432 Class 10 Slides

github.com/THOMASELOVE/2020-432

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Setup

```r
library(magrittr); library(janitor); library(here)

library(skimr)
library(naniar)
library(simputation)
library(broom)
library(rms) # note: also loads Hmisc
library(tidyverse)
```

Today's Data

Heart and Estrogen/Progestin Study (HERS)

- Clinical trial of hormone therapy for the prevention of recurrent heart attacks and deaths among 2763 post-menopausal women with existing coronary heart disease (see Hulley et al 1998 and many subsequent references, including Vittinghoff, Chapter 4.)
- We're exluding the women in the trial with a diabetes diagnosis.

```
hers_raw <- read_csv(here("data/hersdata.csv")) %>%
    clean_names()

hers1 <- hers_raw %>%
    filter(diabetes == "no") %>%
    select(subject, ldl, ht, age, smoking, drinkany, sbp,
           physact, bmi, diabetes)
```

The Codebook (n = 2032)

Variable	Description
`subject`	subject code
`HT`	factor: hormone therapy or placebo
`diabetes`	yes or no (all are no in our sample)
`ldl`	LDL cholesterol in mg/dl
`age`	age in years
`smoking`	yes or no
`drinkany`	yes or no
`sbp`	systolic BP in mm Hg
`physact`	5-level factor, details next slide
`bmi`	body-mass index in kg/m^2

Goal Predict `ldl` using `age`, `smoking`, `drinkany`, `sbp`, `physact` and `bmi`, across both HT levels but restricted to women without `diabetes`.

The `physact` variable

```
hers1 %>% count(physact)
```

```
# A tibble: 5 x 2
  physact                  n
  <chr>                <int>
1 about as active        674
2 much less active       107
3 much more active       252
4 somewhat less active   322
5 somewhat more active   677
```

Comparison is to activity levels for these women just before menopause.

Any missing data?

```
miss_var_summary(hers1)
```

```
# A tibble: 10 x 3
   variable n_miss pct_miss
   <chr>     <int>    <dbl>
 1 ldl           7   0.344
 2 drinkany      2   0.0984
 3 bmi           2   0.0984
 4 subject       0   0
 5 ht            0   0
 6 age           0   0
 7 smoking       0   0
 8 sbp           0   0
 9 physact       0   0
10 diabetes      0   0
```

Single Imputation for `drinkany`, `bmi` and `ldl`

Since `drinkany` is a factor, we have to do some extra work to impute.

```
set.seed(432092)

hers2 <- hers1 %>%
    mutate(drinkany_n =
              ifelse(drinkany == "yes", 1, 0)) %>%
    impute_pmm(drinkany_n ~ age + smoking) %>%
    mutate(drinkany =
              ifelse(drinkany_n == 1, "yes", "no")) %>%
    impute_rlm(bmi ~ age + smoking + sbp) %>%
    impute_rlm(ldl ~ age + smoking + sbp + bmi)
```

Now, check missingness...

```
miss_var_summary(hers2)
```

```
# A tibble: 11 x 3
   variable   n_miss pct_miss
   <chr>       <int>    <dbl>
 1 subject         0        0
 2 ldl             0        0
 3 ht              0        0
 4 age             0        0
 5 smoking         0        0
 6 drinkany        0        0
 7 sbp             0        0
 8 physact         0        0
 9 bmi             0        0
10 diabetes        0        0
11 drinkany_n      0        0
```

Multiple Imputation using `aregImpute` from `Hmisc`

Model to predict all missing values of any variables, using additive regression bootstrapping and predictive mean matching.

Steps are:

1. `aregImpute` draws a sample with replacement from the observations where the target variable is observed, not missing.
2. It then fits a flexible additive model to predict this target variable while finding the optimum transformation of it.
3. It then uses this fitted flexible model to predict the target variable in all of the original observations.
4. Finally, it imputes each missing value of the target variable with the observed value whose predicted transformed value is closest to the predicted transformed value of the missing value.

Fitting a Multiple Imputation Model

```
set.seed(4320132)
dd <- datadist(hers1)
options(datadist = "dd")
fit3 <- aregImpute(~ ldl + age + smoking + drinkany +
                        sbp + physact + bmi,
                    nk = c(0, 3:5), tlinear = FALSE,
                    data = hers1, B = 10, n.impute = 20)
```

```
Iteration 1 Iteration 2 Iteration 3 Iteration 4 Iteration 5 It
```

Multiple Imputation using `aregImpute` from `Hmisc`

`aregImpute` requires specifications of all variables, and several other details:

