ASDA3 Analysis Example Replication Chapter 12

R Code

```
 # Load packages needed
 library(survey)
 library(mice)
 library(haven)
 library(mitools)

 # Read in Nhanes subset, set up for missing data imputation and analysis, data management done in SAS

 nhanesc12  <- read_sas("P:/ASDA3/Replication SAS/c12_nhanes_subset.sas7bdat")
 nhanesc12_sub <- nhanesc12 # make sure to note this is a subset n=5615

 str(nhanesc12_sub)
 md.pattern(nhanesc12_sub)

 # Set survey design
 nhanessvy <- svydesign(strata=~sdmvstra, id=~sdmvpsu, weights=~WTMEC2YR, data=nhanesc12_sub, nest=T)

 # Complete Case Analysis
 # Obtain means for 3 continuous variables without imputation, Table 12.3
 print(ex12_3a <- svymean(~bmxbmi, nhanessvy, se=T, na.rm=T, ci=T))
 show(ex12_3b <- svymean(~BPXDI1, nhanessvy, se=T, na.rm=T, ci=T))
 show(ex12_3c <- svymean(~indfmpir, nhanessvy, se=T, na.rm=T, ci=T))

 # High Blood Pressure Mean, Complete Case, Table 12.4
 (ex12_4 <- svymean(~factor(high_diastolic),nhanessvy, se=T, na.rm=T, deff=T, ci=T, keep.vars=T))
 confint(ex12_4)

 # Logistic Regression Complete Case Analysis with Design Correction, Table 12.5
 mod12_5 <- svyglm(high_diastolic ~ factor(RIDRETH1) + factor(riagendr)+ agec + agecsq,family=quasibinomial,
design=nhanessvy)
 summary(mod12_5)


 # Imputation Method 1 with Design Variables in MI Model, return to original data without the CC high diastolic
blood pressure

 nhanesc12_subm1 <- nhanesc12
 summary(nhanesc12_subm1)
 names(nhanesc12_subm1)

 # Subset variables by number position in data set , drop age and high_diastolic since will be redone once
bpxdi1 is complete
 (nhanesc12_subset  <- nhanesc12[, c(1,2,3,4,5,6,7,8,10,12,13,14)])
 summary(nhanesc12_subset)

 # Use mice to impute and specify type of default method for imputation models
 # Run without custom predictor matrix first,see which variables might not be used in final model

 impm1 <- mice(nhanesc12_subset, n.imp=5, seed=2024, defaultMethod=c("norm","logreg","polyreg"))
 impm1$predictorMatrix
 summary(impm1)

 # Add a predictor matrix to control imputation model predictors for each imputed variable
 pred <- impm1$predictorMatrix
 pred[,"sdmvpsu"] <- 0
```

```
 pred[,"sdmvstra"] <- 0
 pred[,"descode"] <- 1
 pred[,"WTMEC2YR"] <- 1

 pred  #note that certain variables are set to 0 for this matrix

 impm1_pred <- mice(nhanesc12_subset, pred=pred, n.imp=5, seed=2016, defaultMethod=c("norm","logreg","polyreg"))
 summary(impm1_pred)

 # Note small differences between 1st and 2nd implicate
 summary(mice::complete( impm1_pred , 1 )$BPXDI1)
 summary(mice::complete( impm1_pred , 2 )$BPXDI1)

 # Combine all five data.frame objects into a list
 list_of_data_frames <- list(
 mice::complete(impm1_pred , 1 ) ,
 mice::complete( impm1_pred , 2 ) ,
 mice::complete( impm1_pred , 3 ) ,
 mice::complete( impm1_pred , 4 ) ,
 mice::complete( impm1_pred , 5 ))

 # Multiply-imputed design statement
 desnhanesm1 <- svydesign(id = ~ sdmvpsu, strat = ~ sdmvstra , weight = ~ WTMEC2YR ,
  data = imputationList( list_of_data_frames ) , nest = TRUE )
 desnhanesm1

 # Add a new variable to desnhanesm1 using imputed bpxdi1 values
desnhanesm1 <- update(desnhanesm1, high_diastolic = ifelse(BPXDI1 >=90,1,0) )
(desnhanesm1)

 # Combined mean high blood pressure with design adjustment, Table 12.4
 fitm1_mean <- MIcombine(with(desnhanesm1, svymean(~factor(high_diastolic), se=T, ci=T, na.rm=T)))
 fitm1_mean
 confint(fitm1_mean)

 # Run design based logistic model with svyglm using 5 imputed data sets contained in desnhanesm1, Table 12.5
 fitm1 <- MIcombine(with(desnhanesm1, svyglm (factor(high_diastolic) ~ factor(RIDRETH1) + factor(riagendr) +
agec + agecsq, family=quasibinomial)))
 fitm1

 # Obtain means for 3 continuous variables imputed using method 1, Table 12.3 (by each replicate)
 fitm1_ex12_3 <- with(desnhanesm1, svymean(~bmxbmi + BPXDI1 + indfmpir), se=T, na.rm=T, ci=T )
 fitm1_ex12_3


 # Imputation 2 NO design variables in models
 # Return to original data without the CC high diastolic blood pressure

 nhanesc12_submeth2 <- nhanesc12
 names(nhanesc12_submeth2)

 # Subset variables by number position in data set , drop high_diastolic for imputations
 (nhanesc12_subset  <- nhanesc12[, c(1,2,3,4,5,6,7,8,10, 12,13,14)])
