MAR 45% missing - DPMPM

```r
# sample MCAR dataset from PUMS
source("../../utils/sampleMAR45.R")
n = 10000
missing_col = c(1,3,7,9,10,11)
set.seed(3)

output_list <- sampleMAR45(n)
df <- output_list[['df']]
df_observed <- output_list[['df_observed']]

apply(is.na(df_observed), MARGIN = 2, mean)
```

```
##    VEH     MV     NP   RMSP    ENG  MARHT   SCHL RACNUM   AGEP    WKL  PINCP
## 0.4456 0.0000 0.3998 0.0000 0.0000 0.0000 0.4842 0.0000 0.4670 0.4478 0.4384
```

DPMPM

Multiple imputation using NPBayesImputeCat package

Ref: https://cran.r-project.org/web/packages/NPBayesImputeCat/NPBayesImputeCat.pdf

1. Create and initialize the Rcpp_Lcm model object using CreateModel with the following arguments:

- X: dataframe to be imptuted = df
- MCZ: dataframe with the definition of structural zero = NULL
- K: the maximum number of mixture components = 40
- Nmax: An upper truncation limit for the augmented sample size = 0
- aalpha: the hyper parameter alpha in stick-breaking prior = 0.25
- balpha: the hyper parameter beta in stick-breaking prior = 0.25
- seed = 0

2. Set the tracer for the sampling process

- k_star: the effective cluster number
- psi: conditional multinomial probabilties
- ImputedX: imputation result

3. Run the model using the method Run of Rcpp_Lcm class with the following arguments:

- burnin = 10000
- iter = 10000
- thinning = 5

4. Obtain result

```r
N = 40
Mon = 10000
B = 10000
thin.int = 5

# 1. Create and initialize the Rcpp_Lcm model object
model = CreateModel(X = df_observed, MCZ = NULL, K = N, Nmax = 0,
                    aalpha = 0.25, balpha = 0.25, seed = 0)
# 2. Set tracer
```

```r
model$SetTrace(c('k_star', 'psi', 'ImputedX', 'alpha'),Mon)

# 3. Run model using Run(burnin, iter, thinning)
model$Run(B,Mon,thin.int)
```

```r
# Extract results
output <- model$GetTrace()
k_star <- output$k_star
psi <- output$psi
imputed_df <- output$ImputedX
alpha <- output$alpha

#retrieve parameters from the final iteration
result <- model$snapshot

#convert ImputedX matrix to dataframe, using proper factors/names etc.
ImputedX <- GetDataFrame(result$ImputedX,df)
```

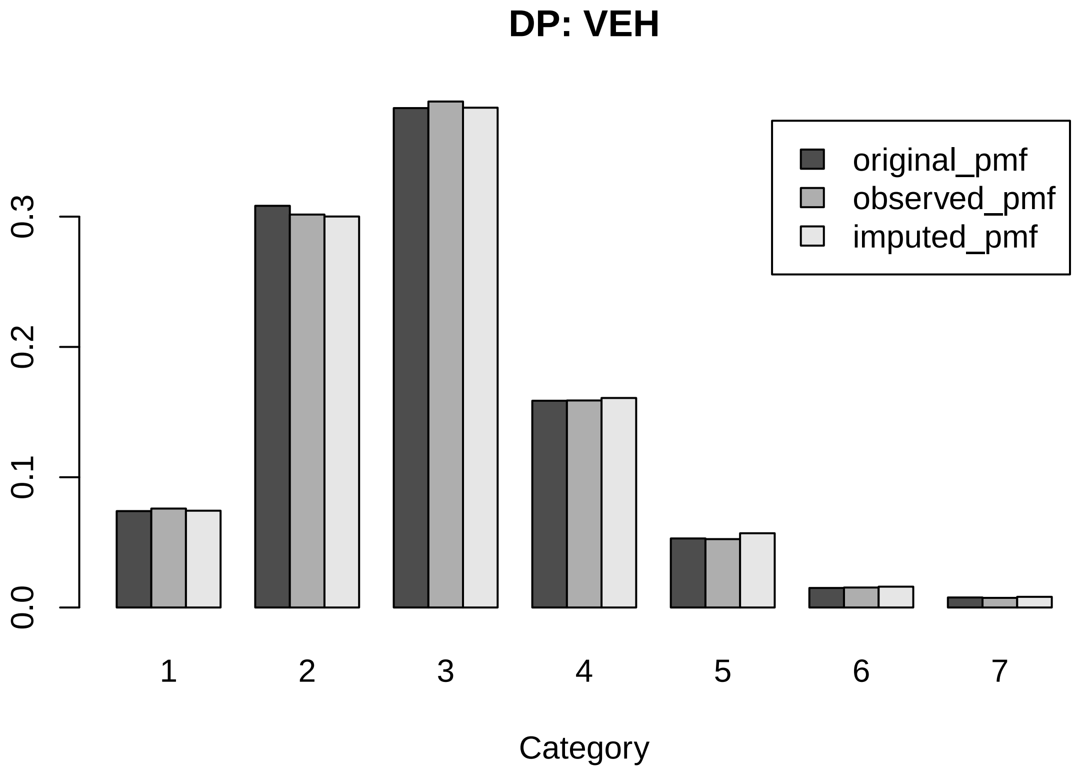
```r
# extract 5 imputed dataset from DP model
imputation_index = as.integer(seq(1,dim(imputed_df)[1], length.out = 5))
imputation_list = list()
levels = c(7,7,7,19,5,4,7,2,17,3,13)
for (index in imputation_index) {
  # need to plus 1 here because the class index of DP function starts at 0
  d = imputed_df[index,] + 1
  dim(d) = dim(t(df_observed))
  d = data.frame(t(d))
  colnames(d) = colnames(df_observed)
  # format columns of d
  for (col_index in 1:ncol(df_observed)) {
    d[,col_index] = factor(d[,col_index], levels = 1:levels[col_index], ordered = TRUE)
  }
  imputation_list[[index]] = d
}
```