- `n.impute` = number of imputations, we'll run 20
- `nk` = number of knots to describe level of complexity, with our choice `nk = c(0, 3:5)` we'll fit both linear models and models with restricted cubic splines with 3, 4, and 5 knots
- `tlinear = FALSE` allows the target variable to have a non-linear transformation when `nk` is 3 or more
- `B = 10` specifies 10 bootstrap samples will be used
- `data` specifies the source of the variables

aregImpute Imputation Results (1 of 4)

```
fit3
```

```
Multiple Imputation using Bootstrap and PMM

aregImpute(formula = ~ldl + age + smoking + drinkany + sbp +
 physact + bmi, data = hers1, n.impute = 20, nk = c(0, 3:5),
 tlinear = FALSE, B = 10)

n: 2032     p: 7    Imputations: 20     nk: 0

Number of NAs:
 ldl   age   smoking drinkany   sbp   physact     bmi
   7     0         0        2     0         0       2
```

`fit3` Imputation Results (2 of 4)

```
R-squares for Predicting Non-Missing Values for Each
Variable Using Last Imputations of Predictors
     ldl drinkany      bmi
   0.041    0.014    0.109
```

`fit3` Imputation Results (3 of 4)

Resampling results for determining the complexity of imputation models

Variable being imputed: ldl

Bootstrap bias-corrrected summaries:

Statistic	nk = 0	nk = 3	nk = 4	nk = 5
R^2	0.0139	0.0149	0.00776	0.0124
mean absolute error	28.3594	42.9139	44.09937	39.8266
median abs. error	22.8301	35.5441	38.85302	32.6386

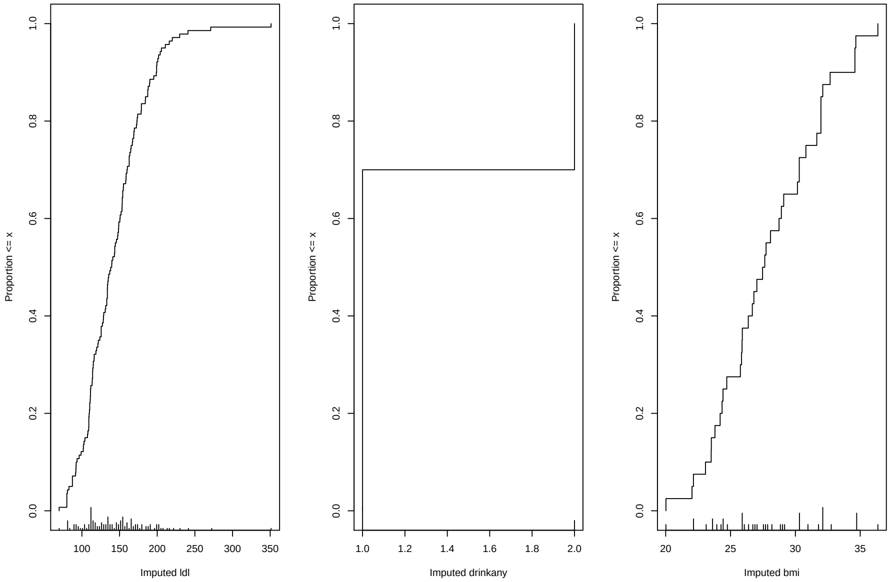
10-fold cross-validated:

Statistic	nk = 0	nk = 3	nk = 4	nk = 5
R^2	0.0214	0.0180	0.01517	0.0191
mean absolute error	145.7176	43.5007	45.02428	44.2456
median abs. error	141.4238	36.4102	38.88053	37.3141

`fit3` Imputation Results (4 of 4)

```
Variable being imputed: drinkany
                            nk=0   nk=3   nk=4    nk=5
Bootstrap  R^2            0.0163 0.0113 0.0102 0.00986
10-fold cv R^2            0.0205 0.0249 0.0163 0.01358
Bootstrap  mean |error|   0.4470 0.4568 0.4558 0.46624
10-fold cv mean |error|   0.4450 0.4454 0.4476 0.44676
Bootstrap median |error|  0.0000 0.0000 0.0000 0.00000
10-fold cv median |error| 0.0000 0.0500 0.1000 0.00000

Variable being imputed: bmi
                             nk=0   nk=3   nk=4   nk=5
Bootstrap  R^2             0.0845 0.0932 0.0946 0.0847
10-fold cv R^2             0.0864 0.0903 0.0968 0.0899
Bootstrap  mean |error|    3.7829 4.8119 4.9226 5.1775
10-fold cv mean |error|   27.6776 4.8359 4.9390 5.1136
Bootstrap median |error|   2.9955 3.9704 3.9371 4.2634
10-fold cv median |error| 27.0143 3.9894 3.9431 4.1876
```

A plot of the imputed values. . . (results)



A plot of the imputed values... (code)

```r
par(mfrow = c(1,3))
plot(fit3)
par(mfrow = c(1,1))
```

- For `ldl`, we imputed most of the 7 missing subjects in most of the 20 imputation runs to values within a range of around 120 through 200, but occasionally, we imputed values that were substantially lower than 100.
- For `drinkany` we imputed about 70% no and 30% yes.
- For `bmi`, we imputed values ranging from about 23 to 27 in many cases, and up near 40 in other cases.
- This method never imputes a value for a variable that doesn't already exist in the data.

