IDA Assignment 3

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Q1.

Consider the `nhanes` dataset in mice. For more information please type help(`nhanes`) in the R console.

a)

(2 marks) What percentage of the cases is incomplete?

Answer :

```
cat("The percentage of incomplete cases is",
    (nrow(nhanes)-nrow(cc(nhanes)))*100/nrow(nhanes))
```

```
## The percentage of incomplete cases is 48
```

b)

(4 marks) Impute the data with `mice` using the defaults with `seed=1`, in step 2 predict `bmi` from `age`, `hyp`, and `chl` by the normal linear regression model, and then pool the results. What are the proportions of variance due to the missing data for each parameter? Which parameters appear to be most affected by the nonresponse?

Answer :

```
pool1 <- pool(with(mice(nhanes, printFlag = F, seed = 1), lm(bmi ~ as.factor(age) + hyp + chl)))
kable(pool1$pooled[,c(1,3,7,8,10)], caption = "Imputation with seed=1") %>%
  kable_styling(latex_options = "hold_position")
```

Table 1: Imputation with seed=1

term	estimate	dfcom	df	lambda
(Intercept)	16.0426979	20	9.743911	0.3071661
as.factor(age)2	-5.2508182	20	5.496624	0.5204870
as.factor(age)3	-6.8779315	20	3.466705	0.6819661
hyp	2.4662556	20	8.463472	0.3606031
chl	0.0544513	20	8.530893	0.3576185

c)

(4 marks) Repeat the analysis for `seed` $\in \{2, 3, 4, 5, 6\}$. Do the conclusions remain the same?

Answer :

```
pool2 <- pool(with(mice(nhanes, printFlag = F, seed = 2), lm(bmi ~ age + hyp + chl)))
pool3 <- pool(with(mice(nhanes, printFlag = F, seed = 3), lm(bmi ~ age + hyp + chl)))
pool4 <- pool(with(mice(nhanes, printFlag = F, seed = 4), lm(bmi ~ age + hyp + chl)))
pool5 <- pool(with(mice(nhanes, printFlag = F, seed = 5), lm(bmi ~ age + hyp + chl)))
pool6 <- pool(with(mice(nhanes, printFlag = F, seed = 6), lm(bmi ~ age + hyp + chl)))

parameters <- c("(Intercept)", "age", "hyp", "chl")
df <- data.frame(parameters, pool2$pooled[,10], pool3$pooled[,10],
                 pool4$pooled[,10], pool5$pooled[,10], pool6$pooled[,10])
colnames(df) <- c("parameters", "seed=2", "seed=3", "seed=4", "seed=5", "seed=6")
kable(df, caption="Imputation with seed=2,3,4,5,6") %>%
  kable_styling(latex_options = "hold_position")
```

Table 2: Imputation with seed=2,3,4,5,6

parameters	seed=2	seed=3	seed=4	seed=5	seed=6
(Intercept)	0.4144454	0.2772900	0.1315114	0.4855733	0.4168136
age	0.4033924	0.5895051	0.2189333	0.4511896	0.6549523
hyp	0.1430995	0.4101152	0.1961083	0.5942866	0.2960364
chl	0.2959966	0.5621346	0.3305334	0.2346065	0.5196295

d)

(4 marks) Repeat the analysis with $M = 100$ with the same seeds. Would you prefer these analyses over those with $M = 5$? Explain why.

Answer :

```
pool1 <- pool(with(mice(nhanes, m = 100, printFlag = F, seed = 1),
                   lm(bmi ~ age + hyp + chl)))
pool2 <- pool(with(mice(nhanes, m = 100, printFlag = F, seed = 2),
                   lm(bmi ~ age + hyp + chl)))
pool3 <- pool(with(mice(nhanes, m = 100, printFlag = F, seed = 3),
                   lm(bmi ~ age + hyp + chl)))
pool4 <- pool(with(mice(nhanes, m = 100, printFlag = F, seed = 4),
                   lm(bmi ~ age + hyp + chl)))
pool5 <- pool(with(mice(nhanes, m = 100, printFlag = F, seed = 5),
                   lm(bmi ~ age + hyp + chl)))
pool6 <- pool(with(mice(nhanes, m = 100, printFlag = F, seed = 6),
                   lm(bmi ~ age + hyp + chl)))

parameters <- c("(Intercept)", "age", "hyp", "chl")
df <- data.frame(parameters, pool1$pooled[,10], pool2$pooled[,10],
                 pool3$pooled[,10], pool4$pooled[,10],
                 pool5$pooled[,10], pool6$pooled[,10])
colnames(df) <- c("parameters", "seed=1", "seed=2", "seed=3", "seed=4",
                  "seed=5", "seed=6")
kable(df, caption="Imputation with seed=1,2,3,4,5,6 and M=100") %>%
  kable_styling(latex_options = "hold_position")
```

Table 3: Imputation with seed=1,2,3,4,5,6 and M=100

parameters	seed=1	seed=2	seed=3	seed=4	seed=5	seed=6
(Intercept)	0.2290445	0.1882474	0.2199607	0.2144722	0.2294356	0.2472607
age	0.4324680	0.4031077	0.3093072	0.3943223	0.3322570	0.4430300
hyp	0.2915346	0.2825108	0.2425105	0.2565132	0.2893046	0.2860700
chl	0.3217837	0.2939693	0.3281911	0.2835232	0.2461956	0.3113085

The pooled estimates is more stable when the value of M is higher. Thus, we would prefer $M = 100$ than $M = 5$

Q2.

(15 marks) Each of the 100 datasets contained in the file dataex2.Rdata was generated in the following way

$$y_i|x_i \overset{\text{ind.}}{\sim} \text{N}(\beta_0 + \beta_1 x_i, 1), \quad x_i \overset{\text{ind.}}{\sim} \text{Unif}(-1, 1), \quad \beta_0 = 1, \quad \beta_1 = 3$$

for $i = 1, \ldots, 100$. Additionally, some of the responses were set to be missing using a MAR mechanism. The goal of this exercise is to study the effect that acknowledging/not acknowledging parameter uncertainty when performing step 1 of multiple imputation might have on the coverage of the corresponding confidence intervals. Further suppose that the analysis of interest in step 2 is to fit the regression model that was used to generate the data, i.e., a normal linear regression model where the response is y and the covariate is x. With the aid of the `mice` package, calculate the empirical coverage probability of the 95% confidence intervals for β_1 under the following two approaches: stochastic regression imputation and the corresponding bootstrap based version. Comment. For both approaches, please consider $m = 20$ and `seed=1`. **NOTE 1:** In order to calculate the empirical coverage probability, you only need to compute the proportion of the time (over the 100 intervals) that the interval contains the true value of the parameter. **NOTE 2:** The data are stored in an array structure such that, for instance, `dataex2[, , 1]`, corresponds to the first dataset (which has 100 rows and 2 columns, with the first column containing the values of x and the second the values of y).

