Testing different imputation methods on PUMS (MAR) - MICE

```r
# load dataset: df
load('../../Datasets/ordinalPUMS.Rdata')

# take 10,000 samples: df
set.seed(0)
n = 10000
sample <- sample(nrow(df), size = 10000)
df <- df[sample,]

# create MCAR scneario with 30% chance of missing: df_observed
missing_prob = 0.3
df_observed <- df
missing_col = c(1,3,7,9,10,11)

# Make VEH and WKL MCAR
missing_col_MCAR = c(1,10)
for (col in missing_col_MCAR) {
  missing_ind <- rbernoulli(n,p = missing_prob)
  df_observed[missing_ind, col] <- NA
}

# Make the rest MAR
numeric_df = sapply(df, as.numeric)
normalized_df = t(t(numeric_df-1)/(apply(numeric_df, MARGIN = 2, FUN = max)-1))
missing_col_MAR = c(3,7,9,11)
fully_observed_col = c(2,4,5,6,8)
beta_NP = c(-0.05, -1.5, 0.6, -2, -0.05)
beta0_NP = -0.05
beta_SCHL = c(-3, 3, -0.75, 0.05, -0.2)
beta0_SCHL = 0.05
beta_AGEP = c(0.05, -0.2, 0.05, -1.25, 1)
beta0_AGEP = -0.05
beta_PINCP = c(3, -0.05, -2.5, 0.05, -1)
beta0_PINCP = -0.05

# missing probability for NP
prob_NP = apply(t(t(normalized_df[, fully_observed_col])*beta_NP)+beta0_NP, MARGIN = 1, sum)
prob_NP = exp(prob_NP)/(exp(prob_NP)+1)
indicator = rbernoulli(n, p = prob_NP)
df_observed[indicator, missing_col_MAR[1]] <- NA

# missing probability for SCHL
prob_SCHL = apply(t(t(normalized_df[, fully_observed_col])*beta_SCHL)+beta0_SCHL, MARGIN = 1, sum)
prob_SCHL = exp(prob_SCHL)/(exp(prob_SCHL)+1)
indicator = rbernoulli(n, p = prob_SCHL)
df_observed[indicator, missing_col_MAR[2]] <- NA
```

```
# missing probability for AGEP
prob_AGEP = apply(t(t(normalized_df[, fully_observed_col])*beta_AGEP)+beta0_AGEP, MARGIN = 1, sum)
prob_AGEP = exp(prob_AGEP)/(exp(prob_AGEP)+1)
indicator = rbernoulli(n, p = prob_AGEP)
df_observed[indicator, missing_col_MAR[3]] <- NA

# missing probability for PINCP
prob_PINCP = apply(t(t(normalized_df[, fully_observed_col])*beta_PINCP)+beta0_PINCP, MARGIN = 1, sum)
prob_PINCP = exp(prob_PINCP)/(exp(prob_PINCP)+1)
indicator = rbernoulli(n, p = prob_PINCP)
df_observed[indicator, missing_col_MAR[4]] <- NA

# 30.58% missing
apply(is.na(df_observed), MARGIN = 2, mean)
```

```
##    VEH     MV     NP   RMSP    ENG  MARHT   SCHL RACNUM   AGEP    WKL  PINCP
## 0.3030 0.0000 0.3121 0.0000 0.0000 0.0000 0.2814 0.0000 0.3355 0.3017 0.3011
```

MICE

Create 5 imputed dataset

```
library(mice)
```

```
##
## Attaching package: 'mice'
```

```
## The following objects are masked from 'package:base':
##
##     cbind, rbind
```

```
imputed_df <-  mice(df_observed,m=5,print=F)
```

```
## Warning: Number of logged events: 150
```