Kitchen Sink Model (Main Effects only)

```
mod_ks <- ols(ldl ~ age + smoking + drinkany + sbp +
               physact + bmi, data = hers2)
anova(mod_ks)
```

```
                Analysis of Variance          Response: ldl

 Factor     d.f. Partial SS  MS          F     P
 age           1    9330.911   9330.911  6.93 0.0085
 smoking       1    8199.755   8199.755  6.09 0.0137
 drinkany      1    6444.424   6444.424  4.79 0.0288
 sbp           1    9274.287   9274.287  6.89 0.0087
 physact       4   10874.528   2718.632  2.02 0.0891
 bmi           1   15876.957  15876.957 11.80 0.0006
 REGRESSION    9   60077.708   6675.301  4.96 <.0001
 ERROR      2022 2721037.890   1345.716
```

Spearman ρ^2 Plot

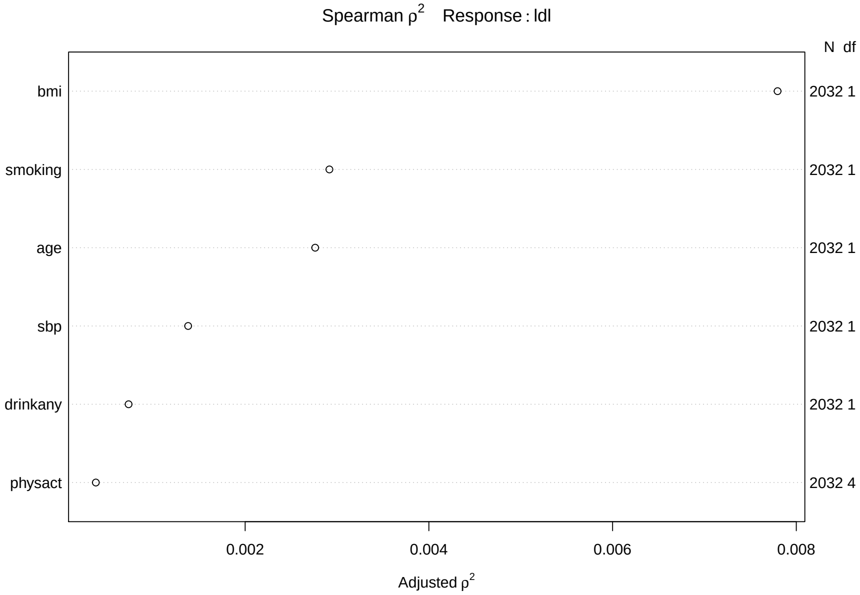
How should we prioritize the degrees of freedom we spend on non-linearity?

```
plot(spearman2(ldl ~ age + smoking + drinkany + sbp +
                    physact + bmi, data = hers2))
```

Plot's on the next page.

- Note the use of the simple imputation `hers2` data here. Why?

Spearman ρ^2 Plot Result



Spending Degrees of Freedom

We're spending 9 degrees of freedom in our kitchen sink model. (We can verify this with `anova` or the plot.)

- Each quantitative main effect costs 1 df to estimate
- Each binary categorical variable also costs 1 df
- Multi-categorical variables with L levels cost L-1 df to estimate

Suppose we're willing to spend up to a total of **14** degrees of freedom (i.e. a combined 5 more on interaction terms and other ways to capture non-linearity.)

What should we choose?

What did we see in the Spearman ρ^2 Plot?

Group 1 (largest adjusted ρ^2)

- `bmi`, a quantitative predictor, is furthest to the right

Group 2 (next largest)

- `smoking`, a binary predictor, is next, followed closely by
- `age`, a quantitative predictor

Other predictors (rest of the group)

- `sbp`, quantitative
- `drinkany`, binary
- `physact`, multi-categorical (5 levels)

Impact of Adding Non-Linearity on Degrees of Freedom Spent

What happens when we add a non-linear term?

- Adding a polynomial of degree D costs D degrees of freedom.
  - So a polynomial of degree 2 (quadratic) costs 2 df, or 1 more than the main effect alone.
- Adding a restricted cubic spline with K knots costs K-1 df.
  - So adding a rcs with 4 knots uses 3 df, or 2 more than the main effect alone.
  - We restrict ourselves to considering splines with 3, 4, or 5 knots.
- Adding an interaction (product term) depends on the main effects of the predictors we are interacting
  - If the product term's predictors have df1 and df2 degrees of freedom, the product term adds df1 $\times$ df2 degrees of freedom to the main effects model.
  - An interaction of a binary and quantitative variable adds $1 \times 1 = 1$ additional degree of freedom to the main effects model.
  - When we use a quantitative variable in a spline and interaction, we'll do the interaction on the main effect, not the spline.