Answer :

```
# initialize a counter
count <- 0
for (i in 1:nrow(dataex2)) {
  #impute values for the ith dataset using M=20
  impute.sri <- mice(dataex2[, , i], m = 20, method = "norm.nob", printFlag = F, seed = 1)
  fit.sri <- with(impute.sri, lm(Y ~ X)) #step 2
  pool.sri <- pool(fit.sri) # step 3
  summary.sri <- summary(pool.sri, conf.int = TRUE)
  if (summary.sri[2, 7] <= 3 & summary.sri[2, 8] >= 3) {
  count <- count + 1 #add to the counter if the the value of beta1 is contained in the
  #confidence interval
  }
}
ecp.sri <- count/nrow(dataex2)
cat("the proportion of the time for Stochastic Imputation is", ecp.sri)
```

```
## the proportion of the time for Stochastic Imputation is 0.88
```

```
# initialize a counter
count <- 0
for (i in 1:nrow(dataex2)) {
  #impute values for the ith dataset, using m=20
  impute.bootstrap <- mice(dataex2[,,i], m = 20, method = "norm.boot",
                           printFlag = FALSE, seed = 1)
  fit.bootstrap <- with(impute.bootstrap, lm(Y ~ X)) #step 2
  pool.bootstrap <- pool(fit.bootstrap) # step 3
  summary.bootstrap <- summary(pool.bootstrap, conf.int = TRUE)
  if (summary.bootstrap[2, c(7)] <= 3 & summary.bootstrap[2, c(8)] >= 3) {
    count = count + 1 #add to the counter if the true value of beta1 is contained in the
  }
}
ecp.bootstrap <- count/nrow(dataex2)
cat("the proportion of the time for Bootstrap is", ecp.bootstrap)
```

```
## the proportion of the time for Bootstrap is 0.95
```

Q3.

(9 marks) Show that for a linear (in the coefficients) regression model, the following two strategies coincide:

(i) Computing the predicted values (point estimates) from each fitted model in step 2 and then pooling them according to Rubin's rule for point estimates (i.e., averaging the predicted values across the imputed datasets).

(ii) Pooling the regression coefficients from each fitted model in step 2 using Rubin's rule for point estimates and then computing the predicted values afterwards

Answer :

We consider a linear regression model given a dataset as $\{y_i, x_{1i}, \ldots, x_{ni}\}$

$$y_i = \beta_0 + \beta_1 x_{1i} + \cdots + \beta_n x_{ni} + \varepsilon_i, \quad \varepsilon_i \sim N(0, \sigma^2)$$

Now we look into Case (i), we compute the predicted values for each fitted model from step 2. Then we obtain as below,

$$\hat{y}_i^{(m)} = \hat{\beta}_0^{(m)} + \hat{\beta}_1^{(m)} x_{1i} + \cdots + \hat{\beta}_n^{(m)} x_{ni}$$

Then we pool them according to Rubin's rule for point estimates.

$$\begin{aligned}
\bar{y}_i &= \frac{1}{M} \sum_{i=1}^{M} \hat{y}^{(m)} \\
&= \frac{1}{M} \sum_{i=1}^{M} \left(\hat{\beta}_0^{(m)} + \hat{\beta}_1^{(m)} x_{1i} + \cdots + \hat{\beta}_n^{(m)} x_{ni} \right) \\
&= \frac{1}{M} \sum_{i=1}^{M} \hat{\beta}_0^{(m)} + \frac{1}{M} \sum_{i=1}^{M} \hat{\beta}_1^{(m)} x_{1i} + \cdots + \frac{1}{M} \sum_{i=1}^{M} \hat{\beta}_n^{(m)} x_{ni} \\
&= \bar{\beta}_0 + \bar{\beta}_1 x_{1i} + \cdots + \bar{\beta}_n x_{ni}
\end{aligned}$$

Now, let us consider Case (ii) to validate if they coincide. We pool the regression coefficients from each fitted model in step 2 using Rubin's rule for point estimates.

$$\begin{aligned}
\bar{\beta}_0 &= \frac{1}{M} \sum_{i=1}^{M} \hat{\beta}_0^{(m)} \\
&\vdots \\
\bar{\beta}_n &= \frac{1}{M} \sum_{i=1}^{M} \hat{\beta}_n^{(m)}
\end{aligned}$$

Then we can compute the predicted values as follow

$$\bar{y}_i = \bar{\beta}_0 + \bar{\beta}_1 x_{1i} + \cdots + \bar{\beta}_n x_{ni}$$

As shown above, the order of the computation of predicted values for each fitted model in step 2 and pooling according to Rubin's rule for point estimates do not matter mathematically. Therefore, we conclude here by saying that both cases coincide.

Q4.

The goal of this exercise is to study different ways of using `mice` when the analysis model of interest/substantive model involves an interaction term between incomplete variables. The model used to generate the data (available in `dataex4.Rdata`), which corresponds to our model of interest in step 2, was the following one:

$$y_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \beta_3 x_{1i} x_{2i} + \varepsilon_i, x_{1i} \overset{\text{iid}}{\sim} \text{N}(0,1), \quad x_{2i} \overset{\text{iid}}{\sim} \text{N}(1.5,1), \quad \varepsilon_i \overset{\text{iid}}{\sim} \text{N}(0,1)$$

for $i = 1, \ldots, 1000$, $\beta_0 = 1.5$, $\beta_1 = 1$, $\beta_2 = 2$ and $\beta_3 = 1$. Additionally, missingness was imposed on y and x_1 and so the interaction variable $x_1 x_2$ also has missing values, although the missingness in this interaction variable is induced by the missing in the covariate x_1. In the following, please use $M = 50$ and `seed=1`.

```
kable(head(dataex4), caption="dataex4 observation")  %>%
  kable_styling(latex_options = "hold_position")
```

Table 4: dataex4 observation

y	x1	x2
NA	NA	1.0983213
4.609476	0.0265944	1.1290673
NA	-1.5165531	1.0748538
1.718231	-1.3626533	1.9411515
NA	1.1784892	0.8272496
1.820674	-0.9341513	1.9166941

a)

(6 marks) By only imputing the y and x_1 variables in step 1, provide the estimates of β_1, β_2, and β_3 along with 95% confidence intervals. Comment. Note that this approach where the interaction variable is left outside the imputation process and calculated afterwards in the analysis model, is known as *Impute, then transform*