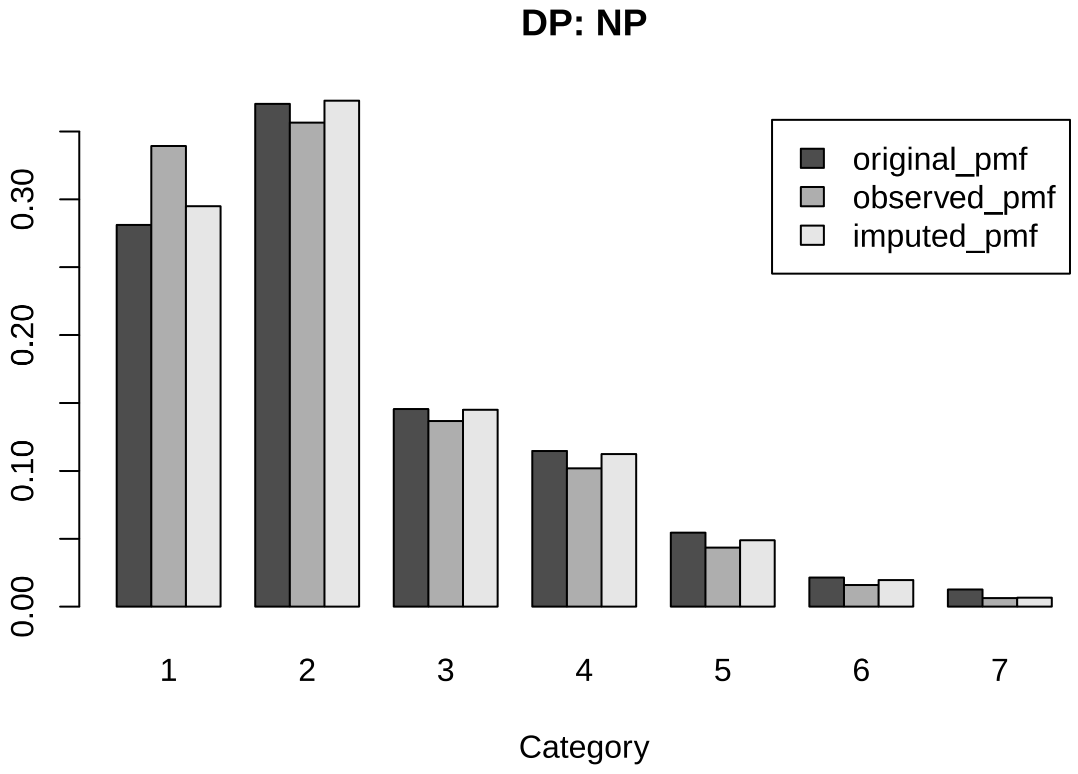
Diagnostics

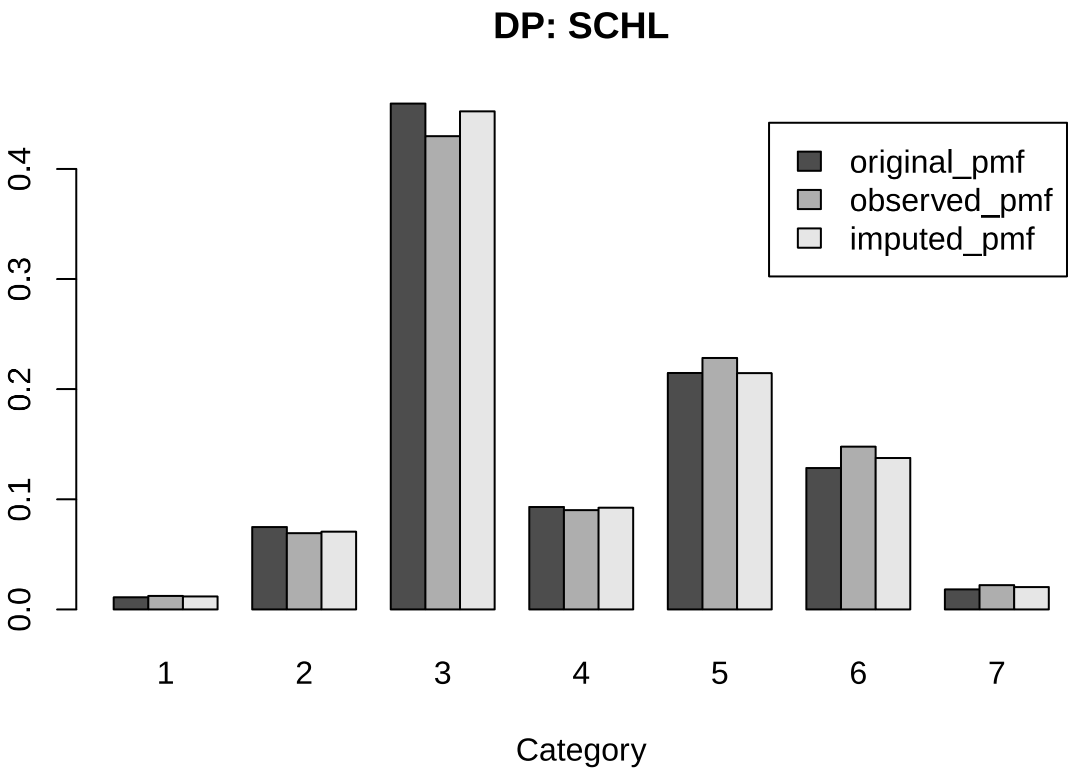
```r
d1 = imputation_list[[1]]
d2 = imputation_list[[2]]
d3 = imputation_list[[3]]
d4 = imputation_list[[4]]
d5 = imputation_list[[5]]
imputed_sets = rbind(d1, d2, d3, d4, d5)
```

