objects and we only need to delete these 10;

the smallest possible subsample is the case that all the missing values of 10 variables occur in different objects, which means each object has exactly 1 missing value, so we have to delete all of them, so 0 in subsample.

3.

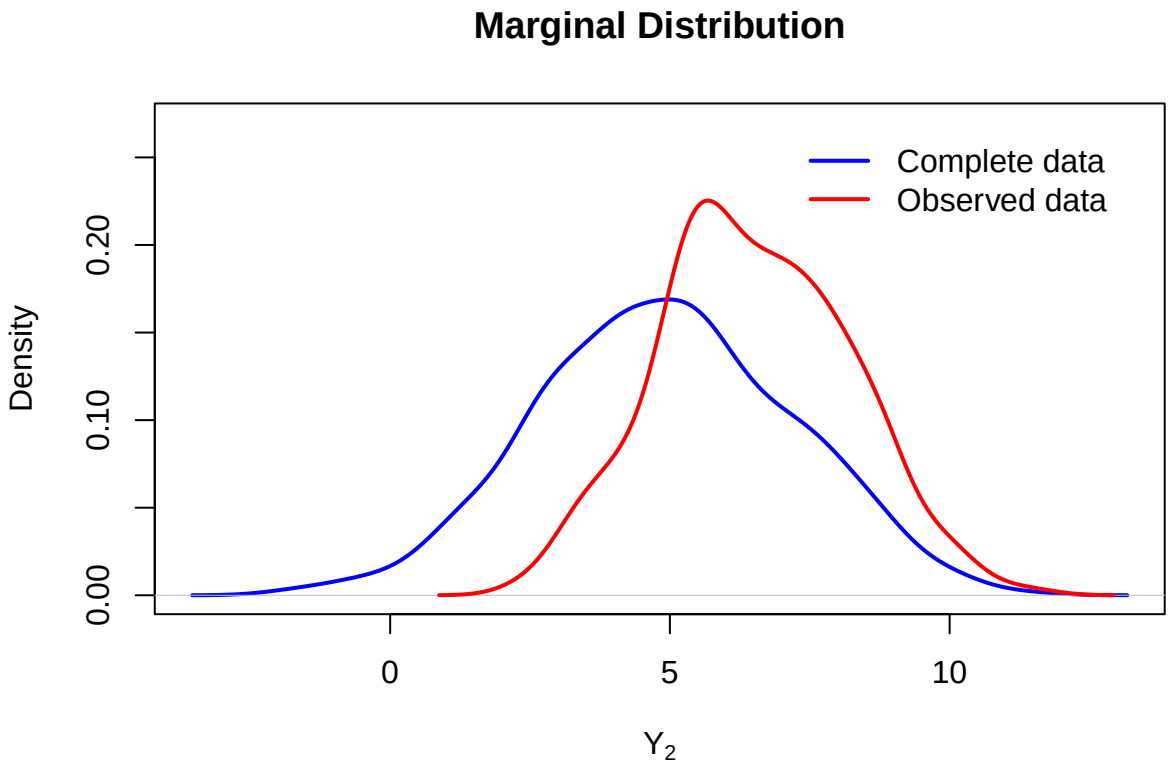
```r
#simulating a complete dataset
set.seed(331)
Z_1 <- rnorm(500,0,1)
Z_2 <- rnorm(500,0,1)
Z_3 <- rnorm(500,0,1)
Y <- list(Z_1 +1, 5 + 2 * Z_1 + Z_2)
y_1 <- Y[[1]]
y_2 <- Y[[2]]
```