Answer :

```
impute.sri <- mice(dataex4, m = 50, seed = 1, printFlag = FALSE)
fit.sri <- with(impute.sri, lm(y ~ x1 + x2 + x1*x2))
pool.sri <- pool(fit.sri)
kable(summary(pool.sri, conf.int = TRUE)[, c(1,2,3,7,8)],
      caption = "Summary Statistics of Imputation of $y$ and $x_1$") %>%
  kable_styling(latex_options = "hold_position")
```

Table 5: Summary Statistics of Imputation of y and x_1

term	estimate	std.error	2.5 %	97.5 %
(Intercept)	1.5929831	0.0954133	1.404501	1.7814655
x1	1.4112333	0.0973291	1.219397	1.6030697
x2	1.9658191	0.0532322	1.860657	2.0709812
x1:x2	0.7550367	0.0570146	0.642302	0.8677715

b)

(10 marks) Now, start by calculating the interaction variable in the incomplete data and append it as a variable to your dataset. Then, use *passive imputation* to impute the interaction variable. Provide the estimates of β_1, β_2, and β_3 along with 95% confidence intervals. Comment.

Answer :

```
x1 <- dataex4$x1; x2 <- dataex4$x2; dataex4$x1x2 <- x1*x2
impute.null <- mice(dataex4, maxit = 0)
method <- impute.null$method
method["x1x2"] <- "~I(x1*x2)"
pred <- impute.null$predictorMatrix
pred[c("x1", "x2"), "x1x2"] <- 0
visit.seq <- impute.null$visitSequence
visit.seq
```

```
## [1] "y"    "x1"   "x2"   "x1x2"
```

```
impute.passive <- mice(dataex4, method = method, predictorMatrix = pred,
                visitSequence = visit.seq, m = 50, seed = 1, printFlag = FALSE)
pool.passive <- pool(with(impute.passive, lm(y ~ x1 + x2 + x1*x2)))
kable(summary(pool.passive, conf.int=TRUE)[,c(1,2,3,7,8)],
      caption = "Summary Statistics of Imputation of $y$ and $x_1$") %>%
  kable_styling(latex_options = "hold_position")
```

Table 6: Summary Statistics of Imputation of y and x_1

term	estimate	std.error	2.5 %	97.5 %
(Intercept)	1.5534782	0.0884221	1.3788626	1.7280939
x1	1.1926170	0.0958435	1.0034980	1.3817360
x2	1.9964402	0.0493658	1.8989468	2.0939336
x1:x2	0.8740573	0.0567852	0.7615712	0.9865434

c)

(10 marks) Now that you have already appended the interaction variable to the dataset, impute it as it was *just another variable* (or like any other variable) in the dataset and use this variable for the interaction term in step 2. Provide the estimates of β_1, β_2 and β_3 along with 95% confidence intervals. Comment.

Answer :

```
impute.jav <- mice(dataex4, m = 50, seed = 1, printFlag = FALSE)
fit.jav <- with(impute.jav, lm(y ~ x1 + x2 + x1x2))
pool.jav <- pool(fit.jav)
kable( summary(pool.jav, conf.int=TRUE)[, c(1,2,3,7,8)],
      caption = "Summary Statistics of Imputation of $y$ and $x_1$") %>%
  kable_styling(latex_options = "hold_position")
```

Table 7: Summary Statistics of Imputation of y and x_1

term	estimate	std.error	2.5 %	97.5 %
(Intercept)	1.499714	0.0782144	1.3452011	1.654227
x1	1.003930	0.0822837	0.8414967	1.166363
x2	2.026180	0.0437161	1.9398113	2.112548
x1x2	1.017793	0.0442807	0.9303479	1.105238

d)

(6 marks) What is the obvious conceptual drawback of the *just another variable* approach for imputing interactions?

Answer :

Q5

(30 marks) The file `NHANES2.Rdata` contains a subset of data from the *National Health and Nutrition Examination Survey* (NHANES), whose goal is to assess the health and nutritional status of adults and children in the United States. The variables in the dataset are the following:

- `wgt`: weight in kg,
- `gender`: male vs female,
- `bili`: bilirubin concentration in mg/dL,
- `age`: in years,
- `chol`: total serum cholestrol in mg/dL,
- `HDL`: High-density lipoprotein cholestrol in mg/dL,
- `hgt`: height in metres,
- `educ`: educational status; 5 ordered categories,
- `race`: 5 unordered categories,
- `SBP`: systolic blood pressure in mmHg,
- `hypten`: hyptertensive status; binary,
- `WC`: waist circumference in cm.

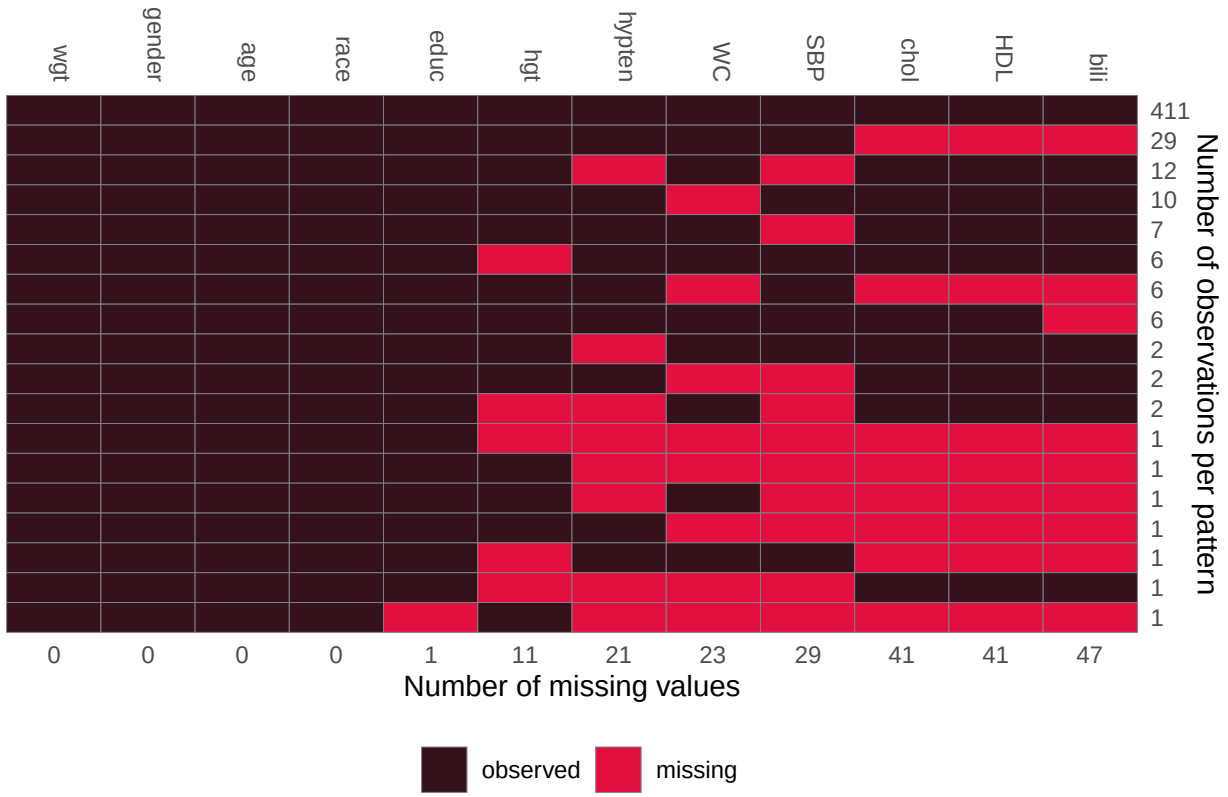
The analysis of interest is the following:

