431 Class 22

Thomas E. Love

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Agenda for Today AND Class 23

- A Three-Way Contingency Table
  - Cochran-Mantel-Haenszel method (and Woolf test)
- Linear Regression for Prediction in our `dm431` data
  - Pre-Modeling Considerations
    - Consideration of Outcome Transformations
    - (Simple) Imputation to deal with Missing Data
    - Partitioning the Data (Development vs. Testing)
  - Building the Model
    - Evaluating Fit in the Development Sample
    - Considering Regression Assumptions
  - Post-Modeling Considerations
    - Evaluating Prediction Quality (Test Sample)
    - Back-Transformation of Outcome Predictions

Our R Setup

```r
library(vcd) # for Woolf test
library(simputation) # for simple imputation
library(car) # for Box-Cox plot
library(GGally) # for scatterplot matrix

library(here); library(magrittr)
library(patchwork); library(janitor); library(broom)
library(tidyverse) # always load tidyverse last

theme_set(theme_bw()) # now all ggplots use theme_bw()
```

Section 1

Three-Way Contingency Tables: A New Example

Alberta Automobile Accidents

Prior to the enactment of seatbelt legislation in the province of Alberta, Canada, a sample of 86,769 auto accident reports were studied. For each report, we categorize:

- driver condition (normal, been drinking)
- was the driver wearing a seatbelt (yes, no)
- the injury level of the driver (none, minimal, minor, or major/fatal)

Source: Jobson JD, Table 6.23 *Applied Multivariate Data Analysis: Volume II: Categorical and Multivariate Methods*

So this is going to become a 2 $\times$ 2 $\times$ 4 table.

A Two-Way Table

Ignoring the driver condition for a moment, here is the 2 × 4 table of seatbelt use and injury level.

–	None	Minimal	Minor	Major	Total
No Seatbelt	65963	4000	2642	303	72908
Seatbelt	12813	647	359	42	13861
Total	78776	4647	3001	345	86769

Calculating Probabilities using the Two-Way Table

We can calculate *marginal* probabilities from the table, like. . .

$$Pr(\text{Seatbelt}) = \frac{13861}{86769} = .160, \text{ and } Pr(\text{No injury}) = \frac{78776}{86769} = .908,$$

and we can calculate *conditional* probabilities, like . . .

$$Pr(\text{No injury}|\text{Seatbelt}) = \frac{12813}{13861} = 0.924$$

and

$$Pr(\text{No injury}|\text{No Seatbelt}) = \frac{65963}{72908} = 0.904$$

Three-Way Contingency Table (four 2 × 2)

We have **four** 2 × 2 tables,

- Injury = None (Odds Ratio = 2.57, 95% CI: 2.29, 2.89)

No Injury	Been Drinking	Normal
No Seatbelt	3992	61971
Seatbelt	313	12500

- Injury = Minimal (Odds Ratio = 1.92, 95% CI: 1.39, 2.65)

Minimal	Been Drinking	Normal
No Seatbelt	481	3519
Seatbelt	43	604

Three-Way Contingency Table (four 2 × 2)

and . . .

- Injury = Minor (Odds Ratio = 3.73, 95% CI: 2.20, 6.34)

Minor	Been Drinking	Normal
No Seatbelt	370	2272
Seatbelt	15	344

- Injury = Major (Odds Ratio = 2.65, 95% CI: 0.91, 7.68)

Major	Been Drinking	Normal
No Seatbelt	66	237
Seatbelt	4	38

Placing the Data in R

```r
condition <- c(rep("Normal", 8), rep("Been_Drinking", 8))
seatbelt <- c(rep(c(rep("Yes", 4), rep("No", 4)), 2))
injury <- c(rep(c("None", "Minimal", "Minor", "Major"), 4))
counts <- c(12500, 604, 344, 38, 61971, 3519, 2272, 237,
            313, 43, 15, 4, 3992, 481, 370, 66)

aaa <- tibble(condition, seatbelt, injury, counts) %>%
  mutate(injury = fct_relevel(injury, "None", "Minimal",
                              "Minor", "Major"))
```

Viewing the Table

```
big_tab <- aaa %$% xtabs(counts ~ seatbelt + condition + injur
big_tab %>% ftable()
```

```
                       injury  None Minimal Minor Major
seatbelt condition
No       Been_Drinking         3992     481   370    66
         Normal               61971    3519  2272   237
Yes      Been_Drinking          313      43    15     4
         Normal               12500     604   344    38
```

We're trying to estimate the odds ratio for "been drinking" given that the driver is "not wearing a seatbelt" as compared to when the driver is wearing a seatbelt, assuming that it is the same across all four injury types. We have:

- row = condition (been drinking or normal)
- column = seatbelt (no or yes)
- strata = injury (four levels)

Can we assume that each injury level has a common odds ratio?

Recall that the sample odds ratios we saw were:

No Injury	Minimal	Minor	Major
2.57	1.92	3.73	2.65

The Woolf test assesses the null hypothesis of a common "condition and seatbelt" odds ratio across the four injury types. This (that a common odds ratio can be assumed to exist for each of the four injury types) is a key assumption of the Cochran-Mantel-Haenszel test.