Extract the 5 imputed dataset

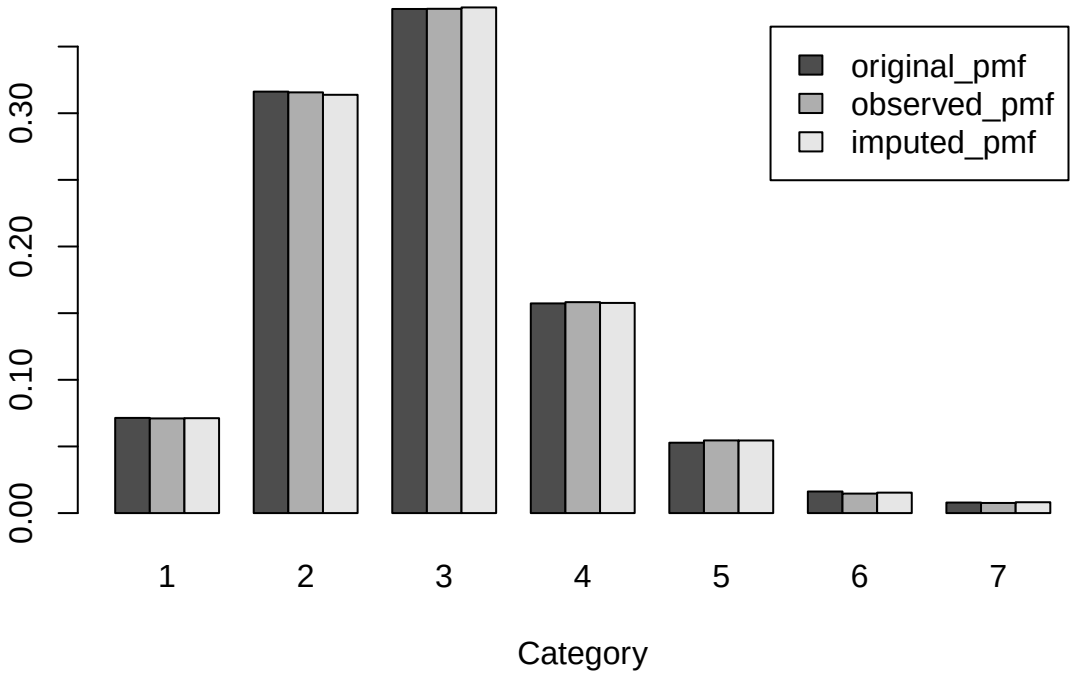
```
d1 <-  complete(imputed_df, 1)
d2 <-  complete(imputed_df, 2)
d3 <-  complete(imputed_df, 3)
d4 <-  complete(imputed_df, 4)
d5 <-  complete(imputed_df, 5)
imputed_sets = rbind(d1, d2, d3, d4, d5)
```