$$\text{wgt} = \beta_0 + \beta_1 \text{gender} + \beta_2 \text{age} + \beta_3 \text{hgt} + \beta_4 \text{WC} + \varepsilon, \quad \varepsilon \sim N(0, \sigma^2).$$

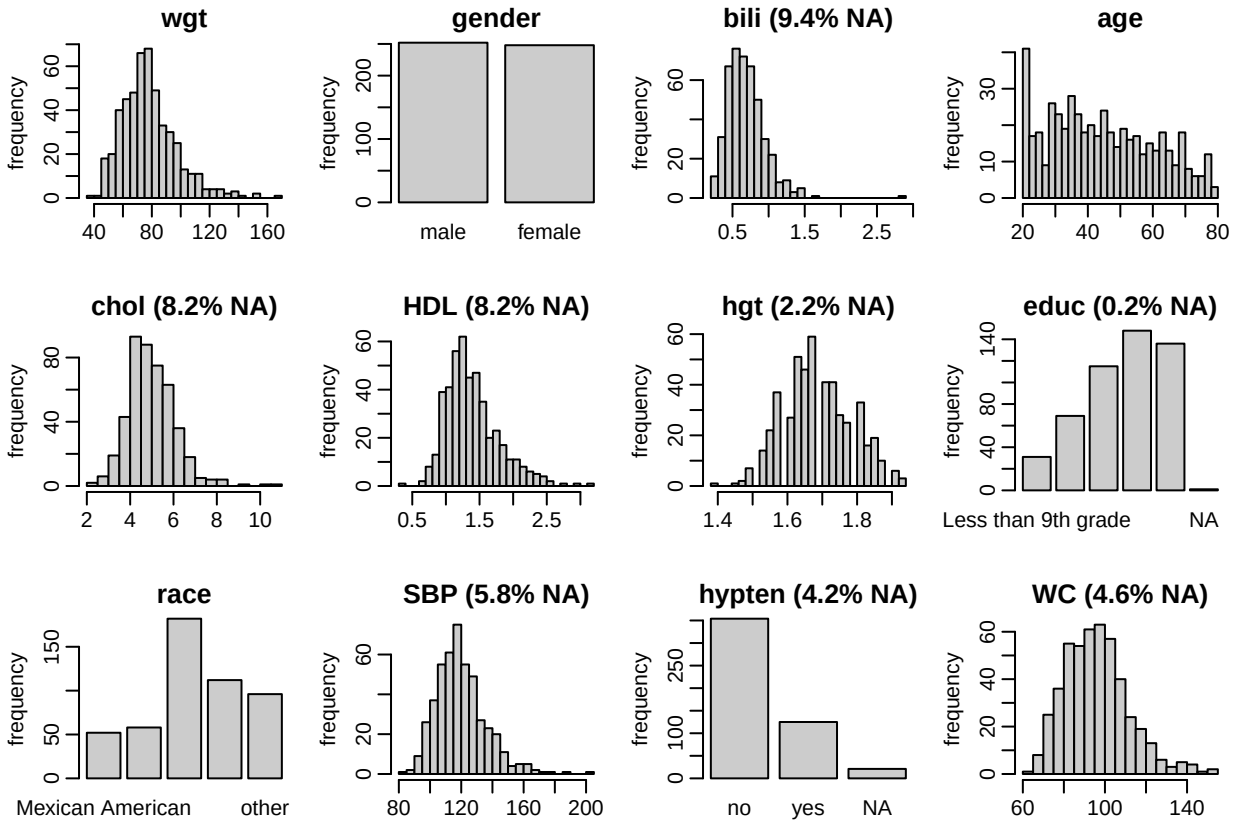
Using multiple imputation and conducting all necessary checks, report your findings.

Answer :

```
nhanes2 <- NHANES2
md_pattern(nhanes2, pattern = FALSE, color = c('#34111b', '#e30f41'))
```




```
par(mar = c(3,3,2,1), mgp = c(2,0.6,0))
plot_all(nhanes2, breaks = 30, ncol = 4)
```




```
impute.null <- mice(nhanes2, maxit = 0)
meth <- impute.null$method
meth["hgt"] <- "norm"
meth
```

```
##       wgt    gender      bili       age      chol       HDL       hgt      educ
##        ""        ""    "pmm"        ""     "pmm"     "pmm"    "norm"    "polr"
##      race       SBP   hypten        WC
##        ""     "pmm" "logreg"     "pmm"
```

```
post <- impute.null$post
post["hgt"] <- "imp[[j]][,i] <- squeeze(imp[[j]][,i], c(1.397, 1.9304))"
# visSeq <- impute.null$visitSequence
```

While inspecting the missing data pattern, we found 411 observations with observed values on all 12 variables. Also, 10 observations for which on `WC` is missing, 6 observations for which on `hgt` is missing Interestingly, we can observe that there are 29 observations for which on `chol`, `HDL` and `bili` are missing.

We can visualise the variables' distributions using `plot_all()`. In the plot above, depicting the distribution of the observed data for the different variables, we could appreciate that `hgt` following a normal distribution is possibly not a completely unreasonable idea. Let us then change the default from predictive mean matching method (`pmm`) to `norm` for the variable `hgt`.

However, we need to be careful, because we do not want to risk imputing a negative value for the height. With the below syntax all imputed values of `hgt` that are outside the interval `(min(nhanes2$hgt), max(nhanes2$hgt))` will be set to those limiting values.