 summary(nhanesc12_subset)

 nhanesc12_subm2 <- nhanesc12_subset

 # Add a predictor matrix to control imputation model predictors for each imputed variable
 pred <- impm2$predictorMatrix
```

```
 pred[,"sdmvpsu"] <- 0
 pred[,"sdmvstra"] <- 0
 pred[,"descode"] <- 0
 pred[,"WTMEC2YR"] <- 0
 impm2$predictorMatrix

 pred

 impm2_pred <- mice(nhanesc12_subm2, pred=pred, n.imp=5, seed=2024, defaultMethod=c("norm","logreg","polyreg"))
 summary(impm2_pred)

 # Small differences between 1st and 2nd implicate
 summary(mice::complete( impm2_pred , 1 )$BPXDI1)
 summary(mice::complete( impm2_pred , 2 )$BPXDI1)

 # Combine all five data.frame objects into a list
 list_of_data_frames2 <-list(
 mice::complete( impm2_pred , 1 ) ,
 mice::complete( impm2_pred , 2 ) ,
 mice::complete( impm2_pred , 3 ) ,
 mice::complete( impm2_pred , 4 ) ,
 mice::complete( impm2_pred , 5 )
 )

 # Multiply-imputed design statement
 desnhanesm2 <-svydesign(id = ~ sdmvpsu, strat = ~ sdmvstra , weight = ~ WTMEC2YR ,
  data = imputationList( list_of_data_frames2 ), nest = TRUE)
 desnhanesm2

 # Add a new variable to desnhanesm2 using imputed blood pressure values
 desnhanesm2 <- update( desnhanesm2, high_diastolic = ifelse(BPXDI1 >=90,1,0))
 (desnhanesm2)

 # Combined mean high blood pressure with NO design adjustment, Table 12.4
 fitm2_mean <- MIcombine(with(desnhanesm2, svymean(~factor(high_diastolic), se=T, na.rm=T, ci=T )))
 fitm2_mean

 confint(fitm2_mean)

 # Run design based logistic model with svyglm using 5 imputed data sets contained in desnhanesm2, Table 12.5
 fitm2 <- MIcombine(with(desnhanesm2, svyglm (factor(high_diastolic) ~ factor(RIDRETH1) + factor(riagendr) +
agec + agecsq, family=quasibinomial)))
 (fitm2)

 # Obtain means for 3 continuous variables imputed using method 2 (NO DESIGN) , Table 12.3 (by each replicate)
 fitm2_ex12_3 <- with(desnhanesm2, svymean(~bmxbmi + BPXDI1 + indfmpir, se=T, na.rm=T, ci=T ))
 fitm2_ex12_3

 # Note: FEFI method not available in R Survey Package, see examples using other software such as SAS PROC
SURVEYIMPUTE
```

R Results

```
> # Chapter 12 Multiple Imputation Using R mice and mitools with Survey Package
>
>  # Load packages needed
>  library(survey)
>  library(mice)
>  library(haven)
>  library(mitools)
>
>  # Read in Nhanes subset, set up for missing data imputation and analysis, data management done in SAS
>
>  nhanesc12  <- read_sas("P:/ASDA3/Replication SAS/c12_nhanes_subset.sas7bdat")
>  nhanesc12_sub <- nhanesc12 # make sure to note this is a subset n=5615
>
>  str(nhanesc12_sub)
tibble [5,615 × 15] (S3: tbl_df/tbl/data.frame)
 $ riagendr      : num [1:5615] 1 2 1 2 1 2 1 1 1 1 ...
  ..- attr(*, "label")= chr "Gender"
 $ RIDRETH1      : num [1:5615] 3 3 5 4 3 3 5 3 5 3 ...
  ..- attr(*, "label")= chr "1=mex 2=oth hisp 3=white 4=black 5=other"
 $ WTMEC2YR      : num [1:5615] 104237 127965 14784 27123 27336 ...
  ..- attr(*, "label")= chr "Full sample 2 year MEC exam weight"
 $ sdmvpsu       : num [1:5615] 1 1 1 2 3 1 2 1 1 1 ...
  ..- attr(*, "label")= chr "Masked variance pseudo-PSU"
 $ sdmvstra      : num [1:5615] 91 94 92 96 90 99 92 95 92 97 ...
  ..- attr(*, "label")= chr "Masked variance pseudo-stratum"
 $ indfmpir      : num [1:5615] 3.15 1.67 0.33 2.02 4.3 5 NA 0.05 5 0.87 ...
  ..- attr(*, "label")= chr "Ratio of family income to poverty"
 $ BPXDI1        : num [1:5615] 82 56 80 70 NA NA 68 72 78 62 ...
  ..- attr(*, "label")= chr "Diastolic: Blood pres (1st rdg) mm Hg"
 $ bmxbmi        : num [1:5615] 23.3 23.2 20.1 33.3 33.9 23.3 20.1 28.5 27.6 27.9 ...
  ..- attr(*, "label")= chr "Body Mass Index (kg/m**2)"
 $ age           : num [1:5615] 22 44 21 43 80 34 51 80 55 35 ...
  ..- attr(*, "label")= chr "Age at Interview in Years"
 $ marcat        : num [1:5615] 3 1 3 3 1 1 1 2 1 1 ...
  ..- attr(*, "label")= chr "1=married 2=prev married 3=never married"
 $ bpxdi1_1      : num [1:5615] 82 56 80 70 0 0 68 72 78 62 ...
 $ agec          : num [1:5615] -24.36 -2.36 -25.36 -3.36 33.64 ...
 $ agecsq        : num [1:5615] 593.41 5.57 643.13 11.29 1131.65 ...
 $ descode       : num [1:5615] 911 941 921 962 903 991 922 951 921 971 ...
 $ high_diastolic: num [1:5615] 0 0 0 0 NA NA 0 0 0 0 ...