(a) MAR

Reason: While a = 2 and b = 0, Y_2 is missing if $2 \times (Y_1 - 1) + Z_3 < 0$, the missing of Y_2 depends only on fully observed data Y_1 and Z_3, but not Y_2 itself, so this mechanism is MAR.

```r
#Stimulate dataset with missing value of MAR
y_2_mis1 <- ifelse(((2 * y_1 - 2 + Z_3) < 0), NA, y_2)

#plotting the marginal distribution
plot(density(y_2), lwd = 2, col = "blue", xlab = expression(Y[2]),
main = "Marginal Distribution", ylim = c(0, 0.27))
lines(density(y_2_mis1, na.rm = TRUE), lwd = 2, col = "red")
legend(7, 0.27, legend = c("Complete data", "Observed data"),
col = c("blue", "red"), lty = c(1,1), lwd = c(2,2), bty ="n")
```



Comment: As expected, the complete data of $Y_2 \sim N(5, 5)$. Under this MAR mechanism, observed data has a greater mean and a smaller variance. It is probably because Y_2 tends to be missing while Y_1 is smaller than the mean 1, i.e., Z_1 is smaller than 0, as a result, smaller Y_2 tends to be missing.

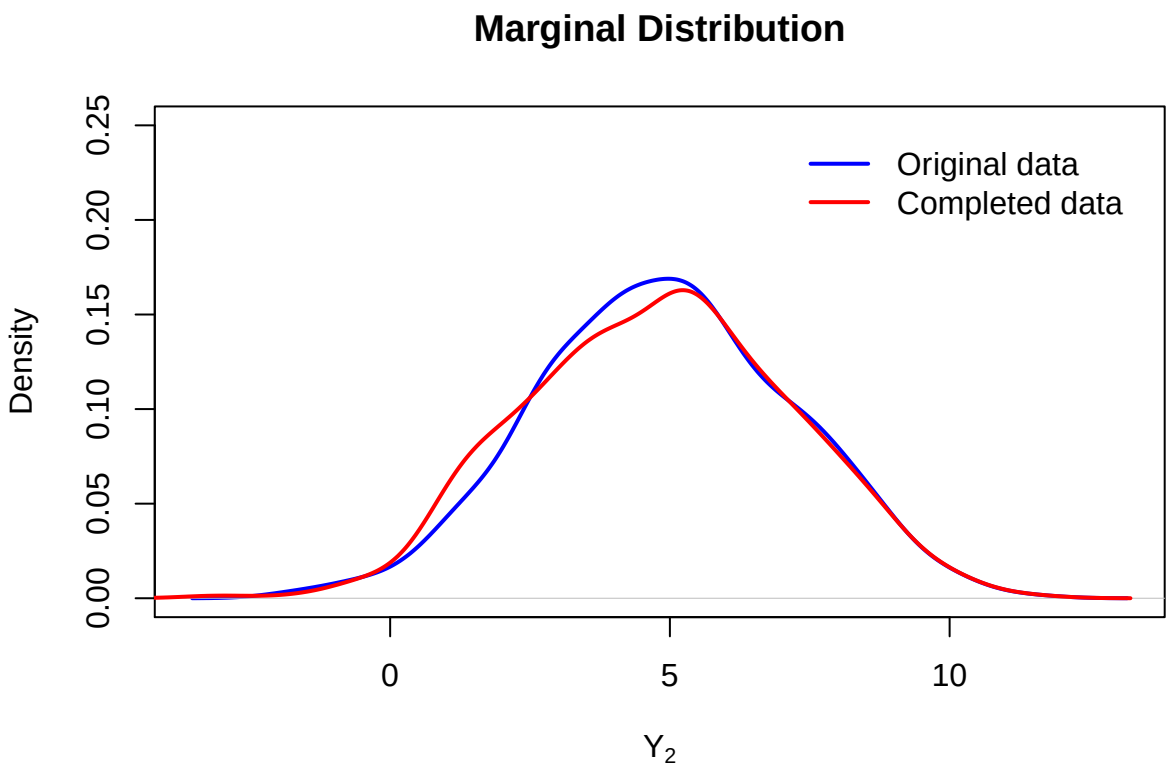
(b)

```r
#stochastic regression imputation
Y_mis1 <- list(y_1, y_2_mis1)

fit1 <- lm(y_2_mis1~y_1)
predicted_sri1 <- predict(fit1, newdata = Y_mis1) + rnorm(length(y_1), 0, sigma(fit1))

y_2_sri1 <- ifelse(((2 * y_1 - 2 + Z_3) < 0), predicted_sri1, y_2)

#the marginal distribution
plot(density(y_2), lwd = 2, col = "blue", xlab = expression(Y[2]),
main = "Marginal Distribution", ylim = c(0, 0.25))
lines(density(y_2_sri1), lwd = 2, col = "red")
legend(7, 0.25, legend = c("Original data", "Completed data"),
col = c("blue", "red"), lty = c(1,1), lwd = c(2,2), bty ="n")
```