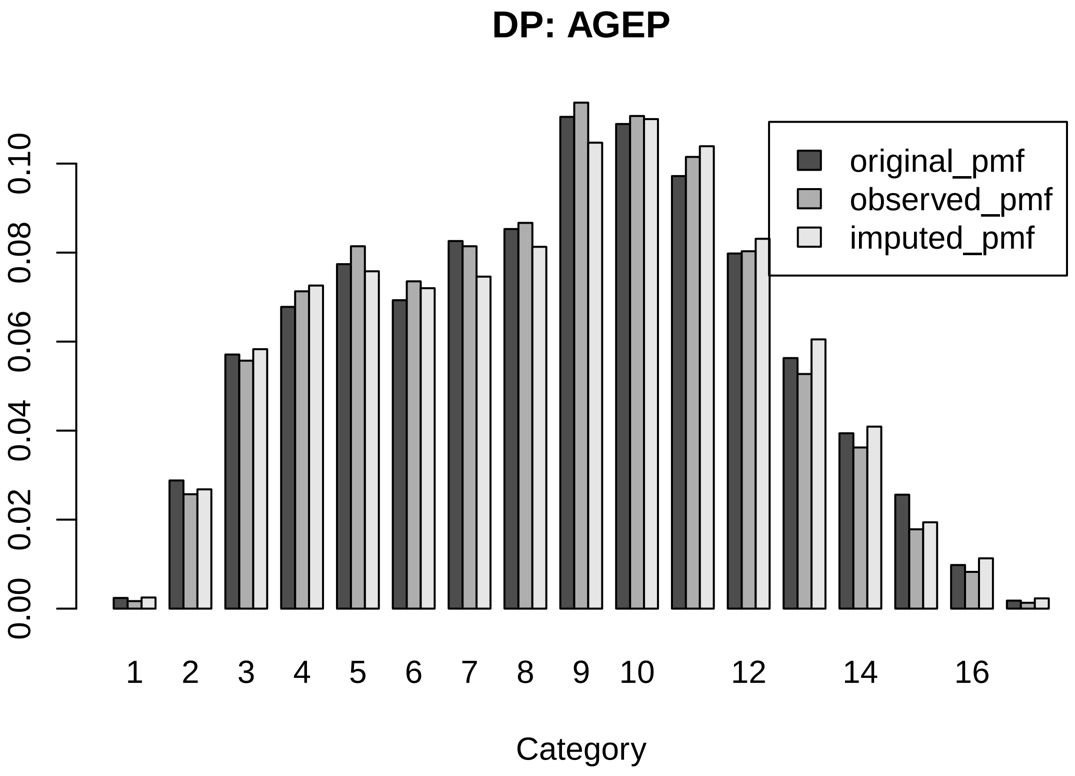
Assess bivariate joint distribution

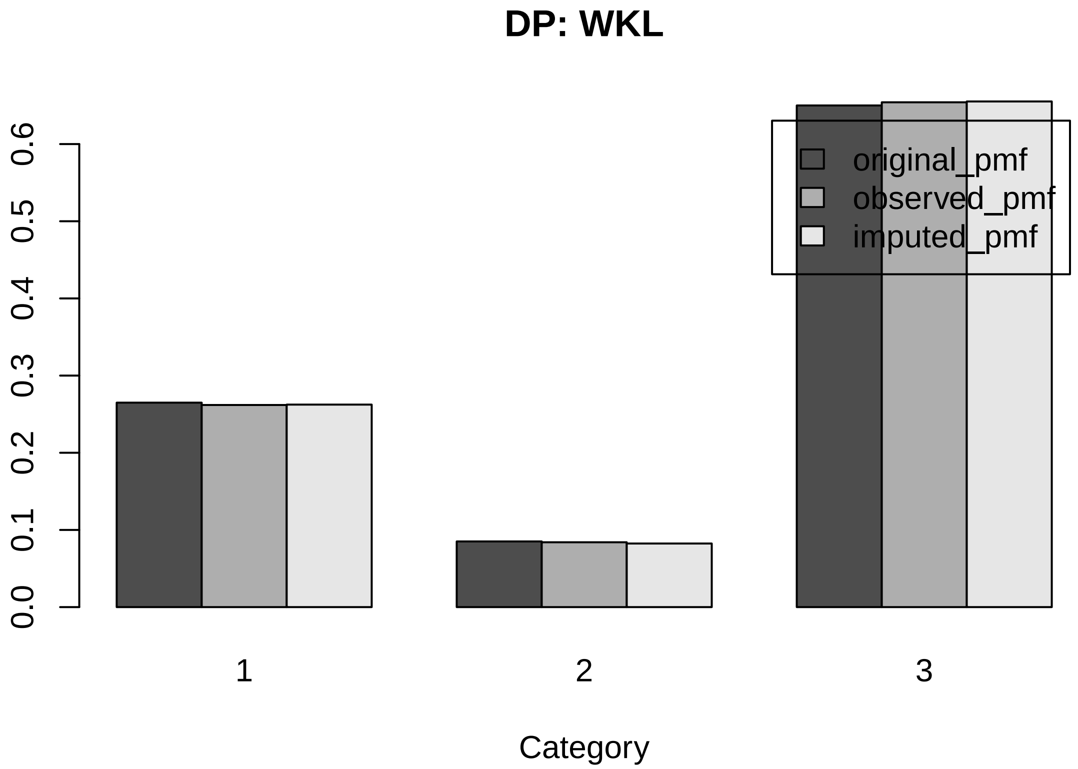
Assess trivariate joint distribution