>  md.pattern(nhanesc12_sub)
     riagendr RIDRETH1 WTMEC2YR sdmvpsu sdmvstra age bpxdi1_1 agec agecsq descode bmxbmi marcat
4430        1        1        1       1        1   1        1    1      1       1      1      1
371         1        1        1       1        1   1        1    1      1       1      1      1
372         1        1        1       1        1   1        1    1      1       1      1      1
60          1        1        1       1        1   1        1    1      1       1      1      1
231         1        1        1       1        1   1        1    1      1       1      1      0
32          1        1        1       1        1   1        1    1      1       1      1      0
21          1        1        1       1        1   1        1    1      1       1      1      0
8           1        1        1       1        1   1        1    1      1       1      1      0
49          1        1        1       1        1   1        1    1      1       1      0      1
12          1        1        1       1        1   1        1    1      1       1      0      1
17          1        1        1       1        1   1        1    1      1       1      0      1
4           1        1        1       1        1   1        1    1      1       1      0      1
7           1        1        1       1        1   1        1    1      1       1      0      0
1           1        1        1       1        1   1        1    1      1       1      0      0
            0        0        0       0        0   0        0    0      0       0     90    300
```

```
     BPXDI1 high_diastolic indfmpir
4430      1              1        1    0
371       1              1        0    1
372       0              0        1    2
60        0              0        0    3
231       1              1        1    1
32        1              1        0    2
21        0              0        1    3
8         0              0        0    4
49        1              1        1    1
12        1              1        0    2
17        0              0        1    3
4         0              0        0    4
7         1              1        1    2
1         0              0        1    4
        483            483      487 1843
>
>  # Set survey design
>  nhanessvy <- svydesign(strata=~sdmvstra, id=~sdmvpsu, weights=~WTMEC2YR, data=nhanesc12_sub, nest=T)



>  # Complete Case Analysis
>  # Obtain means for 3 continuous variables without imputation, Table 12.3
>  print(ex12_3a <- svymean(~bmxbmi, nhanessvy, se=T, na.rm=T, ci=T))
       mean   SE
bmxbmi 28.6 0.21
>  show(ex12_3b <- svymean(~BPXDI1, nhanessvy, se=T, na.rm=T, ci=T))
       mean   SE
BPXDI1 71.4 0.51
>  show(ex12_3c <- svymean(~indfmpir, nhanessvy, se=T, na.rm=T, ci=T))
         mean   SE
indfmpir 2.86 0.11



>  # High Blood Pressure Mean, Complete Case, Table 12.4
>  (ex12_4 <- svymean(~factor(high_diastolic),nhanessvy, se=T, na.rm=T, deff=T, ci=T, keep.vars=T))
                           mean      SE DEff
factor(high_diastolic)0 0.93937 0.00793 5.67
factor(high_diastolic)1 0.06063 0.00793 5.67
>  confint(ex12_4)
                          2.5 %  97.5 %
factor(high_diastolic)0 0.92382 0.95491
factor(high_diastolic)1 0.04509 0.07618


>  # Logistic Regression Complete Case Analysis with Design Correction, Table 12.5
>  mod12_5 <- svyglm(high_diastolic ~ factor(RIDRETH1) + factor(riagendr)+ agec + agecsq,family=quasibinomial,
design=nhanessvy)
>  summary(mod12_5)

Call:
svyglm(formula = high_diastolic ~ factor(RIDRETH1) + factor(riagendr) +
    agec + agecsq, design = nhanessvy, family = quasibinomial)

Survey design:
svydesign(strata = ~sdmvstra, id = ~sdmvpsu, weights = ~WTMEC2YR,
    data = nhanesc12_sub, nest = T)
```

```
Coefficients:
                   Estimate Std. Error t value Pr(>|t|)
(Intercept)       -2.248873   0.198142  -11.35  4.9e-07 ***
factor(RIDRETH1)2 -0.724205   0.245430   -2.95  0.01452 *
factor(RIDRETH1)3  0.131207   0.224460    0.58  0.57180
factor(RIDRETH1)4  0.654740   0.246514    2.66  0.02406 *
factor(RIDRETH1)5  0.050763   0.244587    0.21  0.83975
factor(riagendr)2 -0.549726   0.207123   -2.65  0.02414 *
agec               0.008290   0.006944    1.19  0.26009
agecsq            -0.001624   0.000276   -5.89  0.00015 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 1.02)

Number of Fisher Scoring iterations: 6

>
```

```
>  # Imputation Method 1 with Design Variables in MI Model, return to original data without the CC high
diastolic blood pressure
>
>  nhanesc12_subm1 <- nhanesc12
>  summary(nhanesc12_subm1)
    riagendr       RIDRETH1      WTMEC2YR         sdmvpsu        sdmvstra        indfmpir
 Min.   :1.00   Min.   :1.0   Min.   :  4413   Min.   :1.00   Min.   : 90.0   Min.   :0.0
 1st Qu.:1.00   1st Qu.:3.0   1st Qu.: 16173   1st Qu.:1.00   1st Qu.: 92.0   1st Qu.:0.9
 Median :2.00   Median :3.0   Median : 24567   Median :2.00   Median : 96.0   Median :1.8
 Mean   :1.51   Mean   :3.3   Mean   : 41318   Mean   :1.64   Mean   : 95.9   Mean   :2.4
 3rd Qu.:2.00   3rd Qu.:4.0   3rd Qu.: 45238   3rd Qu.:2.00   3rd Qu.: 99.0   3rd Qu.:3.9
 Max.   :2.00   Max.   :5.0   Max.   :222580   Max.   :3.00   Max.   :103.0   Max.   :5.0
                                                                              NA's   :487
     BPXDI1          bmxbmi          age           marcat        bpxdi1_1          agec
 Min.   :  0.0   Min.   :13.4   Min.   :18.0   Min.   :1.00   Min.   :  0.0   Min.   :-28.36