Can we assume that each injury level has a common odds ratio?

```r
woolf_test(big_tab)
```

```
    Woolf-test on Homogeneity of Odds Ratios (no
    3-Way assoc.)

data:  big_tab
X-squared = 4.9623, df = 3, p-value = 0.1746
```

Our conclusion from the Woolf test is that we are able to retain the null hypothesis of homogeneous odds ratios. So it's not crazy to fit a CMH test (that requires that all of the population odds ratios to be the same.)

Running the Cochran-Mantel-Haenszel test

So, we can use the Cochran-Mantel-Haenszel test to make inferences about the population odds ratio (for the driver having been drinking given no seatbelt rather than seatbelt) accounting for the four injury types. We'll use a 90% confidence interval, and the results appear on the next slide.

```
mantelhaen.test(big_tab, conf.level = .90)
```

Complete CMH output (Edited to fit on the screen)

```r
mantelhaen.test(big_tab, conf.level = .90)
```

```
Mantel-Haenszel chi-squared test with continuity correction

data:  big_tab
Mantel-Haenszel X-squared = 314, df = 1, p-value < 2.2e-16

alt. hypothesis: true common odds ratio is not equal to 1

90 percent confidence interval: 2.327467 2.784538
sample estimates: common odds ratio 2.545765
```

What can we conclude in this case?

Alternate Specification of Three-Way Table

We also have **two** of these 2 × 4 tables:

- Driver had been drinking

Been Drinking	None	Minimal	Minor	Major	Total
No Seatbelt	3992	481	370	66	4909
Seatbelt	313	43	15	4	375
Total	4305	524	385	70	5284

- Driver had not been drinking (was "Normal")

Normal	None	Minimal	Minor	Major	Total
No Seatbelt	61971	3519	2272	237	67999
Seatbelt	12500	604	344	38	13486
Total	74471	4123	2616	275	81485

Could we have run the test changing the roles?

We ran this originally using four (strata) to identify four 2 (row) × 2 (column) tables.

If we did this with two strata (been drinking vs. normal), on a 2 (row - seatbelt or not) × 4 (column - injury type) table, we'd no longer get an odds ratio, but we would be able to obtain a p value for the null hypothesis of no relationship between seatbelt use and injury type, accounting for drinking status.

To get it, we'd just rearrange the big table (strata goes last):

```
big_tab2 <-
  aaa %$% xtabs(counts ~ seatbelt + injury + condition)
```

Results when Strata = drinking status

```r
woolf_test(big_tab2)
```

```

    Woolf-test on Homogeneity of Odds Ratios (no
    3-Way assoc.)

data:  big_tab2
X-squared = 0.21445, df = 1, p-value = 0.6433
```

```r
mantelhaen.test(big_tab2)
```

```

    Cochran-Mantel-Haenszel test

data:  big_tab2
Cochran-Mantel-Haenszel M^2 = 40.213, df = 3,
p-value = 9.601e-09
```

Section 2

Building a "Small" Multiple Regression Model for our `dm431` data

A change to the data!

All this time, we've had an error in the dm431 data, which I'll now call dm431_old.Rds. Can you spot it?

```
dm431_old <- readRDS(here("data", "dm431_old.Rds"))

head(dm431_old, 8)
```

```
# A tibble: 8 x 21
  subject practice   age race_eth sex     a1c insurance
  <chr>   <fct>    <dbl> <fct>    <fct> <dbl> <fct>
1 S-001   Arlingt~    62 Black o~ F       6.3 Commerci~
2 S-002   Bristol     54 Black o~ F      11   Uninsured
3 S-003   Chester     47 Black o~ F       8.7 Uninsured
4 S-004   Dover       53 Non-His~ M       6.5 Commerci~
5 S-005   Franklin    64 Non-His~ F       6.7 Commerci~
6 S-006   Bristol     48 Black o~ F       5.8 Medicare
7 S-006   Franklin    49 Black o~ M       9.6 Commerci~
8 S-008   Dover       63 Black o~ F       6.1 Medicaid
```

So what exactly is the problem?

```
dm431_old %>% nrow()
```

```
[1] 431
```

```
dm431_old %$% n_distinct(subject)
```

```
[1] 430
```

```
dm431_old %>% slice(6:7) %>% select(subject, age)
```

```
# A tibble: 2 x 2
  subject   age
  <chr>   <dbl>
1 S-006      48
2 S-006      49
```

Fixing the Problem

```
dm431_fixed <- dm431_old %>%
  mutate(subject = ifelse(subject == "S-006" & age == 49,
                          "S-007", subject))

dm431_fixed %>% slice(6:7) %>% select(subject, age)
```

```
# A tibble: 2 x 2
  subject   age
  <chr>   <dbl>
1 S-006      48
2 S-007      49
```

```
saveRDS(dm431_fixed, file = here("data", "dm431_fixed.Rds"))
```