Model we'll fit with `ols`

Fitting a model to predict `ldl` using

- `bmi` with a restricted cubic spline, 5 knots
- `age` with a quadratic polynomial
- `sbp` as a linear term
- `drinkany` indicator
- `physact` factor
- `smoking` indicator and its interaction with the main effect of `bmi`

We can fit this to the data

- restricted to complete cases (hers1, effectively)
- after simple imputation (hers2)
- after our multiple imputation (fit3)

Fitting the model to the complete cases

```
d <- datadist(hers1)
options(datadist = "d")

m1 <- ols(ldl ~ rcs(bmi, 5) + pol(age, 2) + sbp +
              drinkany + physact + smoking +
              smoking %ia% bmi, data = hers1,
          x = TRUE, y = TRUE)
```

where `%ia%` identifies the linear interaction alone.

`m1` results (slide 1 of 3)

```
> m1

Frequencies of Missing Values Due to Each Variable
 ldl     bmi     age      sbp drinkany  physact  smoking
   7       2       0        0        2        0        0

Linear Regression Model

ols(formula = ldl ~ rcs(bmi, 5) + pol(age, 2) + sbp +
     drinkany + physact + smoking + smoking %ia% bmi,
     data = hers1, x = TRUE, y = TRUE)

                 Model Likelihood     Discrimination
                    Ratio Test           Indexes
 Obs       2021    LR chi2      52.61    R2       0.026
 sigma36.7430    d.f.            14    R2 adj   0.019
 d.f.      2006    Pr(> chi2) 0.0000    g        6.629
```

m1 results (slide 2 of 3)

	Coef	S.E.	t	Pr(>|t|)
Intercept	121.6057	68.2000	1.78	0.0747
bmi	1.5687	1.0107	1.55	0.1208
bmi'	-8.6685	9.1577	-0.95	0.3440
bmi''	40.5712	37.4468	1.08	0.2787
bmi'''	-55.8872	44.5946	-1.25	0.2103
age	-0.5791	1.9657	-0.29	0.7683
age^2	0.0018	0.0149	0.12	0.9024
sbp	0.1221	0.0453	2.69	0.0072
drinkany=yes	-3.7427	1.6629	-2.25	0.0245
physact=much less active	-4.5660	3.8904	-1.17	0.2407
physact=much more active	-0.3291	2.7521	-0.12	0.9048
physact=somewhat less active	-0.0160	2.5270	-0.01	0.9950
physact=somewhat more active	3.7731	2.0293	1.86	0.0631
smoking=yes	-7.0832	12.0586	-0.59	0.5570
smoking=yes * bmi	0.4961	0.4391	1.13	0.2587

`m1` results (slide 3 of 3)

```
Residuals

     Min       1Q   Median      3Q     Max
-113.440  -24.519   -3.778  20.940 197.087
```

Fitting the model after simple imputation

```
dd <- datadist(hers2)
options(datadist = "dd")

m2 <- ols(ldl ~ rcs(bmi, 5) + pol(age, 2) + sbp +
              drinkany + physact + smoking +
              smoking %ia% bmi, data = hers2,
          x = TRUE, y = TRUE)
```

where, again, %ia% identifies the linear interaction alone.

`m2` results (slide 1 of 2)

```
> m2
Linear Regression Model

 ols(formula = ldl ~ rcs(bmi, 5) + pol(age, 2) + sbp + drinkany +
     physact + smoking + smoking %ia% bmi, data = hers2, x = TRUE,
     y = TRUE)

                Model Likelihood     Discrimination
                   Ratio Test           Indexes
 Obs       2032    LR chi2     53.14    R2       0.026
 sigma36.6503    d.f.           14    R2 adj   0.019
 d.f.      2017    Pr(> chi2) 0.0000    g        6.631

 Residuals

      Min        1Q    Median        3Q       Max
 -113.379  -24.326   -3.835    20.832   197.097
```

`m2` results (slide 2 of 2)

	Coef	S.E.	t	Pr(>|t|)
Intercept	120.2662	67.6113	1.78	0.0754
bmi	1.5508	1.0071	1.54	0.1237
bmi'	-8.4486	9.0978	-0.93	0.3532
bmi''	39.6413	37.1378	1.07	0.2859
bmi'''	-54.8924	44.2677	-1.24	0.2151
age	-0.5249	1.9490	-0.27	0.7877
age^2	0.0014	0.0148	0.10	0.9233
sbp	0.1209	0.0451	2.68	0.0074
drinkany=yes	-3.7023	1.6544	-2.24	0.0253
physact=much less active	-4.7408	3.8621	-1.23	0.2198
physact=much more active	-0.2635	2.7391	-0.10	0.9234
physact=somewhat less active	0.0130	2.5101	0.01	0.9959
physact=somewhat more active	3.8031	2.0193	1.88	0.0598
smoking=yes	-6.8961	12.0196	-0.57	0.5662
smoking=yes * bmi	0.4892	0.4375	1.12	0.2636