Diagnostics

Assess bivariate joint distribution

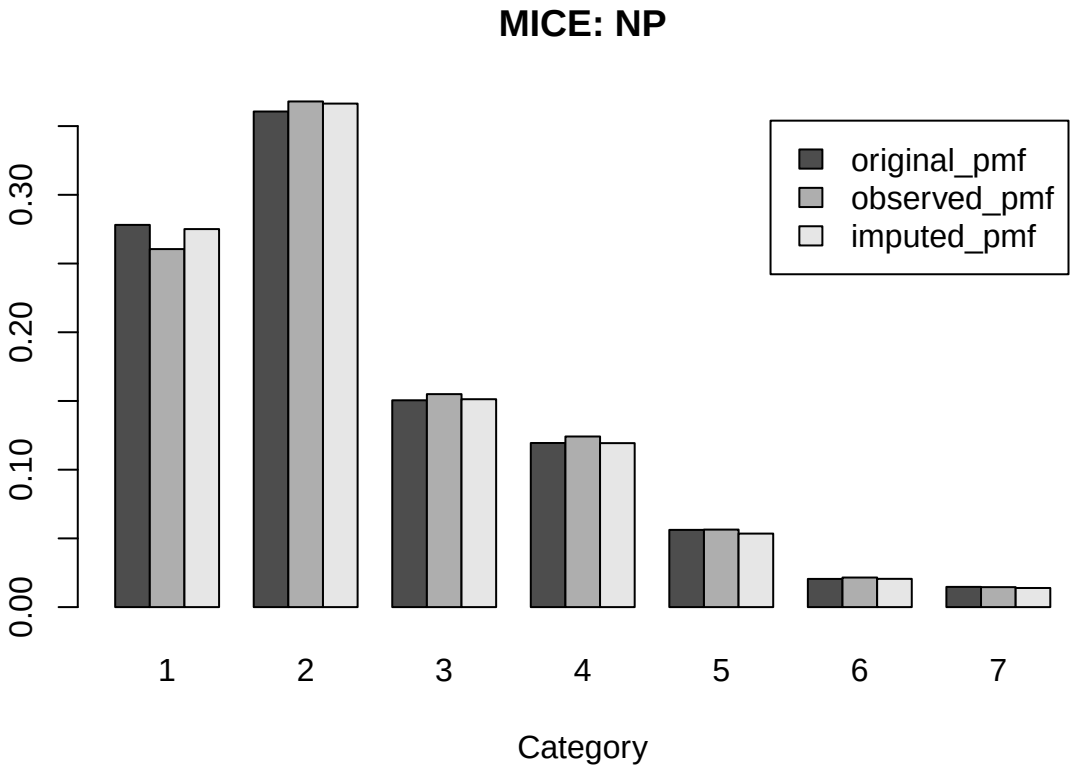
Assess trivariate joint distribution

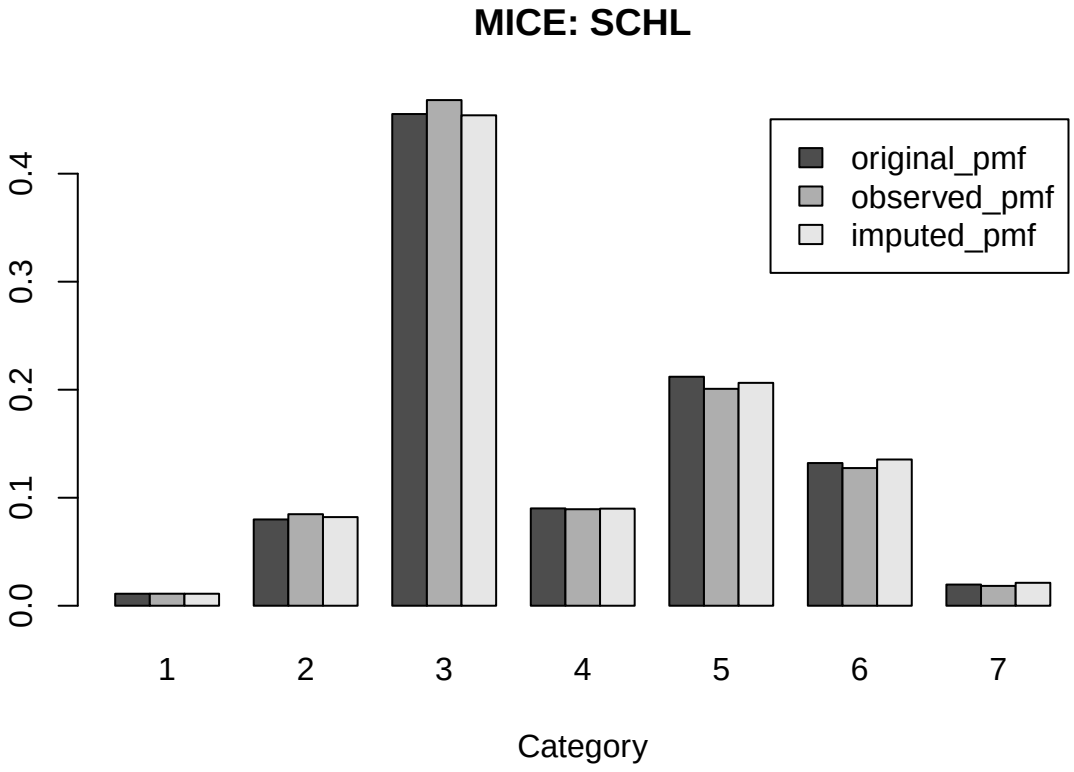
```
# calculate rmse
numeric_df = sapply(df, as.numeric)
normalized_df = t(t(numeric_df-1)/(apply(numeric_df, MARGIN = 2, FUN = max)-1))
numeric_impute = sapply(d1, as.numeric)
normalized_impute = t(t(numeric_impute-1)/(apply(numeric_df, MARGIN = 2, FUN = max)-1))

missing_matrix = is.na(df_observed)
```