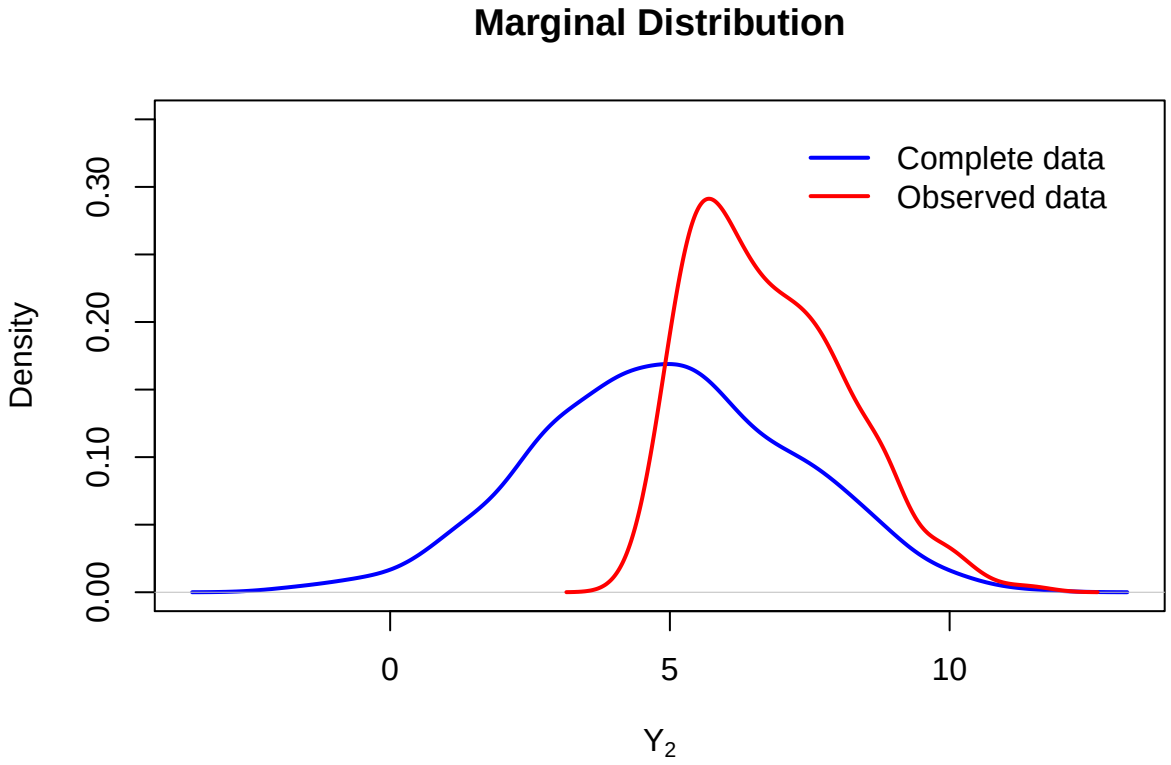
Comment: The data imputed by using stochastic regression imputation is quite similar with the original data especially the right half.