anova(m2) results

```
> anova(m2)
                Analysis of Variance          Response: ldl

 Factor                                           d.f. Partial SS   MS         F    P
 bmi   (Factor+Higher Order Factors)                 5 2.758824e+04 5517.64861 4.11 0.0010
  All Interactions                                   1 1.679813e+03 1679.81344 1.25 0.2636
  Nonlinear                                          3 9.735452e+03 3245.15068 2.42 0.0647
 age                                                 2 9.175762e+03 4587.88077 3.42 0.0330
  Nonlinear                                          1 1.244351e+01   12.44351 0.01 0.9233
 sbp                                                 1 9.657476e+03 9657.47569 7.19 0.0074
 drinkany                                            1 6.726918e+03 6726.91809 5.01 0.0253
 physact                                             4 9.709992e+03 2427.49791 1.81 0.1247
 smoking  (Factor+Higher Order Factors)              2 1.085405e+04 5427.02463 4.04 0.0177
  All Interactions                                   1 1.679813e+03 1679.81344 1.25 0.2636
 smoking * bmi  (Factor+Higher Order Factors)        1 1.679813e+03 1679.81344 1.25 0.2636
 TOTAL NONLINEAR                                     4 9.738807e+03 2434.70175 1.81 0.1237
 TOTAL NONLINEAR + INTERACTION                       5 1.171134e+04 2342.26845 1.74 0.1214
 REGRESSION                                         14 7.178905e+04 5127.78931 3.82 <.0001
 ERROR                                            2017 2.709327e+06 1343.24569
```

Validation of summary statistics

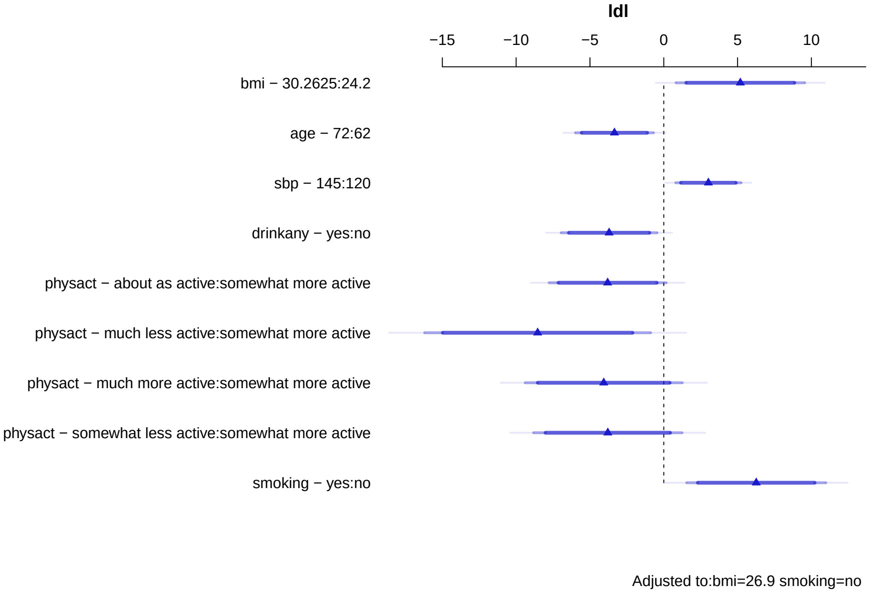
```r
validate(m2)
```

```
          index.orig  training      test optimism
R-square      0.0258    0.0322    0.0193   0.0129
MSE        1333.3300 1331.2658 1342.2160 -10.9502
g             6.6306    7.3074    5.9494   1.3581
Intercept     0.0000    0.0000   25.8305 -25.8305
Slope         1.0000    1.0000    0.8225   0.1775
          index.corrected  n
R-square           0.0129 40
MSE             1344.2801 40
g                  5.2726 40
Intercept         25.8305 40
Slope              0.8225 40
```

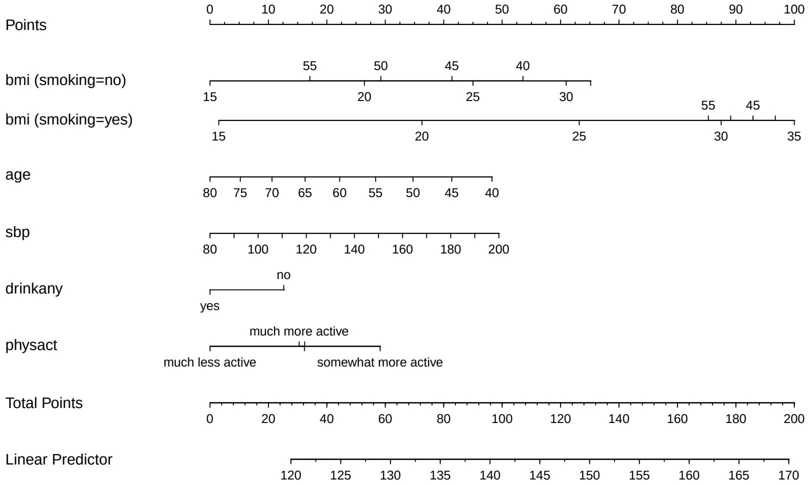
`summary(m2)` results

```
> summary(m2)
             Effects              Response : ldl

 Factor                                                Low   High    Diff.   Effect  S.E.   Lower 0.95 Upper 0.95
 bmi                                                    24.2  30.263  6.0625  5.1862 2.2217   0.82921   9.54330
 age                                                    62.0  72.000 10.0000 -3.3412 1.3450  -5.97890  -0.70357
 sbp                                                   120.0 145.000 25.0000  3.0218 1.1270   0.81165   5.23190
 drinkany - yes:no                                       1.0   2.000      NA -3.7023 1.6544  -6.94690  -0.45779
 physact - about as active:somewhat more active          5.0   1.000      NA -3.8031 2.0193  -7.76310   0.15695
 physact - much less active:somewhat more active         5.0   2.000      NA -8.5439 3.9035 -16.19900  -0.88862
 physact - much more active:somewhat more active         5.0   3.000      NA -4.0666 2.7125  -9.38630   1.25310
 physact - somewhat less active:somewhat more active     5.0   4.000      NA -3.7901 2.5633  -8.81720   1.23690
 smoking - yes:no                                        1.0   2.000      NA  6.2635 2.4009   1.55500  10.97200

Adjusted to: bmi=26.9 smoking=no
```