Focus on Four Variables (+ Subject)

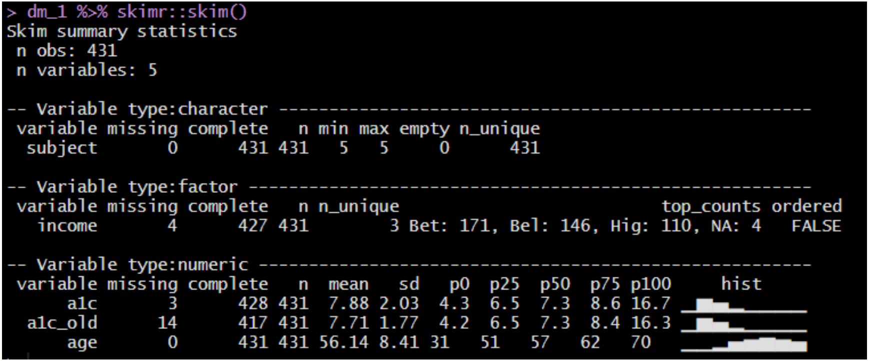
```r
dm431 <- readRDS(here("data", "dm431_fixed.Rds"))

dm_1 <- dm431 %>%
  select(a1c, a1c_old, age, income, subject)
```

Summarizing the dm_1 data set

```r
summary(dm_1)
```

```
      a1c            a1c_old            age       
 Min.   : 4.300   Min.   : 4.200   Min.   :31.00  
 1st Qu.: 6.500   1st Qu.: 6.500   1st Qu.:51.00  
 Median : 7.300   Median : 7.300   Median :57.00  
 Mean   : 7.884   Mean   : 7.712   Mean   :56.14  
 3rd Qu.: 8.600   3rd Qu.: 8.400   3rd Qu.:62.00  
 Max.   :16.700   Max.   :16.300   Max.   :70.00  
 NA's   :3        NA's   :14                      
             income      subject         
 Below_30K      :146   Length:431        
 Between_30-50K :171   Class :character  
 Higher_than_50K:110   Mode  :character  
 NA's           :  4                     
```

dm_1 %>% skimr::skim() results



```
> dm_1 %>% skimr::skim()
Skim summary statistics
 n obs: 431
 n variables: 5

-- Variable type:character -----------------------------------------------------
 variable missing complete   n min max empty n_unique
  subject       0      431 431   5   5     0      431

-- Variable type:factor --------------------------------------------------------
 variable missing complete   n n_unique                          top_counts ordered
   income       4      427 431        3 Bet: 171, Bel: 146, Hig: 110, NA: 4   FALSE

-- Variable type:numeric -------------------------------------------------------
 variable missing complete   n  mean   sd   p0  p25  p50  p75 p100     hist
      a1c       3      428 431  7.88 2.03  4.3  6.5  7.3  8.6 16.7
  a1c_old      14      417 431  7.71 1.77  4.2  6.5  7.3  8.4 16.3
      age       0      431 431 56.14 8.41 31    51   57   62   70
```

What roles will these variables play?

a1c is our outcome, which we'll predict with . . .

1. Model 1: Use a1c_old alone to predict a1c
2. Model 2: Use a1c_old and age together to predict a1c
3. Model 3: Use a1c_old, age, and income together to predict a1c

What will we do about missing data?

```
dm_1 %>% summarise_all(~ sum(is.na(.)))
```

```
# A tibble: 1 x 5
    a1c a1c_old   age income subject
  <int>   <int> <int>  <int>   <int>
1     3      14     0      4       0
```

- We're missing 3 values of a1c, our outcome
- and 14 values of a1c_old, a predictor (Models 1-3)
- and 4 values of income, another predictor (Model 3)

Dealing with outcome missingness

I don't want to impute the outcome. We'll drop the 3 observations missing a1c from our data set.

```
dm_2 <- dm_1 %>% filter(complete.cases(a1c))
dm_2 %>% summarise_all(~ sum(is.na(.)))
```

```
# A tibble: 1 x 5
    a1c a1c_old   age income subject
  <int>   <int> <int>  <int>   <int>
1     0      12     0      4       0
```

How should we deal with the remaining missing values?

Simple Imputation of Missing a1c_old Values

We could use a robust linear model method to impute our quantitative a1c_old values on the basis of age, which is missing no observations in common with a1c_old (in fact, age is missing no observations.)

```
dm_3a <- impute_rlm(dm_2, a1c_old ~ age)

dm_3a %>% select(a1c_old, income) %>% summary()
```

```
    a1c_old                   income   
 Min.   : 4.200   Below_30K      :146  
 1st Qu.: 6.500   Between_30-50K :169  
 Median : 7.300   Higher_than_50K:109  
 Mean   : 7.711   NA's           :  4  
 3rd Qu.: 8.400                        
 Max.   :16.300                        
```