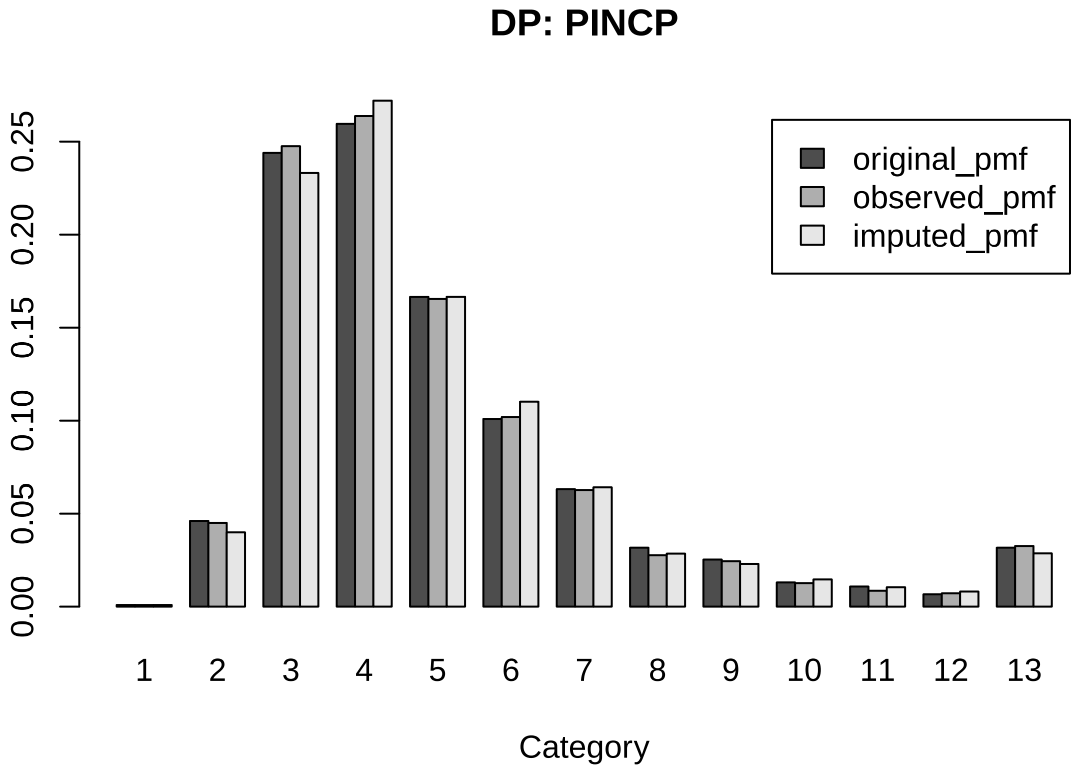

DP: VEH
original_pmf
observed_pmf
imputed_pmf
0.0
0.1
0.2
0.3
1
2
3
4
5
6
7
Category