plot(summary(m2)) results



plot(nomogram(m2))



Making Predictions for an Individual

Suppose now that we want to use R to get a prediction for a new individual subject with `bmi` = 30, `age` = 50, `smoking` = yes and `physact` = about as active, `drinkany`= yes and `sbp` of 150.

```
predict(m2, expand.grid(bmi = 30, age = 50, smoking = "yes",
                        physact = "about as active",
                        drinkany = "yes", sbp = 150),
        conf.int = 0.95, conf.type = "individual")
```

```
$linear.predictors         $lower     $upper
          160.9399       88.48615   233.3936
```

Making Predictions for a Long-Run Mean

The other kind of prediction we might wish to make is for the mean of a series of subjects whose `bmi` = 30, `age` = 50, `smoking` = yes and `physact` = about as active, `drinkany`= yes and `sbp` of 150.

```
predict(m2, expand.grid(bmi = 30, age = 50, smoking = "yes",
                        physact = "about as active",
                        drinkany = "yes", sbp = 150),
        conf.int = 0.95, conf.type = "mean")
```

```
$linear.predictors         $lower      $upper
          160.9399       151.8119    170.0679
```

Of course, the confidence interval will always be narrower than the prediction interval given the same predictor values.

Influential Points?

```
which.influence(m2, cutoff = 0.4)
```

```
$Intercept
[1] 1135

$age
[1] 1135

$smoking
[1] 132

$`smoking * bmi`
[1] 132
```

Fitting the Model using Multiple Imputation

What do we have now?

- An imputation model `fit3`

```
fit3 <- aregImpute(~ ldl + age + smoking + drinkany + sbp +
           physact + bmi, nk = c(0, 3:5), tlinear = FALSE,
           data = hers1, B = 10, n.impute = 20, x = TRUE)
```

- A prediction model

```
m1 <- ols(ldl ~ rcs(bmi, 5) + pol(age, 2) + sbp +
            drinkany + physact + smoking + smoking %ia% bmi,
            x = TRUE, y = TRUE)
```

Now we put them together with the `fit.mult.impute` function...

Linear Regression & Imputation Model

```r
m3imp <-
    fit.mult.impute(ldl ~ rcs(bmi, 5) + pol(age, 2) + sbp +
                        drinkany + physact + smoking +
                        smoking %ia% bmi,
                    fitter = ols, xtrans = fit3,
                    data = hers1)
```

```
Variance Inflation Factors Due to Imputation:

                  Intercept                           bmi
                       1.00                          1.00
                       bmi'                         bmi''
                       1.00                          1.01
                     bmi'''                           age
                       1.01                          1.00
                      age^2                           sbp
                       1.00                          1.01
```

m3imp results (1 of 2)

```
> m3imp
Linear Regression Model

 fit.mult.impute(formula = ldl ~ rcs(bmi, 5) + pol(age, 2) + sbp +
     drinkany + physact + smoking + smoking %ia% bmi, fitter = ols,
     xtrans = fit3, data = hers1)

                Model Likelihood     Discrimination
                   Ratio Test           Indexes
 Obs      2032    LR chi2      53.30    R2       0.026
 sigma36.7128    d.f.            14    R2 adj   0.019
 d.f.     2017    Pr(> chi2) 0.0000    g        6.652

 Residuals

     Min       1Q  Median      3Q     Max
 -113.10   -24.46   -3.81   20.92  197.42
```