Simple Imputation of Missing income Values

We could use a decision tree (CART) method to impute our missing categorical income values, on the basis of age.

```
dm_3b <- impute_cart(dm_2, income ~ age)

dm_3b %>% select(a1c_old, income) %>% summary()
```

```
    a1c_old                   income   
 Min.   : 4.200   Below_30K      :148  
 1st Qu.: 6.500   Between_30-50K :171  
 Median : 7.300   Higher_than_50K:109  
 Mean   : 7.716                        
 3rd Qu.: 8.400                        
 Max.   :16.300                        
 NA's   :12                            
```

Chaining our Simple Imputations

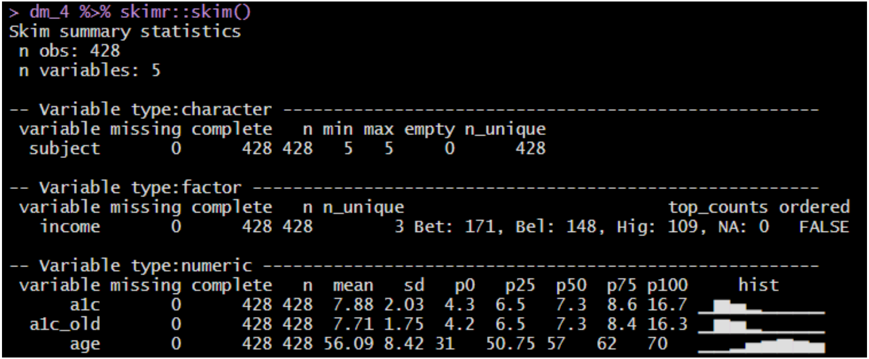
Or we could put all of our imputations together in a chain. I encourage you to try `rlm` for quantitative variables, and `cart` for categorical variables, for now.

```
dm_4 <- dm_2 %>%
  impute_rlm(a1c_old ~ age) %>%
  impute_cart(income ~ age + a1c_old)

dm_4 %>% select(a1c, a1c_old, income) %>%
  summarise_all(~(sum(is.na(.))))
```

```
# A tibble: 1 x 3
    a1c a1c_old income
  <int>   <int>  <int>
1     0       0      0
```

What did we do? What is the result?

dm_4 %>% skimr::skim() results



```
> dm_4 %>% skimr::skim()
Skim summary statistics
 n obs: 428
 n variables: 5

-- Variable type:character ----------------------------------------------------
 variable missing complete   n min max empty n_unique
  subject       0      428 428   5   5     0      428

-- Variable type:factor -------------------------------------------------------
 variable missing complete   n n_unique                          top_counts ordered
   income       0      428 428        3 Bet: 171, Bel: 148, Hig: 109, NA: 0   FALSE

-- Variable type:numeric ------------------------------------------------------
 variable missing complete   n  mean   sd  p0   p25  p50  p75 p100     hist
      a1c       0      428 428  7.88 2.03 4.3  6.5   7.3  8.6 16.7
  a1c_old       0      428 428  7.71 1.75 4.2  6.5   7.3  8.4 16.3
      age       0      428 428 56.09 8.42 31   50.75 57   62   70
```

OK. Ready to proceed?

Section 3

Model Selection (for 431)

How will we decide which of the models is "best"?

Our goal is accurate prediction of `a1c` values.

Which of these models gives us the "best" result?

1. Model 1: Use `a1c_old` alone to predict `a1c`
2. Model 2: Use `a1c_old` and `age` together to predict `a1c`
3. Model 3: Use `a1c_old`, `age`, and `income` together to predict `a1c`

How shall we be guided by our data?

It can scarcely be denied that the supreme goal of all theory is to make the irreducible basic elements as simple and as few as possible without having to surrender the adequate representation of a single datum of experience. (A. Einstein)

- often this is reduced to "make everything as simple as possible but no simpler"

  Entities should not be multiplied without necessity. (Occam's razor)

- often this is reduced to "the simplest solution is most likely the right one"

George Box's aphorisms

On Parsimony: Since all models are wrong the scientist cannot obtain a "correct" one by excessive elaboration. On the contrary following William of Occam he should seek an economical description of natural phenomena. Just as the ability to devise simple but evocative models is the signature of the great scientist so overelaboration and overparameterization is often the mark of mediocrity.
On Worrying Selectively: Since all models are wrong the scientist must be alert to what is importantly wrong. It is inappropriate to be concerned about mice when there are tigers abroad.

- and, the most familiar version…
  … all models are approximations. Essentially, all models are wrong, but some are useful. However, the approximate nature of the model must always be borne in mind.

431 approach: Which model is "most useful"?

1. Split the data into a model development (training) sample of about 70-80% of the observations, and a model test (holdout) sample, containing the remaining observations.
2. Develop candidate models using the development sample.
3. Assess the quality of fit for candidate models within the development sample.
4. Check adherence to regression assumptions in the development sample.
5. When you have candidates, assess them based on the accuracy of the predictions they make for the data held out (and thus not used in building the models.)
6. Select a "final" model for use based on the evidence in steps 3, 4 and especially 5.