Since our model is limited to this, $\text{wgt} = \beta_0 + \beta_1 \text{gender} + \beta_2 \text{age} + \beta_3 \text{hgt} + \beta_4 \text{WC} + \varepsilon, \quad \varepsilon \sim N(0, \sigma^2)$.. We will end our data preprocessing and proceed to the next them in tuning the hyperparameters for imputation

```
seed1.5 <- pool(with(mice(nhanes2, methods = meth, post = post, maxit = 20,
                          m = 5, seed = 1, printFlag = FALSE),
                     lm(wgt ~ gender + age + hgt + WC)))
seed1.10 <- pool(with(mice(nhanes2, methods = meth, post = post, maxit = 20,
                          m = 10, seed = 1, printFlag = FALSE),
                     lm(wgt ~ gender + age + hgt + WC)))
seed1.20 <- pool(with(mice(nhanes2, methods = meth, post = post, maxit = 20,
                          m = 20, seed = 1, printFlag = FALSE),
                     lm(wgt ~ gender + age + hgt + WC)))
seed1.25 <- pool(with(mice(nhanes2, methods = meth, post = post, maxit = 20,
                          m = 25, seed = 1, printFlag = FALSE),
                     lm(wgt ~ gender + age + hgt + WC)))

seed2.5 <- pool(with(mice(nhanes2, methods = meth, post = post, maxit = 20,
                          m = 5, seed = 2, printFlag = FALSE),
                     lm(wgt ~ gender + age + hgt + WC)))
seed2.10 <- pool(with(mice(nhanes2, methods = meth, post = post, maxit = 20,
                          m = 10, seed = 2, printFlag = FALSE),
                     lm(wgt ~ gender + age + hgt + WC)))
seed2.20 <- pool(with(mice(nhanes2, methods = meth, post = post, maxit = 20,
                          m = 20, seed = 2, printFlag = FALSE),
                     lm(wgt ~ gender + age + hgt + WC)))
seed2.25 <- pool(with(mice(nhanes2, methods = meth, post = post, maxit = 20,
                          m = 25, seed = 2, printFlag = FALSE),
                     lm(wgt ~ gender + age + hgt + WC)))
# parameters <- c("(Intercept)", "gender", "age", "hgt", "WC")
# df <- data.frame(parameters, seed1.5$pooled[,10], seed1.10$pooled[,10],
#                  seed1.20$pooled[,10], seed1.25$pooled[,10],
#                  seed2.5$pooled[,10], seed2.10$pooled[,10],
#                  seed2.20$pooled[,10], seed2.25$pooled[,10])
# colnames(df) <- c("parameters", "seed1.5", "seed1.10", "seed1.20", "seed1.25",
#                   "seed2.5", "seed2.10", "seed2.20", "seed2.25")
# kable(df, caption="Imputation with various seed and m values") %>%
#   kable_styling(latex_options = "hold_position")
```

```
kable(data.frame(summary(seed1.5, conf.int = TRUE)[, c(1, 2, 3, 7, 8)],
                 lambda = seed1.5$pooled[,10]), caption = "Seed=1 and m=5") %>%
  kable_styling(latex_options = "hold_position")
```

Table 8: Seed=1 and m=5

term	estimate	std.error	X2.5..	X97.5..	lambda
(Intercept)	-101.0813249	7.5271483	-115.8735738	-86.2890760	0.0220522
genderfemale	-1.3234773	0.8306002	-2.9558739	0.3089192	0.0260571
age	-0.1546038	0.0211511	-0.1961770	-0.1130305	0.0315378
hgt	52.6140997	4.3128656	44.1381775	61.0900219	0.0244407
WC	1.0237576	0.0223515	0.9798302	1.0676850	0.0255510

```
kable(data.frame(summary(seed1.10, conf.int = TRUE)[, c(1, 2, 3, 7, 8)],
                 lambda = seed1.10$pooled[,10]), caption = "Seed=1 and m=10") %>%
  kable_styling(latex_options = "hold_position")
```

Table 9: Seed=1 and m=10

term	estimate	std.error	X2.5..	X97.5..	lambda
(Intercept)	-101.5776334	7.6714365	-116.6579564	-86.4973104	0.0521923
genderfemale	-1.3390581	0.8322271	-2.9744346	0.2963184	0.0240853
age	-0.1567736	0.0214213	-0.1988802	-0.1146671	0.0480265
hgt	52.8057762	4.3828554	44.1902652	61.4212872	0.0508004
WC	1.0262715	0.0224256	0.9822048	1.0703382	0.0212758

```
kable(data.frame(summary(seed1.20, conf.int = TRUE)[, c(1, 2, 3, 7, 8)],
                 lambda = seed1.20$pooled[,10]), caption = "Seed=1 and m=20") %>%
  kable_styling(latex_options = "hold_position")
```

Table 10: Seed=1 and m=20

term	estimate	std.error	X2.5..	X97.5..	lambda
(Intercept)	-101.1011277	7.6726255	-116.1821483	-86.0201072	0.0606764
genderfemale	-1.3545415	0.8305363	-2.9866031	0.2775201	0.0315254
age	-0.1579927	0.0211377	-0.1995300	-0.1164554	0.0326142
hgt	52.5581492	4.3856119	43.9380141	61.1782843	0.0600492
WC	1.0264058	0.0221890	0.9828071	1.0700045	0.0140400

```
kable(data.frame(summary(seed1.25, conf.int = TRUE)[, c(1, 2, 3, 7, 8)],
                 lambda = seed1.25$pooled[,10]), caption = "Seed=1 and m=25") %>%
  kable_styling(latex_options = "hold_position")
```

Table 11: Seed=1 and m=25

term	estimate	std.error	X2.5..	X97.5..	lambda
(Intercept)	-101.3253324	7.7631768	-116.5852572	-86.0654076	0.0721308
genderfemale	-1.3488093	0.8375513	-2.9947043	0.2970857	0.0384292
age	-0.1558489	0.0212148	-0.1975375	-0.1141603	0.0335463
hgt	52.7129195	4.4492421	43.9667212	61.4591178	0.0766404
WC	1.0250900	0.0222574	0.9813569	1.0688232	0.0145306

```
kable(data.frame(summary(seed2.5, conf.int = TRUE)[, c(1, 2, 3, 7, 8)],
                 lambda = seed2.5$pooled[,10]), caption = "Seed=2 and m=5") %>%
  kable_styling(latex_options = "hold_position")
```