 1st Qu.: 64.0   1st Qu.:23.8   1st Qu.:31.0   1st Qu.:1.00   1st Qu.: 60.0   1st Qu.:-15.36
 Median : 72.0   Median :27.4   Median :47.0   Median :1.00   Median : 70.0   Median :  0.64
 Mean   : 70.7   Mean   :28.6   Mean   :47.2   Mean   :1.65   Mean   : 64.7   Mean   :  0.81
 3rd Qu.: 78.0   3rd Qu.:32.0   3rd Qu.:62.0   3rd Qu.:2.00   3rd Qu.: 78.0   3rd Qu.: 15.64
 Max.   :120.0   Max.   :82.1   Max.   :80.0   Max.   :3.00   Max.   :120.0   Max.   : 33.64
 NA's   :483     NA's   :90                    NA's   :300
     agecsq          descode     high_diastolic
 Min.   :   0.1   Min.   : 901   Min.   :0.0
 1st Qu.:  58.4   1st Qu.: 922   1st Qu.:0.0
 Median : 244.6   Median : 961   Median :0.0
 Mean   : 345.1   Mean   : 960   Mean   :0.1
 3rd Qu.: 558.8   3rd Qu.: 992   3rd Qu.:0.0
 Max.   :1131.6   Max.   :1032   Max.   :1.0
                                 NA's   :483
>  names(nhanesc12_subm1)
 [1] "riagendr"       "RIDRETH1"       "WTMEC2YR"       "sdmvpsu"        "sdmvstra"
 [6] "indfmpir"       "BPXDI1"         "bmxbmi"         "age"            "marcat"
[11] "bpxdi1_1"       "agec"           "agecsq"         "descode"        "high_diastolic"
>
>  # Subset variables by number position in data set , drop age and high_diastolic since will be redone once
bpxdi1 is complete
>  (nhanesc12_subset  <- nhanesc12[, c(1,2,3,4,5,6,7,8,10,12,13,14)])
# A tibble: 5,615 × 12
   riagendr RIDRETH1 WTMEC2YR sdmvpsu sdmvstra indfmpir BPXDI1 bmxbmi marcat   agec  agecsq descode
      <dbl>    <dbl>    <dbl>   <dbl>    <dbl>    <dbl>  <dbl>  <dbl>  <dbl>  <dbl>   <dbl>   <dbl>
 1        1        3  104237.       1       91     3.15     82   23.3      3 -24.4   593.       911
 2        2        3  127965.       1       94     1.67     56   23.2      1  -2.36    5.57      941
 3        1        5   14784.       1       92     0.33     80   20.1      3 -25.4   643.       921
 4        2        4   27123.       2       96     2.02     70   33.3      3  -3.36   11.3      962
 5        1        3   27336.       3       90     4.3      NA   33.9      1  33.6  1132.       903
 6        2        3   54203.       1       99     5        NA   23.3      1 -12.4   153.       991
 7        1        5    7851.       2       92    NA        68   20.1      1   4.64   21.5      922
 8        1        3   13190.       1       95     0.05     72   28.5      2  33.6  1132.       951
 9        1        5   17115.       1       92     5        78   27.6      1   8.64   74.6      921
10        1        3   22616.       1       97     0.87     62   27.9      1 -11.4   129.       971
# ℹ 5,605 more rows
# ℹ Use `print(n = ...)` to see more rows
>  summary(nhanesc12_subset)
    riagendr       RIDRETH1      WTMEC2YR         sdmvpsu        sdmvstra        indfmpir
 Min.   :1.00   Min.   :1.0   Min.   :  4413   Min.   :1.00   Min.   : 90.0   Min.   :0.0
 1st Qu.:1.00   1st Qu.:3.0   1st Qu.: 16173   1st Qu.:1.00   1st Qu.: 92.0   1st Qu.:0.9
 Median :2.00   Median :3.0   Median : 24567   Median :2.00   Median : 96.0   Median :1.8
 Mean   :1.51   Mean   :3.3   Mean   : 41318   Mean   :1.64   Mean   : 95.9   Mean   :2.4
 3rd Qu.:2.00   3rd Qu.:4.0   3rd Qu.: 45238   3rd Qu.:2.00   3rd Qu.: 99.0   3rd Qu.:3.9
```

```
 Max.   :2.00   Max.   :5.0   Max.   :222580   Max.   :3.00   Max.   :103.0   Max.   :5.0
                                                                              NA's   :487
     BPXDI1          bmxbmi         marcat          agec            agecsq          descode
 Min.   :  0.0   Min.   :13.4   Min.   :1.00   Min.   :-28.36   Min.   :   0.1   Min.   : 901
 1st Qu.: 64.0   1st Qu.:23.8   1st Qu.:1.00   1st Qu.:-15.36   1st Qu.:  58.4   1st Qu.: 922
 Median : 72.0   Median :27.4   Median :1.00   Median :  0.64   Median : 244.6   Median : 961
 Mean   : 70.7   Mean   :28.6   Mean   :1.65   Mean   :  0.81   Mean   : 345.1   Mean   : 960
 3rd Qu.: 78.0   3rd Qu.:32.0   3rd Qu.:2.00   3rd Qu.: 15.64   3rd Qu.: 558.8   3rd Qu.: 992
 Max.   :120.0   Max.   :82.1   Max.   :3.00   Max.   : 33.64   Max.   :1131.6   Max.   :1032
 NA's   :483     NA's   :90     NA's   :300
>
>  # Use mice to impute and specify type of default method for imputation models
>  # Run without custom predictor matrix first,see which variables might not be used in final model



>  impm1 <- mice(nhanesc12_subset, n.imp=5, seed=2024, defaultMethod=c("norm","logreg","polyreg"))

 iter imp variable
  1   1  indfmpir  BPXDI1  bmxbmi  marcat
  1   2  indfmpir  BPXDI1  bmxbmi  marcat
  1   3  indfmpir  BPXDI1  bmxbmi  marcat
  1   4  indfmpir  BPXDI1  bmxbmi  marcat
  1   5  indfmpir  BPXDI1  bmxbmi  marcat
  2   1  indfmpir  BPXDI1  bmxbmi  marcat
  2   2  indfmpir  BPXDI1  bmxbmi  marcat
  2   3  indfmpir  BPXDI1  bmxbmi  marcat
  2   4  indfmpir  BPXDI1  bmxbmi  marcat
  2   5  indfmpir  BPXDI1  bmxbmi  marcat
  3   1  indfmpir  BPXDI1  bmxbmi  marcat
  3   2  indfmpir  BPXDI1  bmxbmi  marcat
  3   3  indfmpir  BPXDI1  bmxbmi  marcat
  3   4  indfmpir  BPXDI1  bmxbmi  marcat
  3   5  indfmpir  BPXDI1  bmxbmi  marcat
  4   1  indfmpir  BPXDI1  bmxbmi  marcat
  4   2  indfmpir  BPXDI1  bmxbmi  marcat
  4   3  indfmpir  BPXDI1  bmxbmi  marcat
  4   4  indfmpir  BPXDI1  bmxbmi  marcat
  4   5  indfmpir  BPXDI1  bmxbmi  marcat
  5   1  indfmpir  BPXDI1  bmxbmi  marcat
  5   2  indfmpir  BPXDI1  bmxbmi  marcat
  5   3  indfmpir  BPXDI1  bmxbmi  marcat
  5   4  indfmpir  BPXDI1  bmxbmi  marcat