Section 4

Split the data into a model development (training) sample of about 70-80% of the observations, and a model test (holdout) sample, containing the remaining observations.

Partition the imputed data into development/test samples

```r
set.seed(20191114)

dm4_dev <- sample_frac(dm_4, 0.75, replace = FALSE)

dm4_test <- anti_join(dm_4, dm4_dev, by = "subject")
```

```r
nrow(dm_4); nrow(dm4_dev); nrow(dm4_test)
```

```
[1] 428

[1] 321

[1] 107
```

Section 5

Develop candidate models using the development sample.

A look at the outcome (a1c) distribution

We'll study the outcome variable (a1c) in the development sample, to consider whether a transformation might be in order.

I did a little fancy work with the code (continues next slide)...

```
p1 <- ggplot(dm4_dev, aes(x = a1c)) +
  geom_histogram(binwidth = 0.5,
                 fill = "slateblue", col = "white")

p2 <- ggplot(dm4_dev, aes(sample = a1c)) +
  geom_qq(col = "slateblue") + geom_qq_line(col = "red")

p3 <- ggplot(dm4_dev, aes(x = "", y = a1c)) +
  geom_violin(fill = "slateblue", alpha = 0.3) +
  geom_boxplot(fill = "slateblue", width = 0.3,
               outlier.color = "red") +
  labs(x = "") + coord_flip()
```

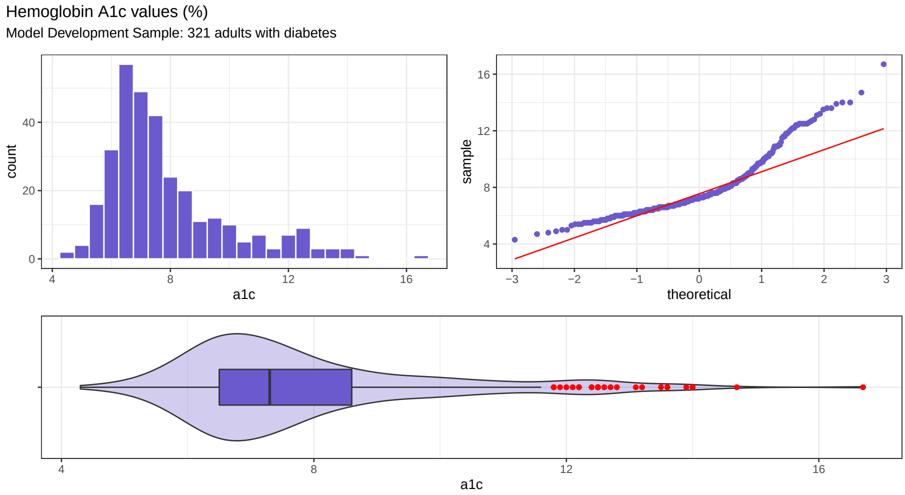
A look at the outcome (`a1c`) distribution

Putting the plots together, and titling them meaningfully…

```
p1 + p2 - p3 +
  plot_layout(ncol = 1, height = c(3, 2)) +
  plot_annotation(title = "Hemoglobin A1c values (%)",
        subtitle = paste0("Model Development Sample: ",
                          nrow(dm4_dev),
                          " adults with diabetes"))
```

Result on the next slide…

Outcome (`a1c`): Model Development Sample



Why Transform the Outcome?

We want to try to identify a good transformation for the conditional distribution of the outcome, given the predictors, in an attempt to make the linear regression assumptions of linearity, Normality and constant variance more appropriate.

Ladder of Especially Useful (and often interpretable) transformations

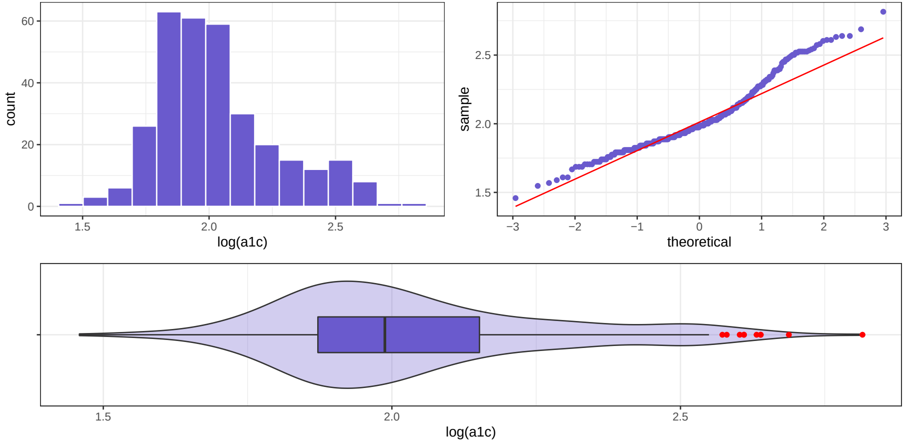
Transformation	y^2	y	$\sqrt{y}$	log(y)	$1/y$	$1/y^2$
λ	2	1	0.5	0	-1	-2

- We see some sign of right skew in the `a1c` data. Let's try a log transformation.