Table 12: Seed=2 and m=5

term	estimate	std.error	X2.5..	X97.5..	lambda
(Intercept)	-100.9966596	7.7300251	-116.2136672	-85.7796520	0.0752096
genderfemale	-1.3775163	0.8404887	-3.0302117	0.2751791	0.0471154
age	-0.1580193	0.0213131	-0.1999240	-0.1161147	0.0436862
hgt	52.5424942	4.4106181	43.8613258	61.2236627	0.0718380
WC	1.0259230	0.0222557	0.9821911	1.0696550	0.0142010

```
kable(data.frame(summary(seed2.10, conf.int = TRUE)[, c(1, 2, 3, 7, 8)],
                 lambda = seed2.10$pooled[,10]), caption = "Seed=2 and m=10") %>%
  kable_styling(latex_options = "hold_position")
```

Table 13: Seed=2 and m=10

term	estimate	std.error	X2.5..	X97.5..	lambda
(Intercept)	-101.5186858	7.5571364	-116.3699779	-86.6673938	0.0311981
genderfemale	-1.3215513	0.8256067	-2.9438439	0.3007412	0.0185686
age	-0.1592563	0.0213802	-0.2012842	-0.1172285	0.0510297
hgt	52.8833997	4.3363259	44.3609058	61.4058936	0.0384335
WC	1.0255032	0.0222773	0.9817285	1.0692778	0.0197263

```
kable(data.frame(summary(seed2.20, conf.int = TRUE)[, c(1, 2, 3, 7, 8)],
                 lambda = seed2.20$pooled[,10]), caption = "Seed=2 and m=20") %>%
  kable_styling(latex_options = "hold_position")
```

Table 14: Seed=2 and m=20

term	estimate	std.error	X2.5..	X97.5..	lambda
(Intercept)	-101.6993777	7.6823878	-116.7986779	-86.600078	0.0547441
genderfemale	-1.3663151	0.8370945	-3.0113631	0.278733	0.0398821
age	-0.1576975	0.0214614	-0.1998791	-0.115516	0.0557808
hgt	53.0055071	4.4023585	44.3525473	61.658467	0.0590317
WC	1.0246288	0.0223533	0.9807051	1.068553	0.0239163

```
kable(data.frame(summary(seed2.25, conf.int = TRUE)[, c(1, 2, 3, 7, 8)],
                 lambda = seed2.25$pooled[,10]), caption = "Seed=2 and m=25") %>%
  kable_styling(latex_options = "hold_position")
```

Table 15: Seed=2 and m=25

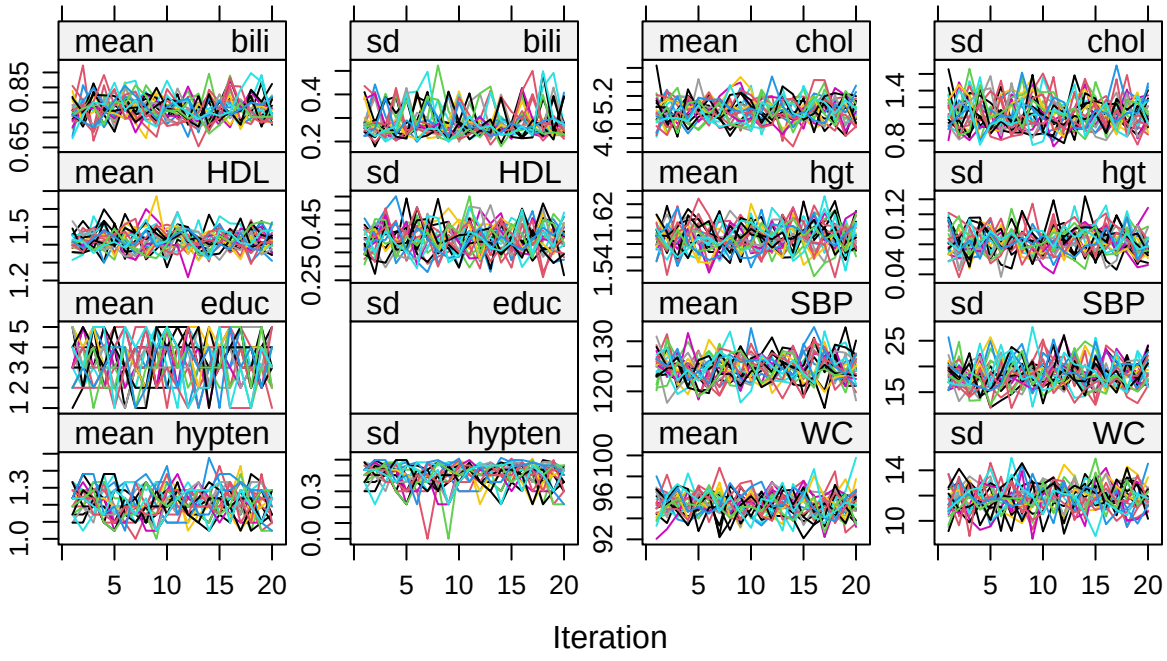
term	estimate	std.error	X2.5..	X97.5..	lambda
(Intercept)	-101.4521949	7.6290783	-116.4452338	-86.4591561	0.0472501
genderfemale	-1.3125011	0.8317349	-2.9468852	0.3218831	0.0303398
age	-0.1585538	0.0213320	-0.2004759	-0.1166316	0.0456505
hgt	52.8201428	4.3724292	44.2269381	61.4133475	0.0516546
WC	1.0255459	0.0223605	0.9816083	1.0694836	0.0243072

Looking at Table 8, the (pooled) estimates, standard errors, and the bounds of the intervals get more stable as M increases and we can be more confident in any one specific run. Note that whatever value of M we choose, there will always be some variation in results between repeat runs. The point is that with a sufficiently large M, the results will with high probability only differ by a small amount.