(c) MNAR

Reason: While a = 0 and b = 2, the missing of Y_2 depends on Z_3 and Y_2 itself, recall that the definition of MNAR is the probability of missing values is related to the specific values that should have been obtained, so this mechanism is MNAR.

```
#Stimlate dataset with missing value of MNAR
y_2_mis2 <- ifelse(((2 * y_2 - 10 + Z_3) < 0), NA, y_2)

#plotting the marginal distribution
plot(density(y_2), lwd = 2, col = "blue", xlab = expression(Y[2]),
main = "Marginal Distribution", ylim = c(0, 0.35))
lines(density(y_2_mis2, na.rm = TRUE), lwd = 2, col = "red")
legend(7, 0.35, legend = c("Complete data", "Observed data"),
col = c("blue", "red"), lty = c(1,1), lwd = c(2,2), bty ="n")
```



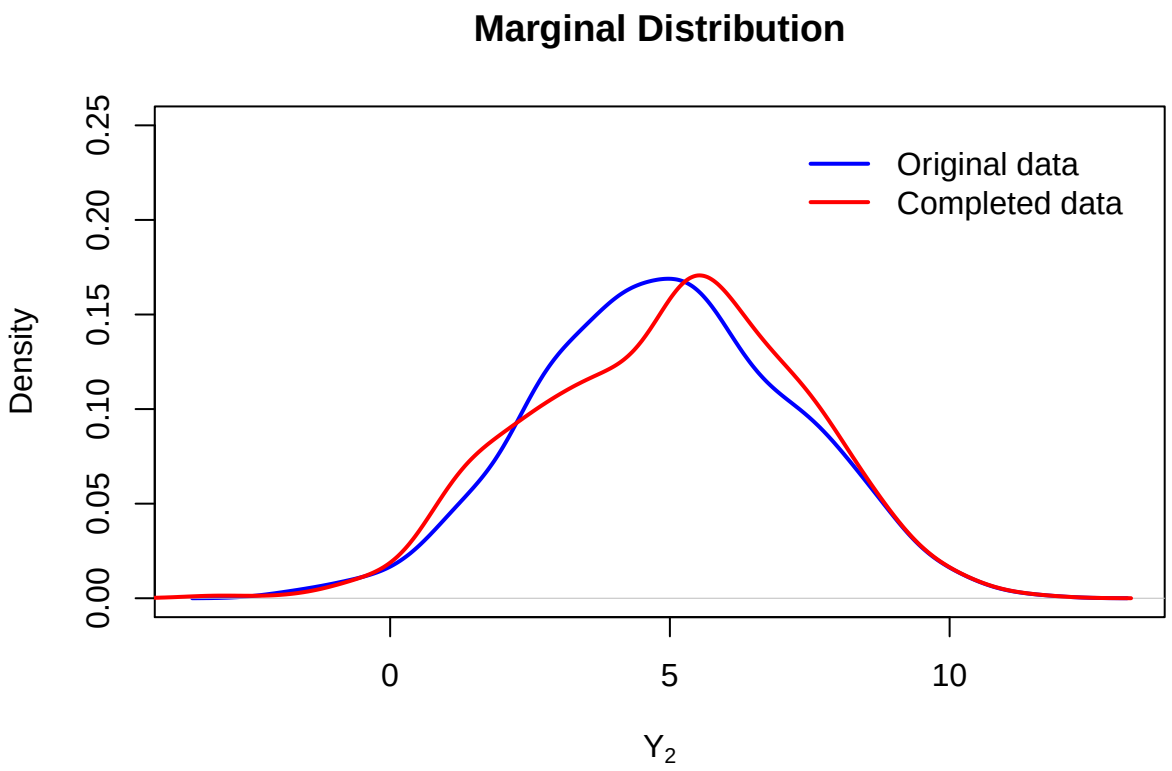
Comment: As we can observe, MNAR case is more extreme in terms of the dissimilarities between the two distributions than the MAR case. Under the MNAR mechanism, the miss dataset are mainly distributed on the left half($Y_2 < 5$). This is probably because Y_2 tends to be missing when $Y_2 < 5$.