  5   5  indfmpir  BPXDI1  bmxbmi  marcat
Warning message:
Number of logged events: 1
>  impm1$predictorMatrix
         riagendr RIDRETH1 WTMEC2YR sdmvpsu sdmvstra indfmpir BPXDI1 bmxbmi marcat agec agecsq
riagendr        0        1        1       1        1        1      1      1      1    1      1
RIDRETH1        1        0        1       1        1        1      1      1      1    1      1
WTMEC2YR        1        1        0       1        1        1      1      1      1    1      1
sdmvpsu         1        1        1       0        1        1      1      1      1    1      1
sdmvstra        1        1        1       1        0        1      1      1      1    1      1
indfmpir        1        1        1       1        1        0      1      1      1    1      1
BPXDI1          1        1        1       1        1        1      0      1      1    1      1
bmxbmi          1        1        1       1        1        1      1      0      1    1      1
marcat          1        1        1       1        1        1      1      1      0    1      1
agec            1        1        1       1        1        1      1      1      1    0      1
agecsq          1        1        1       1        1        1      1      1      1    1      0
```

```
descode         1        1        1       1        1        1      1      1      1    1      1
         descode
riagendr       0
RIDRETH1       0
WTMEC2YR       0
sdmvpsu        0
sdmvstra       0
indfmpir       0
BPXDI1         0
bmxbmi         0
marcat         0
agec           0
agecsq         0
descode        0
>  summary(impm1)
Class: mids
Number of multiple imputations:  5
Imputation methods:
riagendr RIDRETH1 WTMEC2YR  sdmvpsu sdmvstra indfmpir   BPXDI1   bmxbmi   marcat     agec   agecsq
      ""       ""       ""       ""       ""    "norm"   "norm"   "norm"   "norm"       ""       ""
 descode
      ""
PredictorMatrix:
         riagendr RIDRETH1 WTMEC2YR sdmvpsu sdmvstra indfmpir BPXDI1 bmxbmi marcat agec agecsq
riagendr        0        1        1       1        1        1      1      1      1    1      1
RIDRETH1        1        0        1       1        1        1      1      1      1    1      1
WTMEC2YR        1        1        0       1        1        1      1      1      1    1      1
sdmvpsu         1        1        1       0        1        1      1      1      1    1      1
sdmvstra        1        1        1       1        0        1      1      1      1    1      1
indfmpir        1        1        1       1        1        0      1      1      1    1      1
         descode
riagendr       0
RIDRETH1       0
WTMEC2YR       0
sdmvpsu        0
sdmvstra       0
indfmpir       0
Number of logged events:  1
  it im dep      meth     out
1  0  0     collinear descode
>
>  # Add a predictor matrix to control imputation model predictors for each imputed variable
>  pred <- impm1$predictorMatrix
>  pred[,"sdmvpsu"] <- 0
>  pred[,"sdmvstra"] <- 0
>  pred[,"descode"] <- 1
>  pred[,"WTMEC2YR"] <- 1
>
>  pred  #note that certain variables are set to 0 for this matrix
         riagendr RIDRETH1 WTMEC2YR sdmvpsu sdmvstra indfmpir BPXDI1 bmxbmi marcat agec agecsq
riagendr        0        1        1       0        0        1      1      1      1    1      1
RIDRETH1        1        0        1       0        0        1      1      1      1    1      1
WTMEC2YR        1        1        1       0        0        1      1      1      1    1      1
sdmvpsu         1        1        1       0        0        1      1      1      1    1      1
sdmvstra        1        1        1       0        0        1      1      1      1    1      1
indfmpir        1        1        1       0        0        0      1      1      1    1      1
BPXDI1          1        1        1       0        0        1      0      1      1    1      1
bmxbmi          1        1        1       0        0        1      1      0      1    1      1
marcat          1        1        1       0        0        1      1      1      0    1      1
```

```
agec            1        1        1       0        0        1      1      1      1    0      1
agecsq          1        1        1       0        0        1      1      1      1    1      0
descode         1        1        1       0        0        1      1      1      1    1      1
         descode
riagendr       1
RIDRETH1       1
WTMEC2YR       1
sdmvpsu        1
sdmvstra       1
indfmpir       1
BPXDI1         1
bmxbmi         1
marcat         1
agec           1
agecsq         1
descode        1
>
>  impm1_pred <- mice(nhanesc12_subset, pred=pred, n.imp=5, seed=2016,
defaultMethod=c("norm","logreg","polyreg"))

 iter imp variable
  1   1  indfmpir  BPXDI1  bmxbmi  marcat
  1   2  indfmpir  BPXDI1  bmxbmi  marcat
  1   3  indfmpir  BPXDI1  bmxbmi  marcat
  1   4  indfmpir  BPXDI1  bmxbmi  marcat
  1   5  indfmpir  BPXDI1  bmxbmi  marcat
  2   1  indfmpir  BPXDI1  bmxbmi  marcat
  2   2  indfmpir  BPXDI1  bmxbmi  marcat
  2   3  indfmpir  BPXDI1  bmxbmi  marcat
  2   4  indfmpir  BPXDI1  bmxbmi  marcat
  2   5  indfmpir  BPXDI1  bmxbmi  marcat
  3   1  indfmpir  BPXDI1  bmxbmi  marcat
  3   2  indfmpir  BPXDI1  bmxbmi  marcat
  3   3  indfmpir  BPXDI1  bmxbmi  marcat
  3   4  indfmpir  BPXDI1  bmxbmi  marcat
  3   5  indfmpir  BPXDI1  bmxbmi  marcat
  4   1  indfmpir  BPXDI1  bmxbmi  marcat
  4   2  indfmpir  BPXDI1  bmxbmi  marcat
  4   3  indfmpir  BPXDI1  bmxbmi  marcat