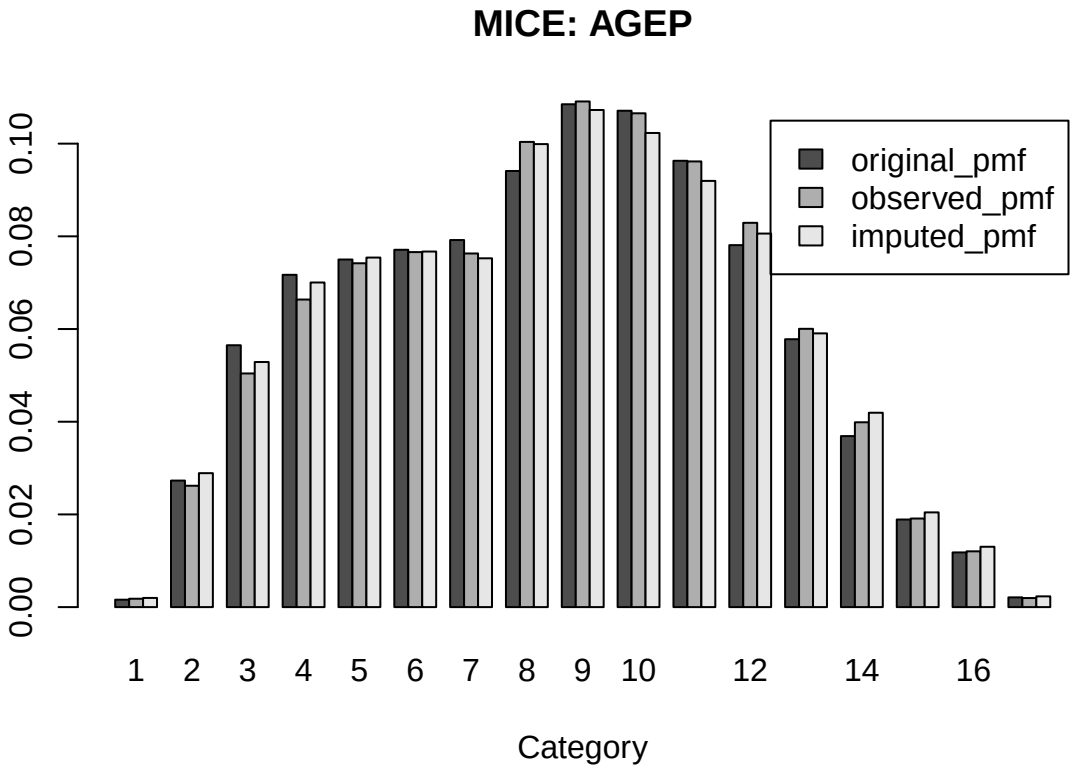


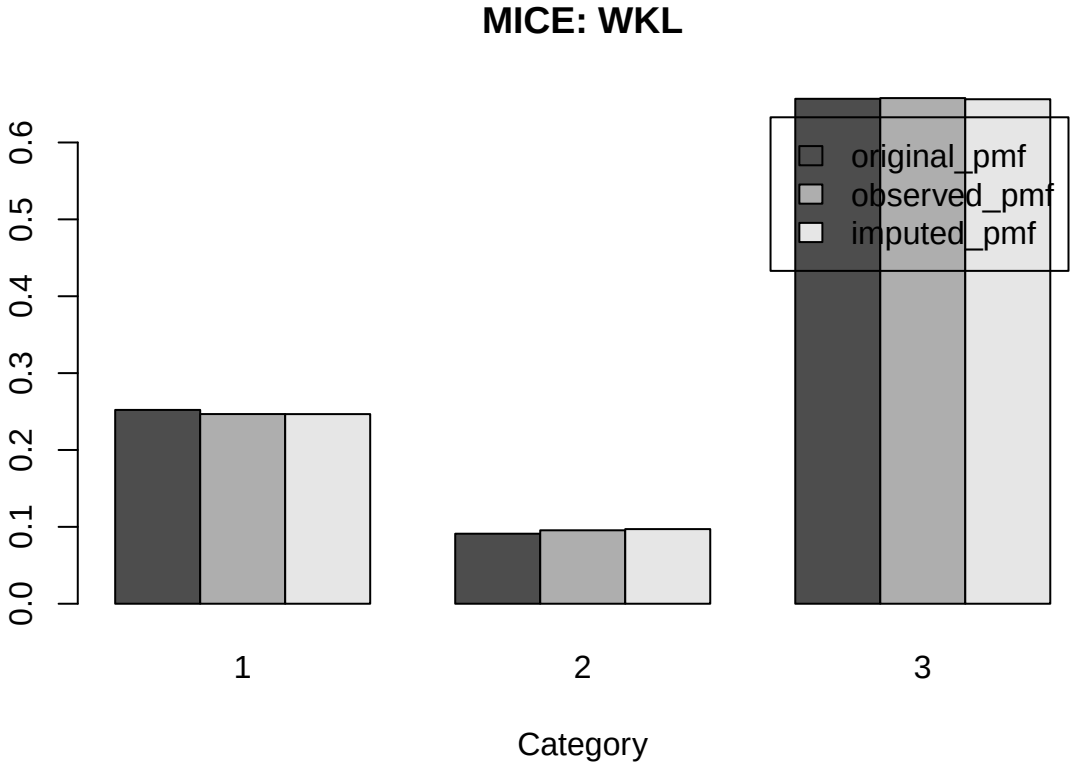

```
rmse = sqrt(sum((normalized_df[missing_matrix] - normalized_impute[missing_matrix])^2)/sum(missing_matri
rmse
```