Consider a log transformation?

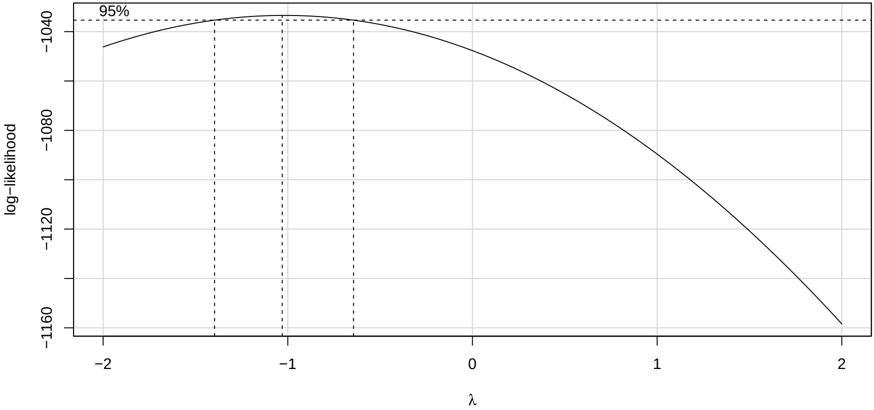
Natural Logarithm of Hemoglobin A1c

Model Development Sample: 321 adults with diabetes



Using Box-Cox to help select a transformation?

```
mod_0 <- lm(a1c ~ a1c_old + age + income, data = dm4_dev)

boxCox(mod_0)
```

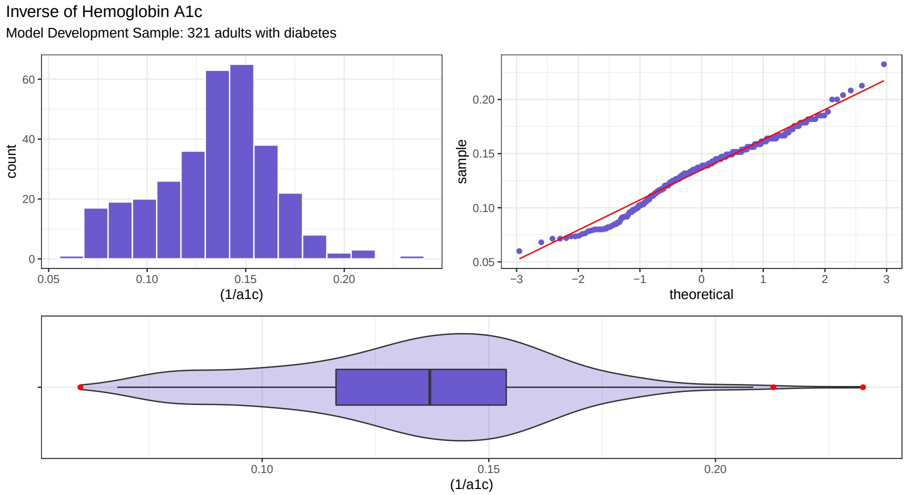


Using Box-Cox to help select a transformation?

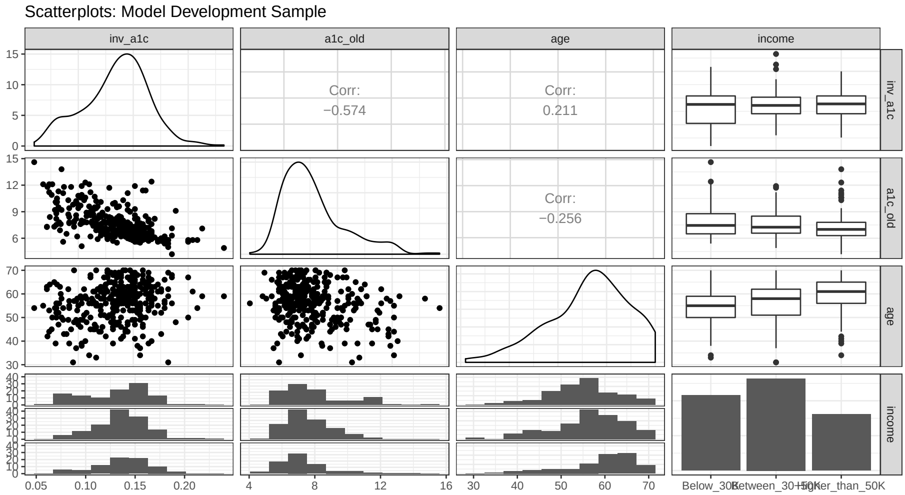
```
summary(powerTransform(mod_0))
```

```
bcPower Transformation to Normality
   Est Power Rounded Pwr Wald Lwr Bnd Wald Upr Bnd
Y1    -1.019          -1      -1.3953      -0.6427

Likelihood ratio test that transformation parameter is equal t
 (log transformation)
                           LRT df       pval
LR test, lambda = (0) 28.53961  1 9.1801e-08

Likelihood ratio test that no transformation is needed
                           LRT df       pval
LR test, lambda = (1) 112.3945  1 < 2.22e-16
```

Consider the inverse?