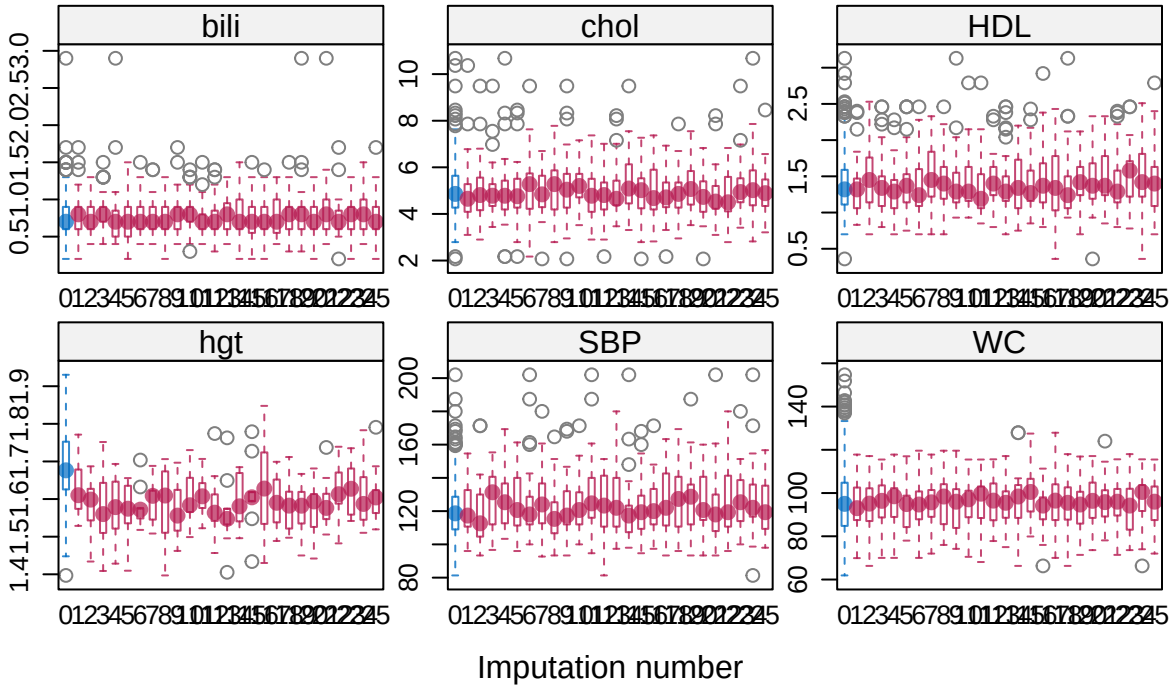
```
imp <- mice(nhanes2, method = meth, post = post, maxit = 20,
            m = 25, seed = 1, printFlag = FALSE)
imp$loggedEvents
```

```
## NULL
```