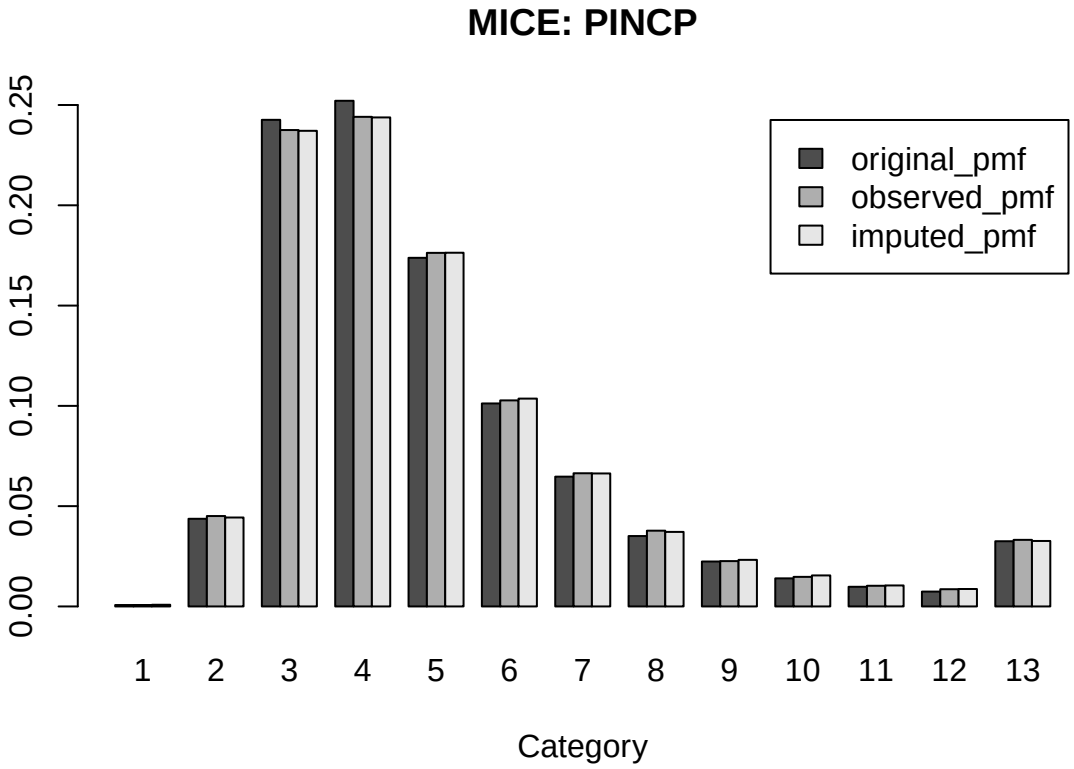
```
## [1] 0.3187519
```

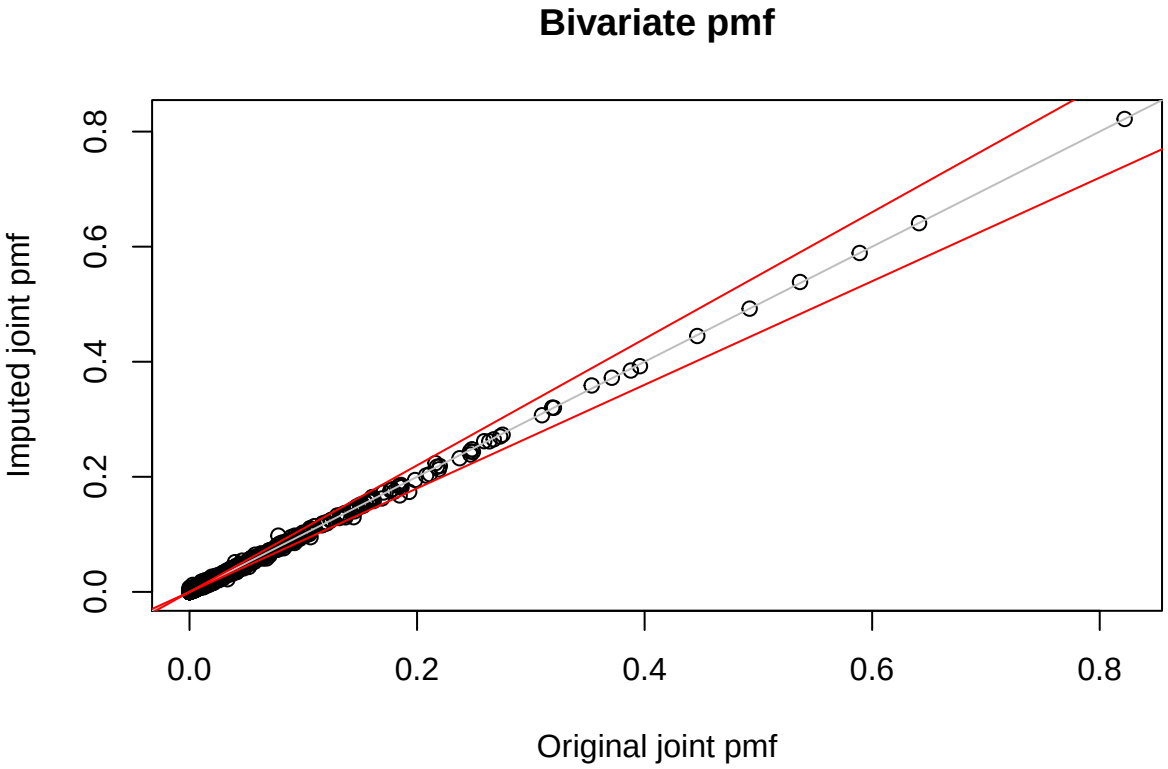

MICE: NP
original_pmf
observed_pmf
imputed_pmf
0.00
0.10
0.20
0.30
1
2
3
4
5
6
7
Category

