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36-402/608 ADA-II  
Breakout #5 Results

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**Question 1:** Figure out how the code works, and what the results are telling us about the missing data in this dataset.

The “mice” multiple imputation package contains a dataset called “boys” which contains measurements of 9 variables for 748 Dutch boys. The first five are “demographics”: age, height, weight, body mass index, and head circumference. The last one is region of the country. The other three are measures of the stage of puberty: genital Tanner stage, pubic hair stage, and testicular volume.

```
> library(mice)
> round( 100 * sapply(boys, function(x){mean(is.na(x))}), 1)
age hgt wgt bmi hc gen phb tv reg
0.0 2.7 0.5 2.8 6.1 67.2 67.2 69.8 0.4

> round( 100 * apply(boys, 2, function(x){mean(is.na(x))}), 1)
age hgt wgt bmi hc gen phb tv reg
0.0 2.7 0.5 2.8 6.1 67.2 67.2 69.8 0.4

> table( apply(boys, 1, function(x){sum(is.na(x))}) )
 0  1  2  3  4  5  6  7
223 20  1 438 47 17  1  1

> boys[1,]
  age hgt wgt bmi hc gen phb tv reg
0.035 50.1 3.65 14.54 33.7 <NA> <NA> NA south

> is.na(boys[1,])
  age hgt wgt bmi hc gen phb tv reg
FALSE FALSE FALSE FALSE FALSE TRUE TRUE TRUE FALSE

> 1 + is.na(boys[1,])
  age hgt wgt bmi hc gen phb tv reg
  1  1  1  1  1  2  2  2  1

> c("P","M")[1+is.na(boys[1,])]
[1] "P" "P" "P" "P" "P" "M" "M" "M" "P"

> paste( c("P","M")[1+is.na(boys[1,])], collapse="")
[1] "PPPPMMMP"
```

```

> apply(boys, 1, function(x) {
  paste(c("P","M")[1+is.na(x)], collapse="")} [1:5]
[1] "PPPPPMMP" "PPPPPMMP" "PPPPPMMP" "PPPPPMMP" "PPPPPMMP"

> patterns = apply(boys, 1, function(x) {
  paste(c("P","M")[1+is.na(x)], collapse="")}
> table(patterns)
PMMMMMMMP PMMMPPPP PMMMPPPP PMPMMMMMP PMPMPMMMP PPMPPMMMP PPPMMMMMP
      1      1      1      1      16      1      43
PPPPPMMP PPPPPMMP PPPPPMMP PPPPPMMP PPPPPMMP PPPPPMMP
      3      437      1      1      19      223

> table(substring(patterns,6,8)=="MMM")
FALSE TRUE
  246   502

# aggregate() has three arguments: The first, a vector or matrix, is
# what is analyzed (per column for a matrix). The analysis is to
# apply the function that is the third argument, e.g., mean(), length(),
# or a user defined (often anonymous) function. The second argument,
# which must be a list, contains one or more vectors of the same length
# as the first argument, and each unique value (or set of values for
# a list with more than one element) determines a subset of the
# first argument on which the function is applied.

# Test case:
> aggregate(boys[,2:3], list(under12=boys$age<12, region=boys$reg), mean)
  under12 region      hgt      wgt
1  FALSE north 179.7451 68.44314
2   TRUE north      NA 18.25133
3  FALSE east 174.7308 61.95077
4   TRUE east      NA 20.02818
5  FALSE west      NA      NA
6   TRUE west      NA      NA
7  FALSE south 175.2263 61.96579
8   TRUE south      NA 16.33717
9  FALSE city 170.8655 58.75172
10  TRUE city      NA 17.67207