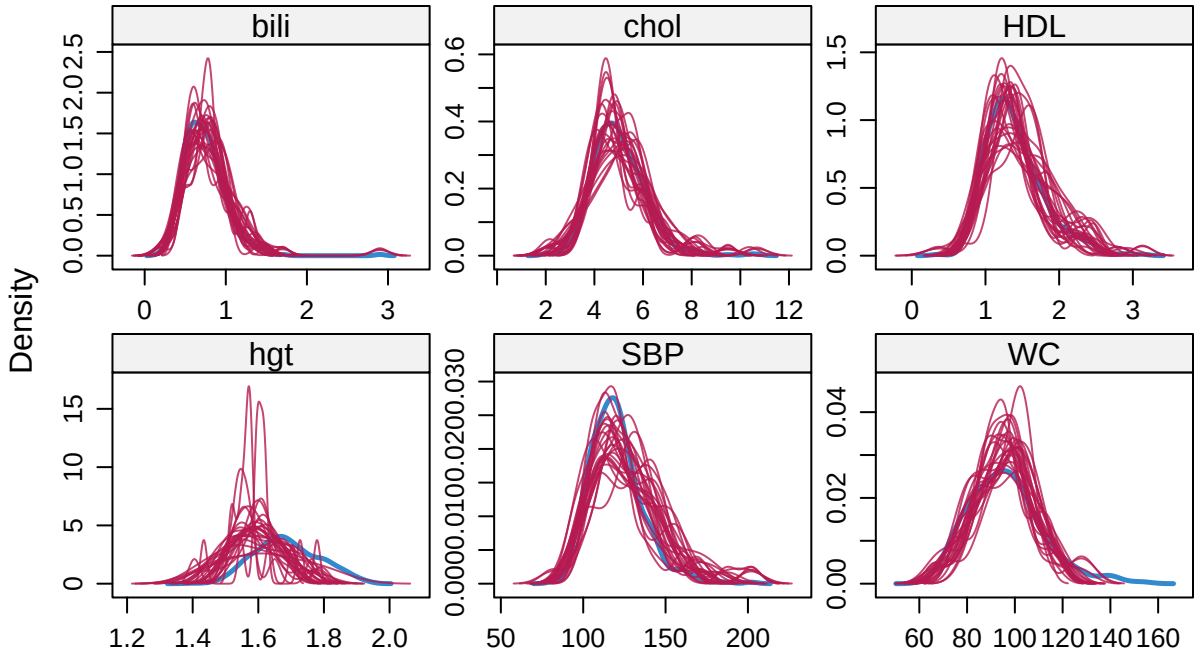
```
plot(imp, layout=c(4,4))
```



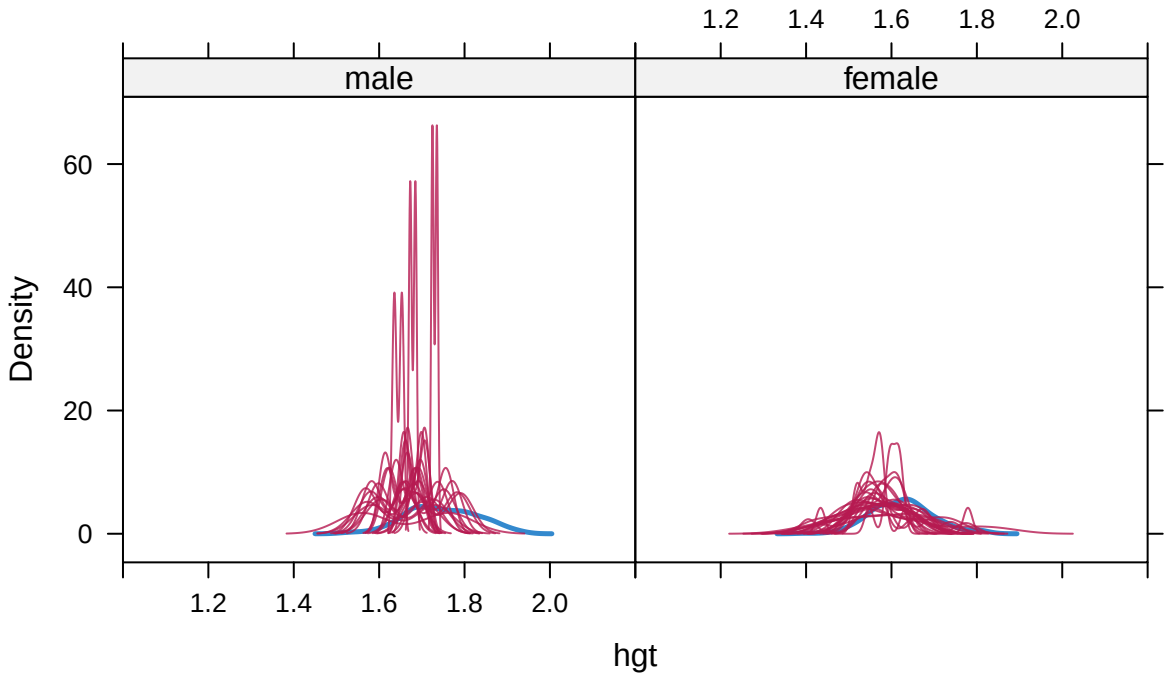

```
bwplot(imp)[c(2,4,5,6,7,8)]
```



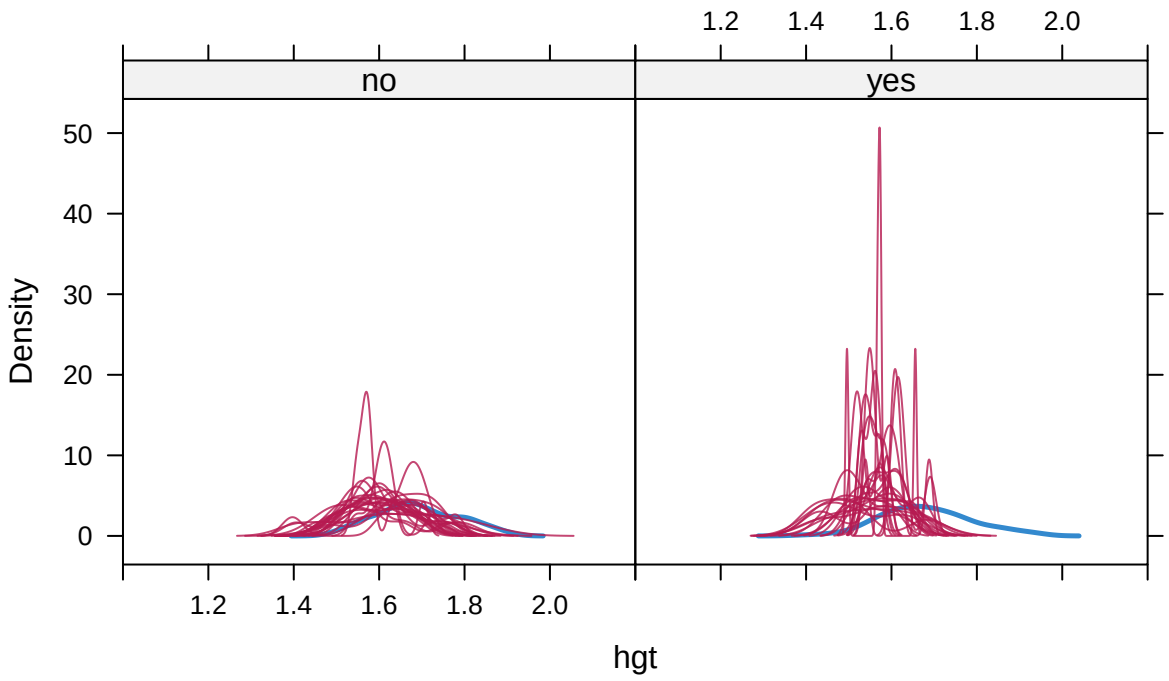

```
densityplot(imp)
```



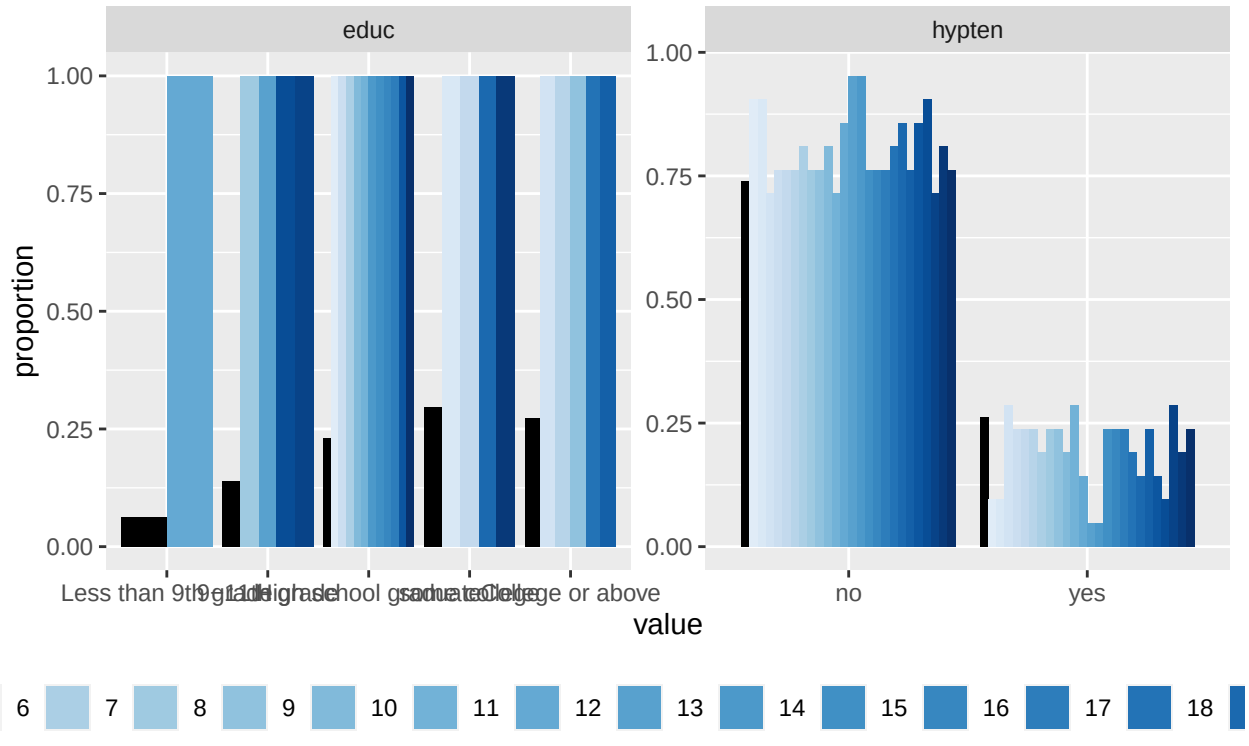

```
densityplot(imp,~hgt|gender, xlim = c(1, 2.2))
```




```
densityplot(imp,~hgt|hypten, xlim = c(1, 2.2))
```




```
propplot(imp)
```




```
fit <- with(imp, lm(wgt ~ gender + age + hgt + WC))
```