Scatterplot Matrix



Scatterplot Matrix (Code)

```
dm4_dev %>%
  mutate(inv_a1c = 1/a1c) %>%
  select(inv_a1c, a1c_old, age, income) %>%
  ggpairs(., title = "Scatterplot Matrix for Model Development
          lower = list(combo = wrap("facethist", bins = 10)))
```

Note that ggpairs comes from the GGally package.

Three Regression Models We'll Fit

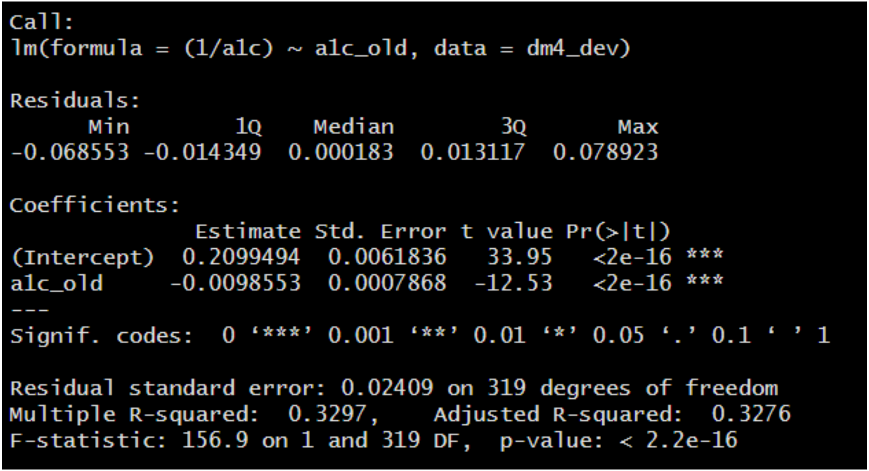
Remember we're using the model development sample here.

```r
mod_1 <- lm((1/a1c) ~ a1c_old, data = dm4_dev)

mod_2 <- lm((1/a1c) ~ a1c_old + age, data = dm4_dev)

mod_3 <- lm((1/a1c) ~ a1c_old + age + income,
            data = dm4_dev)
```

Section 6

Assess the quality of fit for candidate models within the development sample.

summary(mod_1) (edited to fit on screen)



```
Call:
lm(formula = (1/a1c) ~ a1c_old, data = dm4_dev)

Residuals:
      Min        1Q    Median        3Q       Max
-0.068553 -0.014349  0.000183  0.013117  0.078923

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.2099494  0.0061836   33.95   <2e-16 ***
a1c_old     -0.0098553  0.0007868  -12.53   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.02409 on 319 degrees of freedom
Multiple R-squared:  0.3297,    Adjusted R-squared:  0.3276
F-statistic: 156.9 on 1 and 319 DF,  p-value: < 2.2e-16
```

Summary of Fit Quality (mod_1)

```
g1 <- glance(mod_1) %>%
  mutate(name = "mod_1") %>%
  select(name, r.squared, adj.r.squared,
         sigma, AIC, BIC) %>%
  knitr::kable(digits = c(0, 3, 3, 3, 0, 0))

g1
```

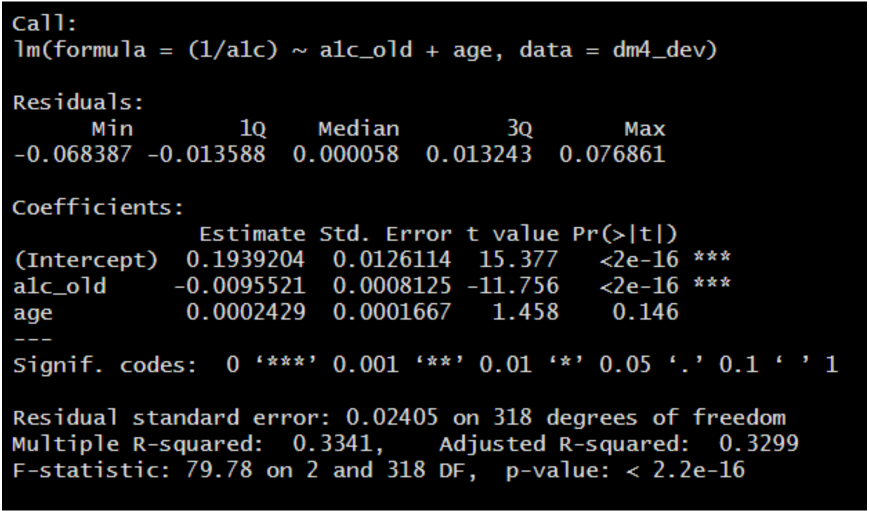
name	r.squared	adj.r.squared	sigma	AIC	BIC
mod_1	0.33	0.328	0.024	-1477	-1466