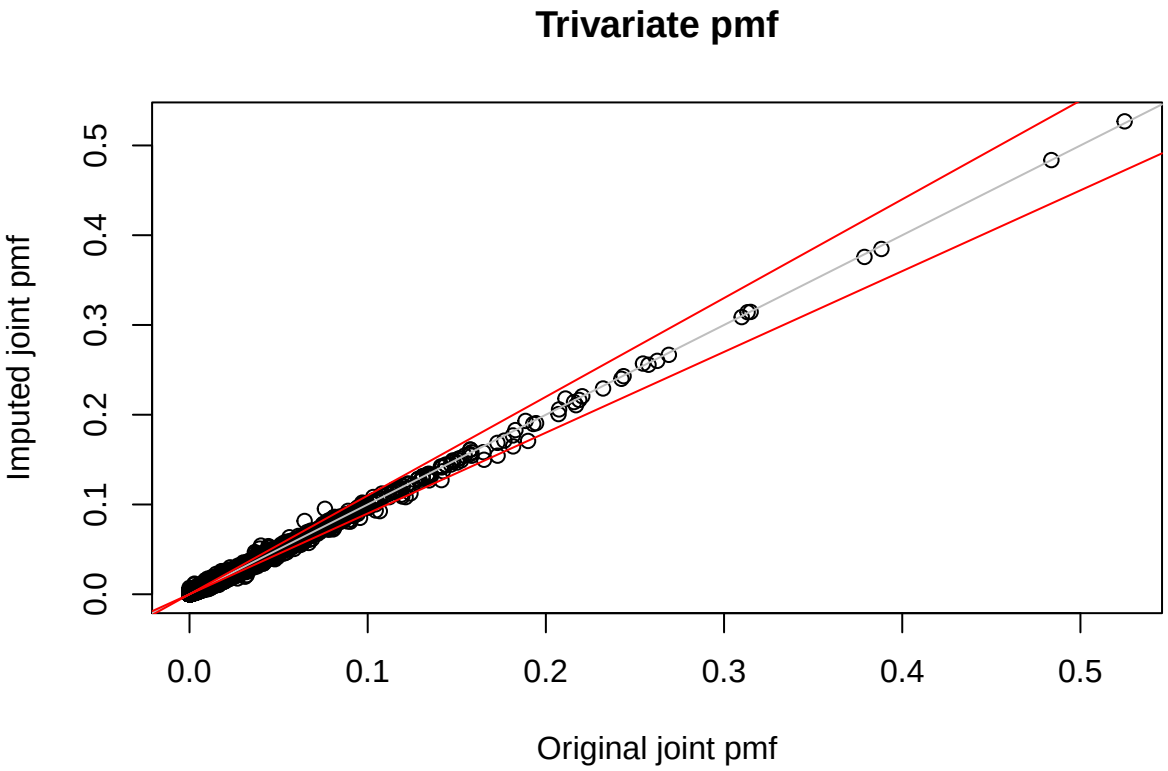

MICE: SCHL
original_pmf
observed_pmf
imputed_pmf
0.0
0.1
0.2
0.3
0.4
1
2
3
4
5
6
7
Category


MICE: AGEP
0.00
0.02
0.04
0.06
0.08
0.10
1
2
3
4
5
6
7
8
9
10
12
14
16
original_pmf
observed_pmf
imputed_pmf
Category


MICE: WKL
0.0
0.1
0.2
0.3
0.4
0.5
0.6
1
2
3
original_pmf
observed_pmf
imputed_pmf
Category


MICE: PINCP
original_pmf
observed_pmf
imputed_pmf
0.00
0.05
0.10
0.15
0.20
0.25
1
2
3
4
5
6
7
8
9
10
11
12
13
Category


Bivariate pmf
Imputed joint pmf
0.0
0.2
0.4
0.6
0.8
Original joint pmf


Trivariate pmf
Imputed joint pmf
Original joint pmf
0.0
0.1
0.2
0.3
0.4
0.5