```

```

> aggregate(boys[,1:5], list(miss3=substring(patterns,6,8)=="MMM"), mean, na.rm=TRUE)
  miss3      age      hgt      wgt      bmi      hc
1 FALSE 14.016533 164.9537 53.64549 19.06549 55.29592
2  TRUE  6.778416 115.6153 29.10494 17.56493 49.47418

> table(round(boys$age))
 0  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21
91 87 59 35 19  5 10  8  9 23 28 30 28 38 48 56 50 32 29 36 23  4

> agecut = cut(boys$age, seq(0,24,4))
> table(agecut)
 (0,4]  (4,8]  (8,12] (12,16] (16,20] (20,24]
   286     37    100    178    135     12

> aggregate(substring(patterns,6,8)=="MMM", list(ages=agecut), mean)
  ages      x
1  (0,4] 1.000000
2  (4,8] 0.9729730
3  (8,12] 0.2200000
4 (12,16] 0.4438202
5 (16,20] 0.5259259
6 (20,24] 0.6666667

> aggregate(substring(patterns,6,8)=="MMM", list(ages=cut(boys$age,8:16))), mean)
  ages      x
1  (8,9] 0.4285714
2  (9,10] 0.1724138
3 (10,11] 0.2333333
4 (11,12] 0.2058824
5 (12,13] 0.2962963
6 (13,14] 0.4468085
7 (14,15] 0.4693878
8 (15,16] 0.4909091

```

**Question 2:** Figure out how the code works, and what the results are telling us about predicting body mass index from age, hypertension, and cholesterol.

```
> round( 100 * apply(nhanes, 2, function(x){mean(is.na(x))}), 1)
age bmi hyp chl
  0  36  32  40
```

```
> table( apply(nhanes, 1, function(x){sum(is.na(x))}) )
  0  1  2  3
13  4  1  7
```

```
> patterns = apply(nhanes, 1, function(x) {
  paste(c("P","M")[1+is.na(x)], collapse="")})
> table(patterns)
PMMM PMMP PMPP PPPM PPPP
  7   1   1   3  13
```

```
> nhanes5 = mice(nhanes, 5, printFlag=FALSE)
> nhanes5lm = with(nhanes5, lm(bmi ~ age+hyp+chl))
> summary(nhanes5lm)
## summary of imputation 1 :
...
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) 19.50020    3.20307   6.088 4.85e-06 ***
age          -3.65876    0.78889  -4.638 0.000142 ***
hyp           0.24298    1.80267   0.135 0.894061
chl           0.07387    0.01700   4.345 0.000285 ***
```

```
...
## summary of imputation 2 :
...
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) 20.25075    3.16735   6.394 2.45e-06 ***
age          -3.69148    0.81501  -4.529 0.000183 ***
hyp           0.62913    1.82420   0.345 0.733614
chl           0.06560    0.01828   3.589 0.001729 **
```

```

> nhanes5pool = pool(nhanes5lm)
> summary(nhanes5pool)

```

	est	se	t	df	Pr(> t )
(Intercept)	19.80287222	3.45264062	5.7355730	12.474896	0.000080651
age	-3.84997696	0.98008080	-3.9282240	11.066091	0.002332770
hyp	0.69663077	2.12866914	0.3272612	9.572933	0.750513844
chl	0.06891952	0.01835404	3.7550043	15.430643	0.001828751

  

	lo 95	hi 95	missing	fmi
(Intercept)	12.31185362	27.2938908	NA	0.2682756
age	-6.00554946	-1.6944045	0	0.3137279
hyp	-4.07517784	5.4684394	8	0.3675757
chl	0.02989367	0.1079454	10	0.1825114

  

```

# Where the above comes from:
> nhanes5pool$qbar

```

	age	hyp	chl
(Intercept)	19.80287222	-3.84997696	0.69663077
age	0.69663077	0.06891952	
hyp			
chl			

  

```

> round(nhanes5pool$t,4)

```

	(Intercept)	age	hyp	chl
(Intercept)	11.9207	0.8997	-2.9507	-0.0505
age	0.8997	0.9606	-1.1413	-0.0065
hyp	-2.9507	-1.1413	4.5312	-0.0020
chl	-0.0505	-0.0065	-0.0020	0.0003

  

```

> sqrt(diag(nhanes5pool$t))

```

	age	hyp	chl
(Intercept)	3.45264062	0.98008080	2.12866914
age	0.98008080	2.12866914	0.01835404
hyp	2.12866914	0.01835404	
chl	0.01835404		

  

```

> nhanes5pool$df

```

	age	hyp	chl
(Intercept)	12.474896	11.066091	9.572933
age	11.066091	9.572933	15.430643
hyp	9.572933	15.430643	
chl	15.430643		