(d)

```
#stochastic regression imputation
Y_mis2 <- list(y_1, y_2_mis2)

fit2 <- lm(y_2_mis2~y_1)
predicted_sri2 <- predict(fit2, newdata = Y_mis2) + rnorm(length(y_1), 0, sigma(fit2))
y_2_sri2 <- ifelse(((2 * y_2 - 10 + Z_3) < 0), predicted_sri1, y_2)

#the marginal distribution
plot(density(y_2), lwd = 2, col = "blue", xlab = expression(Y[2]),
main = "Marginal Distribution", ylim = c(0, 0.25))
lines(density(y_2_sri2), lwd = 2, col = "red")
legend(7, 0.25, legend = c("Original data", "Completed data"),
col = c("blue", "red"), lty = c(1,1), lwd = c(2,2), bty ="n")
```



Comment: We can observe that data after imputation shows more difference on both left half and right half compared with 3(b). So it seems that the performance of stochastic regression imputation on MNAR case is not as good as on MAR case.

4.

(a) The overall recovery time mean provided by a complete case analysis is 19.27273 and the associated standard error is 2.603013.

The correlations between the recovery time and the dose is 0.2391256,

The correlations between the recovery time and blood pressure is -0.01952862.

```
#load data
load("databp.Rdata")

#complete case analysis
ind_cc <- which(is.na((databp$recovtime)) == FALSE)
data_cc=databp[ind_cc,]

#mean value of the recovery time
Rmean <- mean(data_cc$recovtime)
Rmean
```

```
## [1] 19.27273
```

```
#standard error  of the recovery time
sd(data_cc$recovtime)/sqrt(nrow(data_cc))
```

```
## [1] 2.603013
```

```
#correlations between the recovery time and the dose
cor(data_cc$recovtime, data_cc$logdose, use = "complete")
```

```
## [1] 0.2391256
```

```
#correlations between the recovery time and blood pressure
cor(data_cc$recovtime, data_cc$bloodp, use = "complete")
```

```
## [1] -0.01952862
```

(b) The mean recovery time using mean imputation is 19.27273.

The overall recovery time mean provided by mean imputation is 2.284135 and the associated standard error is 2.284135.

The correlations between the recovery time and the dose is 0.2150612,

The correlations between the recovery time and blood pressure is -0.01934126.

```
#mean imputation
Recovtime_mi <- ifelse(is.na(databp$recovtime), Rmean, databp$recovtime)

#mean value of the recovery time after mean imputation
mean(Recovtime_mi)
```

```
## [1] 19.27273
```

```
#standard error  of the recovery time after mean imputation
sd(Recovtime_mi)/sqrt(length(Recovtime_mi))
```

```
## [1] 2.284135
```

```
#correlations between the recovery time and the dose after mean imputation
cor(Recovtime_mi, databp$logdose)
```

```
## [1] 0.2150612
```

```
#correlations between the recovery time and blood pressure after mean imputation
cor(Recovtime_mi, databp$bloodp)
```

```
## [1] -0.01934126
```

(c) The overall recovery time mean provided by mean regression imputation is 19.44428 and the associated standard error is 2.312845

The correlations between the recovery time and the dose is 0.2801835,

The correlations between the recovery time and blood pressure is -0.01113646

```
#mean regression imputation
fit <- lm(databp$recovtime ~ databp$logdose + databp$bloodp, data = databp)
predicted_ri <- predict(fit, newdata = databp)
Recovtime_ri <- ifelse(is.na(databp$recovtime), predicted_ri, databp$recovtime)

#mean value of the recovery time after regression imputation
mean(Recovtime_ri)
```

```
## [1] 19.44428
```

```
#standard error  of the recovery time after regression imputation
sd(Recovtime_ri)/sqrt(length(Recovtime_ri))
```

```
## [1] 2.312845
```

```
#correlations between the recovery time and the dose after regression imputation
cor(Recovtime_ri, databp$logdose)
```

```
## [1] 0.2801835
```

```
#correlations between the recovery time and blood pressure after regression imputation
cor(Recovtime_ri, databp$bloodp)
```

```
## [1] -0.0111364
```

(d) The overall recovery time mean provided by stochastic regression imputation is 20.05764 and the associated standard error is 2.40414.