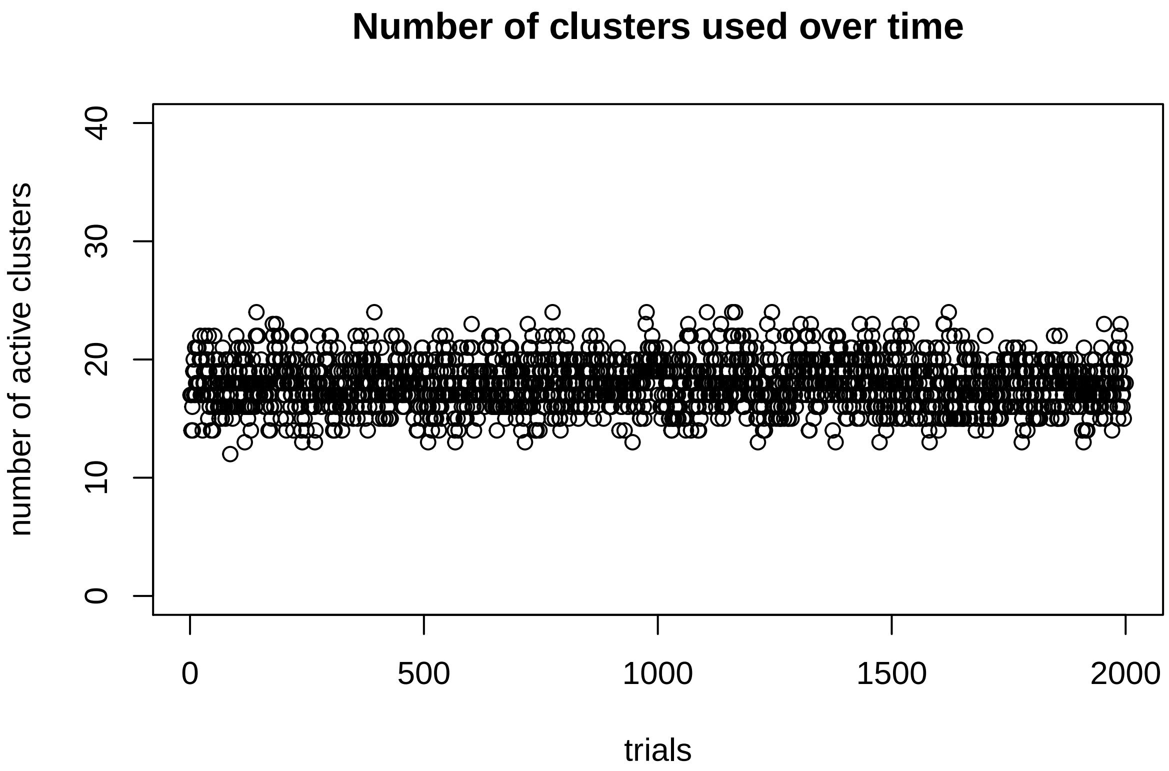

DP: NP
original_pmf
observed_pmf
imputed_pmf
0.00
0.10
0.20
0.30
1
2
3
4
5
6
7
Category


DP: 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