  4   4  indfmpir  BPXDI1  bmxbmi  marcat
  4   5  indfmpir  BPXDI1  bmxbmi  marcat
  5   1  indfmpir  BPXDI1  bmxbmi  marcat
  5   2  indfmpir  BPXDI1  bmxbmi  marcat
  5   3  indfmpir  BPXDI1  bmxbmi  marcat
  5   4  indfmpir  BPXDI1  bmxbmi  marcat
  5   5  indfmpir  BPXDI1  bmxbmi  marcat
>  summary(impm1_pred)
Class: mids
Number of multiple imputations:  5
Imputation methods:
riagendr RIDRETH1 WTMEC2YR  sdmvpsu sdmvstra indfmpir   BPXDI1   bmxbmi   marcat     agec   agecsq
      ""        ""        ""        ""        ""   "norm"   "norm"   "norm"   "norm"       ""        ""
 descode
      ""
PredictorMatrix:
         riagendr RIDRETH1 WTMEC2YR sdmvpsu sdmvstra indfmpir BPXDI1 bmxbmi marcat agec agecsq
riagendr        0        1        1       0        0        1      1      1      1    1      1
RIDRETH1        1        0        1       0        0        1      1      1      1    1      1
WTMEC2YR        1        1        0       0        0        1      1      1      1    1      1
```

```
sdmvpsu         1        1        1       0        0        1      1      1      1    1      1
sdmvstra        1        1        1       0        0        1      1      1      1    1      1
indfmpir        1        1        1       0        0        0      1      1      1    1      1
         descode
riagendr       1
RIDRETH1       1
WTMEC2YR       1
sdmvpsu        1
sdmvstra       1
indfmpir       1


>  # Note small differences between 1st and 2nd implicate
>  summary(mice::complete( impm1_pred , 1 )$BPXDI1)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    0.0    64.0    72.0    70.7    78.0   120.0
>  summary(mice::complete( impm1_pred , 2 )$BPXDI1)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    0.0    64.0    72.0    70.8    78.0   120.0


>  # Combine all five data.frame objects into a list
>  list_of_data_frames <- list(
+  mice::complete(impm1_pred , 1 ) ,
+  mice::complete( impm1_pred , 2 ) ,
+  mice::complete( impm1_pred , 3 ) ,
+  mice::complete( impm1_pred , 4 ) ,
+  mice::complete( impm1_pred , 5 ))


>  # Multiply-imputed design statement
>  desnhanesm1 <- svydesign(id = ~ sdmvpsu, strat = ~ sdmvstra , weight = ~ WTMEC2YR ,
+   data = imputationList( list_of_data_frames ) , nest = TRUE )
>  desnhanesm1
Multiple (5) imputations: svydesign(id = ~sdmvpsu, strat = ~sdmvstra, weight = ~WTMEC2YR,
    data = imputationList(list_of_data_frames), nest = TRUE)


>  # Add a new variable to desnhanesm1 using imputed bpxdi1 values
> desnhanesm1 <- update(desnhanesm1, high_diastolic = ifelse(BPXDI1 >=90,1,0) )
> (desnhanesm1)
Multiple (5) imputations: svydesign(id = ~sdmvpsu, strat = ~sdmvstra, weight = ~WTMEC2YR,
    data = imputationList(list_of_data_frames), nest = TRUE)

>  # Combined mean high blood pressure with design adjustment, Table 12.4
>  fitm1_mean <- MIcombine(with(desnhanesm1, svymean(~factor(high_diastolic), se=T, ci=T, na.rm=T)))
>  fitm1_mean
Multiple imputation results:
      with(desnhanesm1, svymean(~factor(high_diastolic), se = T, ci = T,
    na.rm = T))
      MIcombine.default(with(desnhanesm1, svymean(~factor(high_diastolic),
    se = T, ci = T, na.rm = T)))
                       results      se
factor(high_diastolic)0 0.93795 0.00773
factor(high_diastolic)1 0.06205 0.00773
>  confint(fitm1_mean)
                        2.5 % 97.5 %
factor(high_diastolic)0 0.9228 0.9531
factor(high_diastolic)1 0.0469 0.0772
```

```
>  # Run design based logistic model with svyglm using 5 imputed data sets contained in desnhanesm1, Table 12.5
>  fitm1 <- MIcombine(with(desnhanesm1, svyglm (factor(high_diastolic) ~ factor(RIDRETH1) + factor(riagendr) +
agec + agecsq, family=quasibinomial)))
>  fitm1
Multiple imputation results:
      with(desnhanesm1, svyglm(factor(high_diastolic) ~ factor(RIDRETH1) +
    factor(riagendr) + agec + agecsq, family = quasibinomial))
      MIcombine.default(with(desnhanesm1, svyglm(factor(high_diastolic) ~
    factor(RIDRETH1) + factor(riagendr) + agec + agecsq, family = quasibinomial)))
                     results        se
(Intercept)       -2.242033 0.2131718
factor(RIDRETH1)2 -0.553521 0.3382193
factor(RIDRETH1)3  0.149216 0.2418729
factor(RIDRETH1)4  0.612931 0.2544578
factor(RIDRETH1)5  0.106958 0.2742154
factor(riagendr)2 -0.492720 0.1897702
agec               0.008941 0.0067064
agecsq            -0.001697 0.0002728


>  # Obtain means for 3 continuous variables imputed using method 1, Table 12.3 (by each replicate)
>  fitm1_ex12_3 <- with(desnhanesm1, svymean(~bmxbmi + BPXDI1 + indfmpir), se=T, na.rm=T, ci=T )
>  fitm1_ex12_3
[[1]]
          mean   SE
bmxbmi   28.62 0.21
BPXDI1   71.30 0.46
indfmpir  2.86 0.10

[[2]]
          mean   SE
bmxbmi   28.63 0.21
BPXDI1   71.45 0.47
indfmpir  2.84 0.10

[[3]]
          mean   SE
bmxbmi   28.61 0.21
BPXDI1   71.36 0.45
indfmpir  2.85 0.10

[[4]]
          mean   SE
bmxbmi   28.63 0.21
BPXDI1   71.36 0.47
indfmpir  2.85 0.10

[[5]]
          mean   SE
bmxbmi   28.63 0.21
BPXDI1   71.32 0.44
indfmpir  2.84 0.10

attr(,"call")
with(desnhanesm1, svymean(~bmxbmi + BPXDI1 + indfmpir), se = T,
    na.rm = T, ci = T)
>
```

```
>  # Imputation 2 NO design variables in models
>  # Return to original data without the CC high diastolic blood pressure
>
>  nhanesc12_submeth2 <- nhanesc12
>  names(nhanesc12_submeth2)
 [1] "riagendr"       "RIDRETH1"       "WTMEC2YR"       "sdmvpsu"        "sdmvstra"
 [6] "indfmpir"       "BPXDI1"         "bmxbmi"         "age"            "marcat"