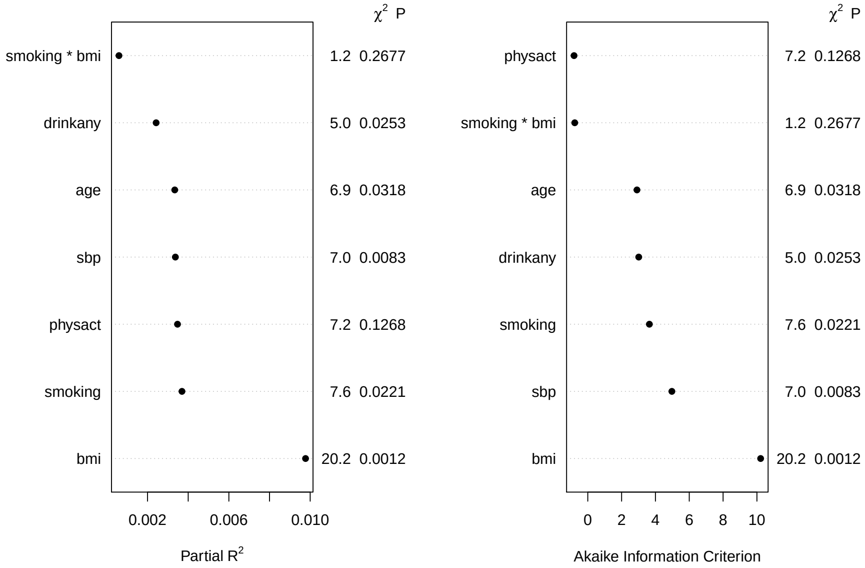
m3imp results (2 of 2)

	Coef	S.E.	t	Pr(>|t|)
Intercept	121.1499	67.7998	1.79	0.0741
bmi	1.5445	1.0097	1.53	0.1263
bmi'	-8.2945	9.1027	-0.91	0.3623
bmi''	39.0890	37.3055	1.05	0.2949
bmi'''	-54.2119	44.4779	-1.22	0.2230
age	-0.5521	1.9547	-0.28	0.7776
age^2	0.0016	0.0148	0.11	0.9119
sbp	0.1216	0.0453	2.69	0.0073
drinkany=yes	-3.7404	1.6625	-2.25	0.0246
physact=much less active	-4.7426	3.8692	-1.23	0.2204
physact=much more active	-0.2665	2.7455	-0.10	0.9227
physact=somewhat less active	0.0313	2.5214	0.01	0.9901
physact=somewhat more active	3.8060	2.0257	1.88	0.0604
smoking=yes	-6.9198	12.0472	-0.57	0.5658
smoking=yes * bmi	0.4917	0.4388	1.12	0.2626

anova(m3imp)

```
> anova(m3imp)
                Analysis of Variance          Response: ldl

 Factor                                          d.f. Partial SS   MS        F    P
 bmi  (Factor+Higher Order Factors)                 5   27514.6406 5502.9281 4.08 0.0011
  All Interactions                                  1    1692.6044 1692.6044 1.26 0.2626
  Nonlinear                                         3    9741.6194 3247.2065 2.41 0.0653
 age                                                2    9078.9851 4539.4926 3.37 0.0347
  Nonlinear                                         1      16.5032   16.5032 0.01 0.9119
 sbp                                                1    9721.1667 9721.1667 7.21 0.0073
 drinkany                                           1    6822.3861 6822.3861 5.06 0.0246
 physact                                            4    9690.3632 2422.5908 1.80 0.1267
 smoking  (Factor+Higher Order Factors)             2   10845.6127 5422.8063 4.02 0.0180
  All Interactions                                  1    1692.6044 1692.6044 1.26 0.2626
 smoking * bmi  (Factor+Higher Order Factors)       1    1692.6044 1692.6044 1.26 0.2626
 TOTAL NONLINEAR                                    4    9747.0966 2436.7741 1.81 0.1246
 TOTAL NONLINEAR + INTERACTION                      5   11717.3715 2343.4743 1.74 0.1225
 REGRESSION                                        14   71571.1297 5112.2236 3.79 <.0001
 ERROR                                           2017 2718570.0412 1347.8285
```

Evaluation via Partial R^2 and AIC (result)



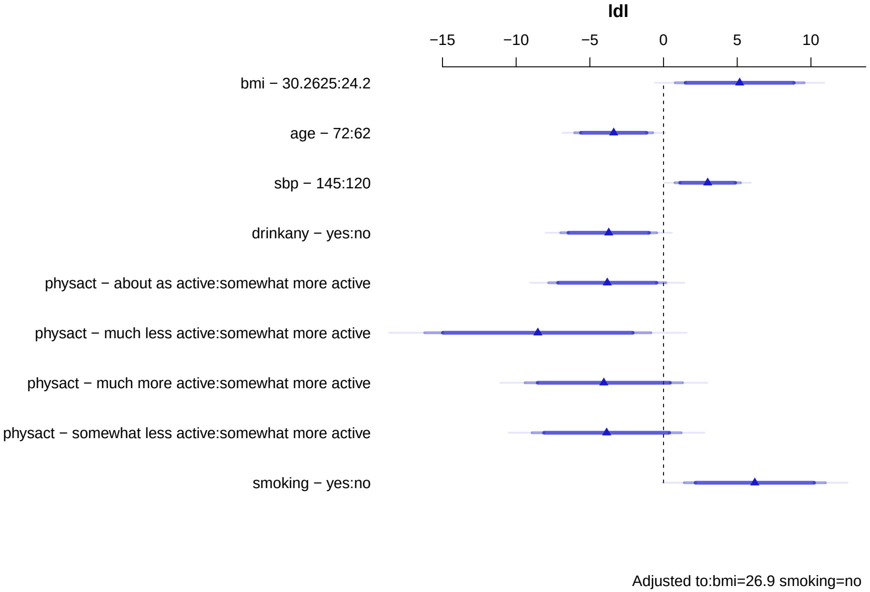
Evaluation via Partial R^2 and AIC (code)

```
par(mfrow = c(1,2))
plot(anova(m3imp), what="partial R2")
plot(anova(m3imp), what="aic")
par(mfrow = c(1,1))
```