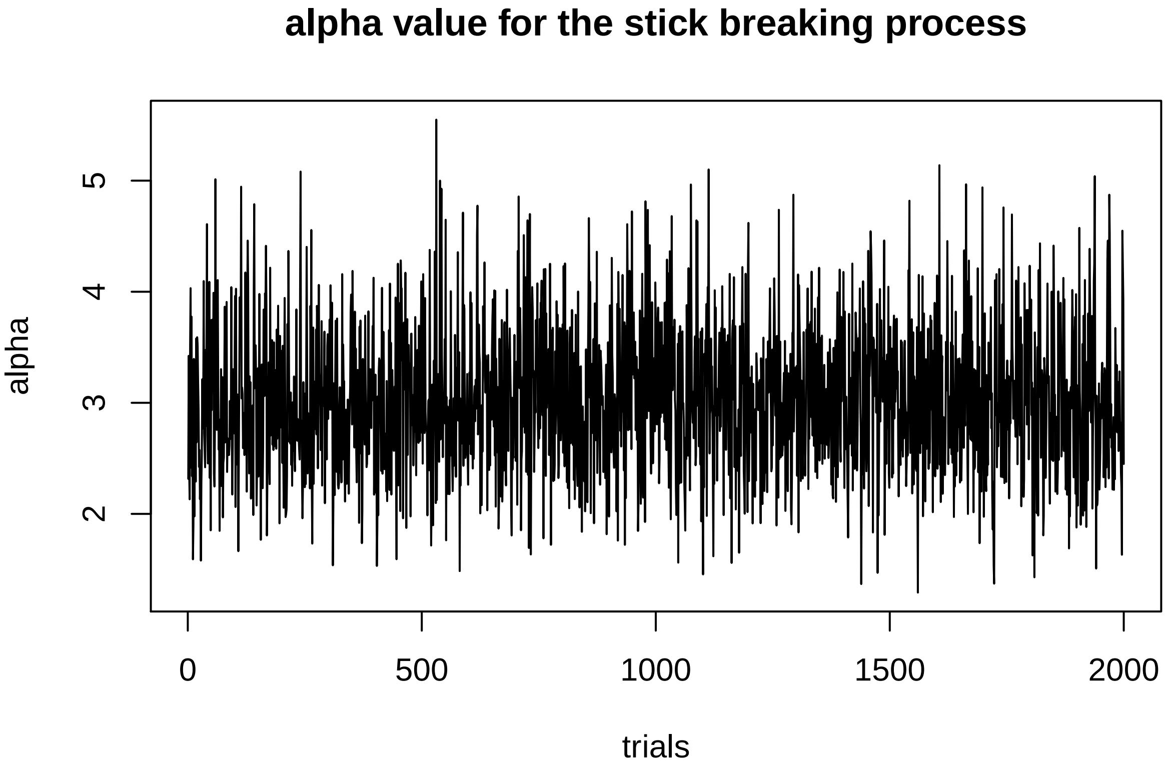

DP: AGEP
original_pmf
observed_pmf
imputed_pmf
0.00
0.02
0.04
0.06
0.08
0.10
1
2
3
4
5
6
7
8
9
10
12
14
16
Category