[11] "bpxdi1_1"       "agec"           "agecsq"         "descode"        "high_diastolic"
>
>  # Subset variables by number position in data set , drop high_diastolic for imputations
>  (nhanesc12_subset  <- nhanesc12[, c(1,2,3,4,5,6,7,8,10, 12,13,14)])
# A tibble: 5,615 × 12
   riagendr RIDRETH1 WTMEC2YR sdmvpsu sdmvstra indfmpir BPXDI1 bmxbmi marcat   agec  agecsq descode
      <dbl>    <dbl>    <dbl>   <dbl>    <dbl>    <dbl>  <dbl>  <dbl>  <dbl>  <dbl>   <dbl>   <dbl>
 1        1        3  104237.       1       91     3.15     82   23.3      3 -24.4   593.       911
 2        2        3  127965.       1       94     1.67     56   23.2      1  -2.36    5.57     941
 3        1        5   14784.       1       92     0.33     80   20.1      3 -25.4   643.       921
 4        2        4   27123.       2       96     2.02     70   33.3      3  -3.36   11.3      962
 5        1        3   27336.       3       90     4.3      NA   33.9      1  33.6  1132.       903
 6        2        3   54203.       1       99     5        NA   23.3      1 -12.4   153.       991
 7        1        5    7851.       2       92    NA        68   20.1      1   4.64   21.5      922
 8        1        3   13190.       1       95     0.05     72   28.5      2  33.6  1132.       951
 9        1        5   17115.       1       92     5        78   27.6      1   8.64   74.6      921
10        1        3   22616.       1       97     0.87     62   27.9      1 -11.4   129.       971
# ℹ 5,605 more rows
# ℹ Use `print(n = ...)` to see more rows
>  summary(nhanesc12_subset)
    riagendr       RIDRETH1      WTMEC2YR         sdmvpsu        sdmvstra        indfmpir
 Min.   :1.00   Min.   :1.0   Min.   :  4413   Min.   :1.00   Min.   : 90.0   Min.   :0.0
 1st Qu.:1.00   1st Qu.:3.0   1st Qu.: 16173   1st Qu.:1.00   1st Qu.: 92.0   1st Qu.:0.9
 Median :2.00   Median :3.0   Median : 24567   Median :2.00   Median : 96.0   Median :1.8
 Mean   :1.51   Mean   :3.3   Mean   : 41318   Mean   :1.64   Mean   : 95.9   Mean   :2.4
 3rd Qu.:2.00   3rd Qu.:4.0   3rd Qu.: 45238   3rd Qu.:2.00   3rd Qu.: 99.0   3rd Qu.:3.9
 Max.   :2.00   Max.   :5.0   Max.   :222580   Max.   :3.00   Max.   :103.0   Max.   :5.0
                                                                              NA's   :487
     BPXDI1          bmxbmi         marcat          agec            agecsq          descode
 Min.   :  0.0   Min.   :13.4   Min.   :1.00   Min.   :-28.36   Min.   :   0.1   Min.   : 901
 1st Qu.: 64.0   1st Qu.:23.8   1st Qu.:1.00   1st Qu.:-15.36   1st Qu.:  58.4   1st Qu.: 922
 Median : 72.0   Median :27.4   Median :1.00   Median :  0.64   Median : 244.6   Median : 961
 Mean   : 70.7   Mean   :28.6   Mean   :1.65   Mean   :  0.81   Mean   : 345.1   Mean   : 960
 3rd Qu.: 78.0   3rd Qu.:32.0   3rd Qu.:2.00   3rd Qu.: 15.64   3rd Qu.: 558.8   3rd Qu.: 992
 Max.   :120.0   Max.   :82.1   Max.   :3.00   Max.   : 33.64   Max.   :1131.6   Max.   :1032
 NA's   :483     NA's   :90     NA's   :300
>
>  nhanesc12_subm2 <- nhanesc12_subset
>
>  # Add a predictor matrix to control imputation model predictors for each imputed variable
>  pred <- impm2$predictorMatrix
Error: object 'impm2' not found
>  pred[,"sdmvpsu"] <- 0
>  pred[,"sdmvstra"] <- 0
>  pred[,"descode"] <- 0
>  pred[,"WTMEC2YR"] <- 0
>  impm2$predictorMatrix
Error: object 'impm2' not found
>
>  pred
         riagendr RIDRETH1 WTMEC2YR sdmvpsu sdmvstra indfmpir BPXDI1 bmxbmi marcat agec agecsq
riagendr        0        1        0       0        0        1      1      1      1    1      1
```

```
RIDRETH1        1        0        0       0        0        1      1      1      1    1      1
WTMEC2YR        1        1        0       0        0        1      1      1      1    1      1
sdmvpsu         1        1        0       0        0        1      1      1      1    1      1
sdmvstra        1        1        0       0        0        1      1      1      1    1      1
indfmpir        1        1        0       0        0        0      1      1      1    1      1
BPXDI1          1        1        0       0        0        1      0      1      1    1      1
bmxbmi          1        1        0       0        0        1      1      0      1    1      1
marcat          1        1        0       0        0        1      1      1      0    1      1
agec            1        1        0       0        0        1      1      1      1    0      1
agecsq          1        1        0       0        0        1      1      1      1    1      0
descode         1        1        0       0        0        1      1      1      1    1      1
         descode
riagendr       0
RIDRETH1       0
WTMEC2YR       0
sdmvpsu        0
sdmvstra       0
indfmpir       0
BPXDI1         0
bmxbmi         0
marcat         0
agec           0
agecsq         0
descode        0
>
>  impm2_pred <- mice(nhanesc12_subm2, pred=pred, n.imp=5, seed=2024,
defaultMethod=c("norm","logreg","polyreg"))

 iter imp variable
  1   1  indfmpir  BPXDI1  bmxbmi  marcat
  1   2  indfmpir  BPXDI1  bmxbmi  marcat
  1   3  indfmpir  BPXDI1  bmxbmi  marcat
  1   4  indfmpir  BPXDI1  bmxbmi  marcat
  1   5  indfmpir  BPXDI1  bmxbmi  marcat
  2   1  indfmpir  BPXDI1  bmxbmi  marcat
  2   2  indfmpir  BPXDI1  bmxbmi  marcat
  2   3  indfmpir  BPXDI1  bmxbmi  marcat
  2   4  indfmpir  BPXDI1  bmxbmi  marcat
  2   5  indfmpir  BPXDI1  bmxbmi  marcat
  3   1  indfmpir  BPXDI1  bmxbmi  marcat