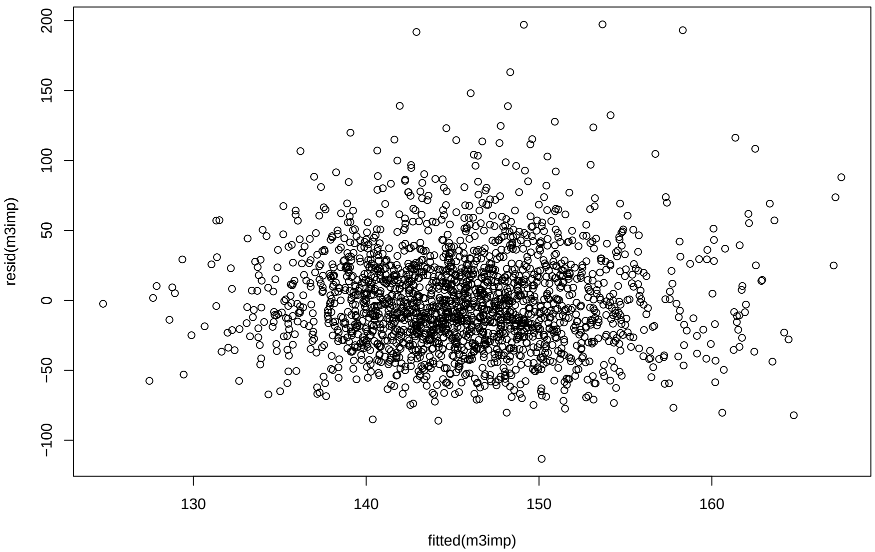
summary(m3imp)

```
> summary(m3imp)
             Effects              Response : ldl

 Factor                                              Low   High    Diff.   Effect  S.E.   Lower 0.95 Upper 0.95
 bmi                                                  24.2  30.263  6.0625  5.2108 2.2283   0.84072    9.58080
 age                                                  62.0  72.000 10.0000 -3.3219 1.3498  -5.96910   -0.67463
 sbp                                                 120.0 145.000 25.0000  3.0394 1.1317   0.81989    5.25880
 drinkany - yes:no                                     1.0   2.000      NA -3.7404 1.6625  -7.00080   -0.47996
 physact - about as active:somewhat more active        5.0   1.000      NA -3.8060 2.0257  -7.77860    0.16663
 physact - much less active:somewhat more active       5.0   2.000      NA -8.5486 3.9114 -16.21900   -0.87779
 physact - much more active:somewhat more active       5.0   3.000      NA -4.0724 2.7198  -9.40640    1.26160
 physact - somewhat less active:somewhat more active   5.0   4.000      NA -3.7746 2.5773  -8.82900    1.27980
 smoking - yes:no                                      1.0   2.000      NA  6.3067 2.4196   1.56150   11.05200

Adjusted to: bmi=26.9 smoking=no
```

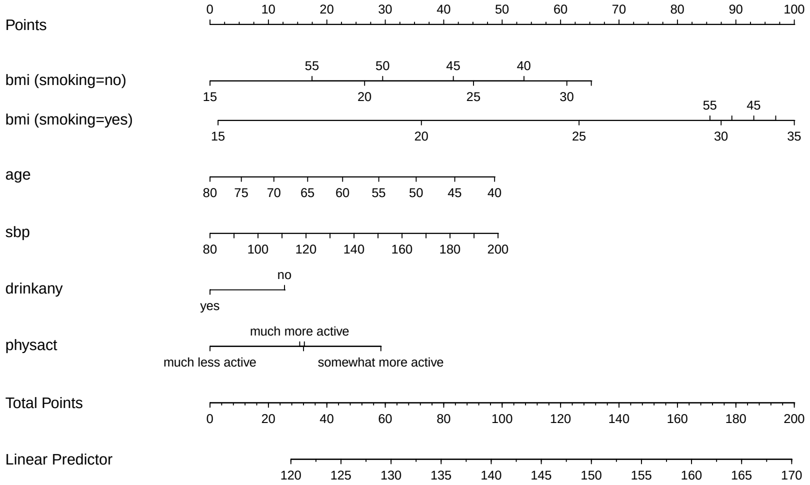
plot(summary(m3imp))



plot(resid(m3imp) ~ fitted(m3imp))



plot(nomogram(m3imp))



Next Step

Can we do all of this for a logistic regression model?