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

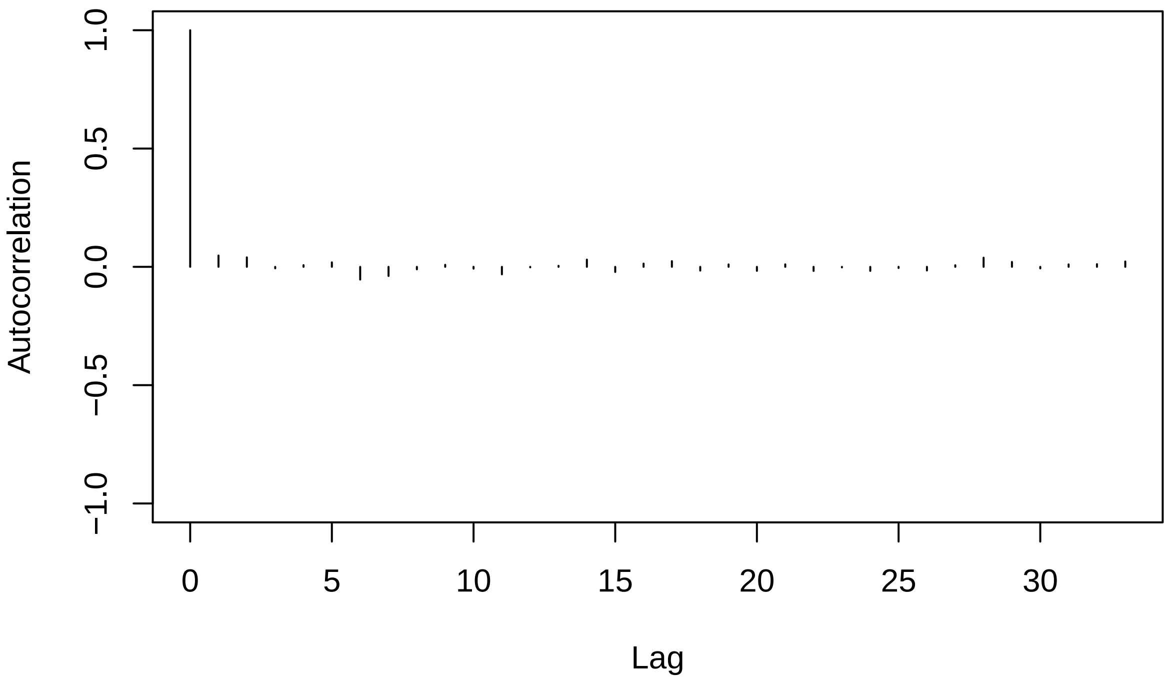

DP: PINCP
0.00
0.05
0.10
0.15
0.20
0.25
1
2
3
4
5
6
7
8
9
10
11
12
13
Category
original_pmf
observed_pmf
imputed_pmf