The correlations between the recovery time and the dose is 0.2701687,

The correlations between the recovery time and blood pressure is 0.02455702.

```
#stochastic regression imputation
predicted_sri <- predict(fit, newdata = databp) + rnorm(nrow(databp), 0, sigma(fit))
Recovtime_sri <- ifelse(is.na(databp$recovtime), predicted_sri, databp$recovtime)

#mean value of the recovery time after regression imputation
mean(Recovtime_sri)
```

```
## [1] 20.05764
```

```
#standard error  of the recovery time after regression imputation
sd(Recovtime_sri)/sqrt(length(Recovtime_sri))
```

```
## [1] 2.40414
```

```
#correlations between the recovery time and the dose after regression imputation
cor(Recovtime_sri, databp$logdose)
```

```
## [1] 0.2701687
```

```
#correlations between the recovery time and blood pressure after regression imputation
cor(Recovtime_sri, databp$bloodp)
```

```
## [1] 0.02455702
```

Extra care: In some cases/examples,stochastic regression imputation can lead to implausible predictions by adding a random noise term. For instance, in this example, it may impute a negative value for the recovery time, which does not make sense.

(e) The overall recovery time mean provided by predictive mean matching is 19.52 and the associated standard error is 2.3238767

The correlations between the recovery time and the dose is 0.2908267,

The correlations between the recovery time and blood pressure is -0.009406132

```
#predictive mean matching
#get the donor list by previous predicted data predicted_ri
donor = 1:nrow(databp)
predicted_mis = ifelse(is.na(databp$recovtime), NA, predicted_ri)

for (i in 1:nrow(databp)){
  donor[i] = databp$recovtime[which.min((predicted_mis - predicted_ri[[i]])**2)]
}

Recovtime_pmm <- ifelse(is.na(databp$recovtime), donor, databp$recovtime)

#mean value of the recovery time after regression imputation
mean(Recovtime_pmm)
```

```
## [1] 19.44
```

```
#standard error  of the recovery time after regression imputation
sd(Recovtime_pmm)/sqrt(length(Recovtime_pmm))
```

```
## [1] 2.464467
```

```
#correlations between the recovery time and the dose after regression imputation
cor(Recovtime_pmm, databp$logdose)
```

```
## [1] 0.3037945
```

```
#correlations between the recovery time and blood pressure after regression imputation
cor(Recovtime_pmm, databp$bloodp)
```

```
## [1] -0.03208685
```

(f) **Advantage of predictive mean matching:** It can avoid some implausible imputation because it choose a closest value to the predicted value from the original dataset, so every single imputation is proper. Predictive mean matching combines the advantages of stochastic regression imputation and hot deck imputation.

Potential problem: Like stochastic regression imputation, it will also attenuate standard errors of the estimates and increase the correlations between variables.

APPENDIX

As for question 4, the position and values of imputation of each method is:

```
#position
ind <- which(is.na((databp$recovtime)) == TRUE)
ind
```

```
## [1]  4 10 22
```

```
#mean imputation
Recovtime_mi[ind]
```

```
## [1] 19.27273 19.27273 19.27273
```

```
#mean regression imputation
Recovtime_ri[ind]
```

```
## [1] 14.26254 21.51562 26.32896
```

```
#stochastic regression imputation
Recovtime_sri[ind]
```

```
## [1] 18.44350 37.95871 21.03881
```

```
#predictive mean matching
Recovtime_pmm[ind]
```

```
## [1] 13 10 39
```