  3   2  indfmpir  BPXDI1  bmxbmi  marcat
  3   3  indfmpir  BPXDI1  bmxbmi  marcat
  3   4  indfmpir  BPXDI1  bmxbmi  marcat
  3   5  indfmpir  BPXDI1  bmxbmi  marcat
  4   1  indfmpir  BPXDI1  bmxbmi  marcat
  4   2  indfmpir  BPXDI1  bmxbmi  marcat
  4   3  indfmpir  BPXDI1  bmxbmi  marcat
  4   4  indfmpir  BPXDI1  bmxbmi  marcat
  4   5  indfmpir  BPXDI1  bmxbmi  marcat
  5   1  indfmpir  BPXDI1  bmxbmi  marcat
  5   2  indfmpir  BPXDI1  bmxbmi  marcat
  5   3  indfmpir  BPXDI1  bmxbmi  marcat
  5   4  indfmpir  BPXDI1  bmxbmi  marcat
  5   5  indfmpir  BPXDI1  bmxbmi  marcat
>  summary(impm2_pred)
Class: mids
Number of multiple imputations:  5
Imputation methods:
riagendr RIDRETH1 WTMEC2YR  sdmvpsu sdmvstra indfmpir   BPXDI1   bmxbmi   marcat     agec   agecsq
```

```
      ""       ""       ""       ""       ""   "norm"   "norm"   "norm"   "norm"       ""       ""
 descode
      ""
PredictorMatrix:
         riagendr RIDRETH1 WTMEC2YR sdmvpsu sdmvstra indfmpir BPXDI1 bmxbmi marcat agec agecsq
riagendr        0        1        0       0        0        1      1      1      1    1      1
RIDRETH1        1        0        0       0        0        1      1      1      1    1      1
WTMEC2YR        1        1        0       0        0        1      1      1      1    1      1
sdmvpsu         1        1        0       0        0        1      1      1      1    1      1
sdmvstra        1        1        0       0        0        1      1      1      1    1      1
indfmpir        1        1        0       0        0        0      1      1      1    1      1
         descode
riagendr       0
RIDRETH1       0
WTMEC2YR       0
sdmvpsu        0
sdmvstra       0
indfmpir       0
>
>  # Small differences between 1st and 2nd implicate
>  summary(mice::complete( impm2_pred , 1 )$BPXDI1)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    0.0    64.0    72.0    70.8    78.0   120.0
>  summary(mice::complete( impm2_pred , 2 )$BPXDI1)
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    0.0    64.0    71.7    70.7    78.0   120.0


>  # Combine all five data.frame objects into a list
>  list_of_data_frames2 <-list(
+  mice::complete( impm2_pred , 1 ) ,
+  mice::complete( impm2_pred , 2 ) ,
+  mice::complete( impm2_pred , 3 ) ,
+  mice::complete( impm2_pred , 4 ) ,
+  mice::complete( impm2_pred , 5 )
+  )

>  # Multiply-imputed design statement
>  desnhanesm2 <-svydesign(id = ~ sdmvpsu, strat = ~ sdmvstra , weight = ~ WTMEC2YR ,
+   data = imputationList( list_of_data_frames2 ), nest = TRUE)
>  desnhanesm2
Multiple (5) imputations: svydesign(id = ~sdmvpsu, strat = ~sdmvstra, weight = ~WTMEC2YR,
    data = imputationList(list_of_data_frames2), nest = TRUE)

>  # Add a new variable to desnhanesm2 using imputed blood pressure values
>  desnhanesm2 <- update( desnhanesm2, high_diastolic = ifelse(BPXDI1 >=90,1,0))
>  (desnhanesm2)
Multiple (5) imputations: svydesign(id = ~sdmvpsu, strat = ~sdmvstra, weight = ~WTMEC2YR,
    data = imputationList(list_of_data_frames2), nest = TRUE)
```

```
>  # Combined mean high blood pressure with NO design adjustment, Table 12.4
>  fitm2_mean <- MIcombine(with(desnhanesm2, svymean(~factor(high_diastolic), se=T, na.rm=T, ci=T )))

>  fitm2_mean
Multiple imputation results:
      with(desnhanesm2, svymean(~factor(high_diastolic), se = T, na.rm = T,
    ci = T))
      MIcombine.default(with(desnhanesm2, svymean(~factor(high_diastolic),
    se = T, na.rm = T, ci = T)))
                        results       se
factor(high_diastolic)0 0.93931 0.006851
factor(high_diastolic)1 0.06069 0.006851


>  # Run design based logistic model with svyglm using 5 imputed data sets contained in desnhanesm2, Table 12.5
>  fitm2 <- MIcombine(with(desnhanesm2, svyglm (factor(high_diastolic) ~ factor(RIDRETH1) + factor(riagendr) +
agec + agecsq, family=quasibinomial)))

>  (fitm2)
Multiple imputation results:
      with(desnhanesm2, svyglm(factor(high_diastolic) ~ factor(RIDRETH1) +
    factor(riagendr) + agec + agecsq, family = quasibinomial))
      MIcombine.default(with(desnhanesm2, svyglm(factor(high_diastolic) ~
    factor(RIDRETH1) + factor(riagendr) + agec + agecsq, family = quasibinomial)))
                     results        se
(Intercept)       -2.246027 0.2209162
factor(RIDRETH1)2 -0.627261 0.2862377
factor(RIDRETH1)3  0.149691 0.2387049
factor(RIDRETH1)4  0.644521 0.2527741
factor(RIDRETH1)5  0.064117 0.2469976
factor(riagendr)2 -0.541073 0.2045024
agec               0.007834 0.0066280
agecsq            -0.001691 0.0003141


>  # Obtain means for 3 continuous variables imputed using method 2 (NO DESIGN) , Table 12.3 (by each replicate)
>  fitm2_ex12_3 <- with(desnhanesm2, svymean(~bmxbmi + BPXDI1 + indfmpir, se=T, na.rm=T, ci=T ))
>  fitm2_ex12_3
[[1]]
          mean   SE
bmxbmi   28.61 0.21
BPXDI1   71.41 0.43
indfmpir  2.83 0.10

[[2]]
          mean   SE
bmxbmi   28.62 0.21
BPXDI1   71.25 0.42
indfmpir  2.83 0.10

[[3]]
          mean   SE
bmxbmi   28.62 0.21
BPXDI1   71.31 0.46
indfmpir  2.83 0.10

[[4]]
          mean   SE
bmxbmi   28.62 0.21
```

```
BPXDI1   71.36 0.44
indfmpir  2.82 0.10

[[5]]
          mean   SE
bmxbmi   28.62 0.21
BPXDI1   71.27 0.47
indfmpir  2.82 0.10

attr(,"call")
with(desnhanesm2, svymean(~bmxbmi + BPXDI1 + indfmpir, se = T,
    na.rm = T, ci = T))

>  # Note: FEFI method not available in R Survey Package, see examples using other software such as SAS PROC
SURVEYIMPUTE
```