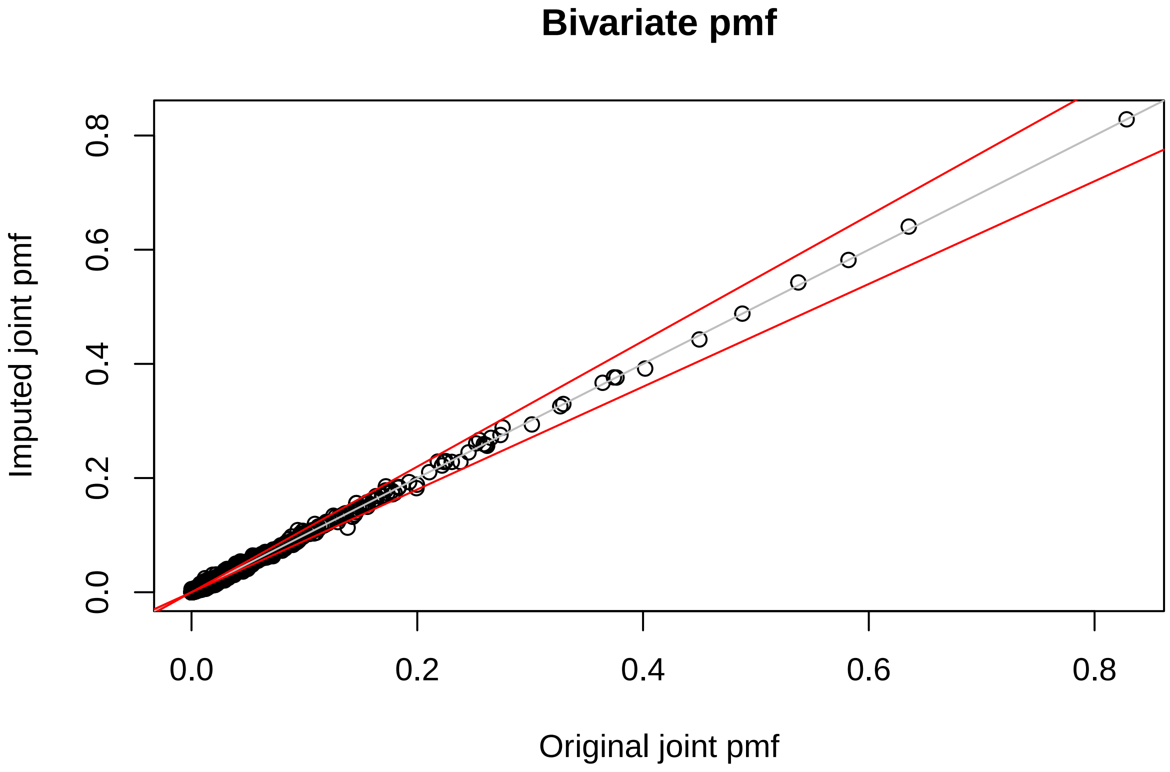


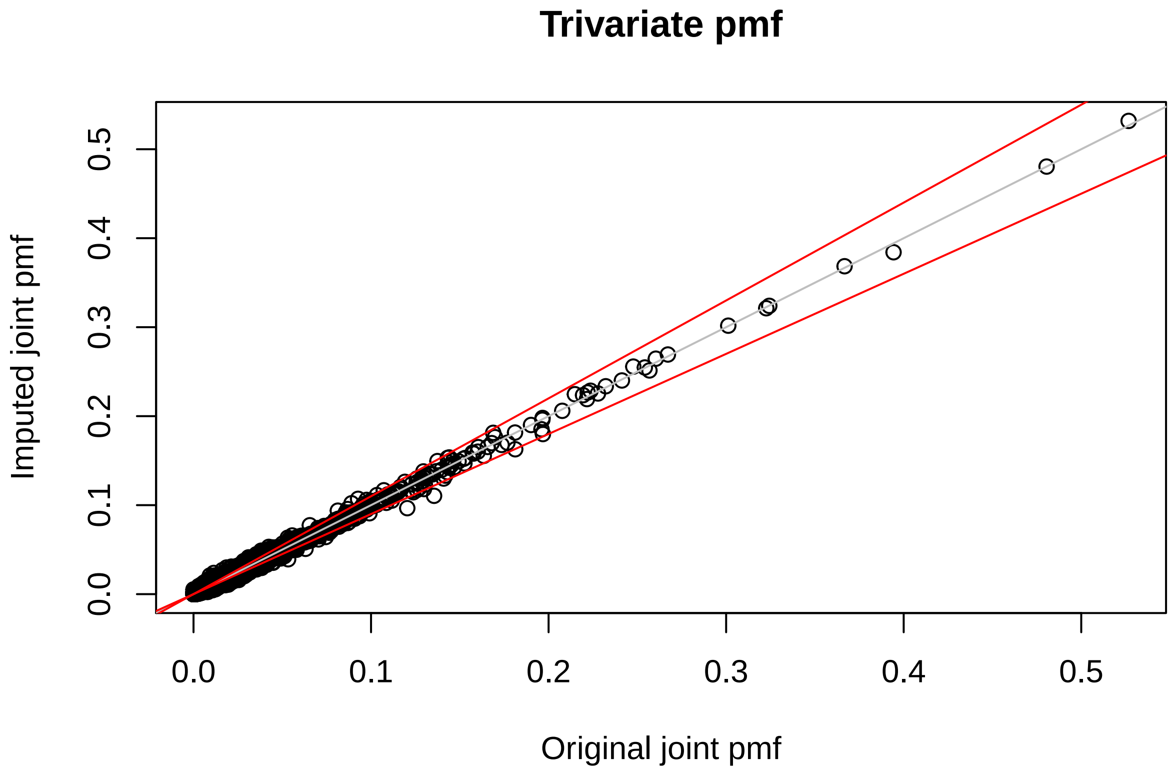
Number of clusters used over time



alpha value for the stick breaking process


Autocorrelation
1.0
0.5
0.0
−0.5
−1.0
0
5
10
15
20
25
30
Lag


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


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