Tidied coefficients (mod_1)

```
tidy(mod_1, conf.int = TRUE, conf.level = 0.95) %>%
  select(term, estimate, std.error, p.value,
         conf.low, conf.high) %>%
  knitr::kable(digits = c(0, 4, 4, 4, 4, 4))
```

term	estimate	std.error	p.value	conf.low	conf.high
(Intercept)	0.2099	0.0062	0	0.1978	0.2221
a1c_old	-0.0099	0.0008	0	-0.0114	-0.0083

summary(mod_2) (edited to fit on screen)



```
Call:
lm(formula = (1/a1c) ~ a1c_old + age, data = dm4_dev)

Residuals:
      Min        1Q    Median        3Q       Max 
-0.068387 -0.013588  0.000058  0.013243  0.076861 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept)  0.1939204  0.0126114  15.377   <2e-16 ***
a1c_old     -0.0095521  0.0008125 -11.756   <2e-16 ***
age          0.0002429  0.0001667   1.458    0.146    
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.02405 on 318 degrees of freedom
Multiple R-squared:  0.3341,    Adjusted R-squared:  0.3299 
F-statistic: 79.78 on 2 and 318 DF,  p-value: < 2.2e-16
```

Summary of Fit Quality (mod_2)

```
g2 <- glance(mod_2) %>%
  mutate(name = "mod_2") %>%
  select(name, r.squared, adj.r.squared,
         sigma, AIC, BIC) %>%
  knitr::kable(digits = c(0, 3, 3, 3, 0, 0))

g2
```

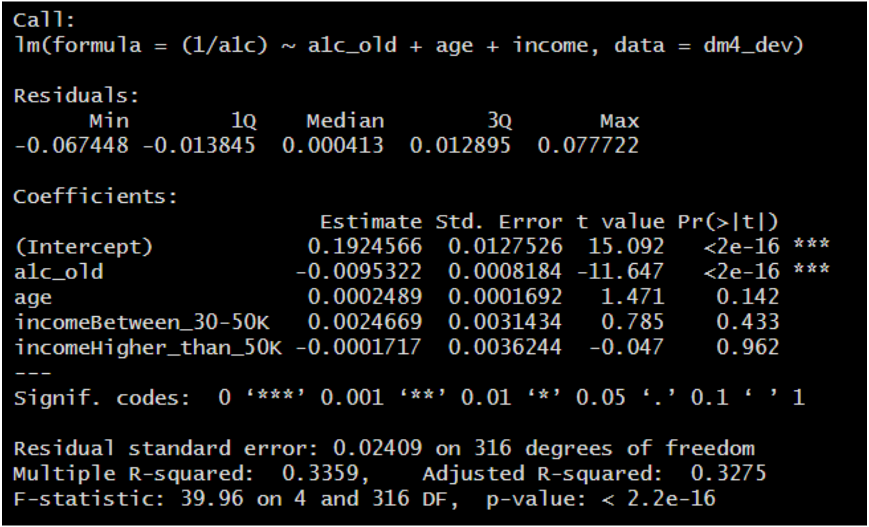
name	r.squared	adj.r.squared	sigma	AIC	BIC
mod_2	0.334	0.33	0.024	-1477	-1462

Tidied coefficients (mod_2)

```r
tidy(mod_2, conf.int = TRUE, conf.level = 0.95) %>%
  select(term, estimate, std.error, p.value,
         conf.low, conf.high) %>%
  knitr::kable(digits = c(0, 4, 4, 4, 4, 4))
```

term	estimate	std.error	p.value	conf.low	conf.high
(Intercept)	0.1939	0.0126	0.000	0.1691	0.2187
a1c_old	-0.0096	0.0008	0.000	-0.0112	-0.0080
age	0.0002	0.0002	0.146	-0.0001	0.0006

summary(mod_3) (edited to fit on screen)



```
Call:
lm(formula = (1/alc) ~ alc_old + age + income, data = dm4_dev)

Residuals:
      Min        1Q    Median        3Q       Max 
-0.067448 -0.013845  0.000413  0.012895  0.077722 

Coefficients:
                        Estimate Std. Error t value Pr(>|t|)    
(Intercept)            0.1924566  0.0127526  15.092   <2e-16 ***
alc_old               -0.0095322  0.0008184 -11.647   <2e-16 ***
age                    0.0002489  0.0001692   1.471    0.142    
incomeBetween_30-50K   0.0024669  0.0031434   0.785    0.433    
incomeHigher_than_50K -0.0001717  0.0036244  -0.047    0.962    
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.02409 on 316 degrees of freedom
Multiple R-squared:  0.3359,    Adjusted R-squared:  0.3275 
F-statistic: 39.96 on 4 and 316 DF,  p-value: < 2.2e-16
```

Summary of Fit Quality (mod_3)

```
g3 <- glance(mod_3) %>%
  mutate(name = "mod_3") %>%
  select(name, r.squared, adj.r.squared,
         sigma, AIC, BIC) %>%
  knitr::kable(digits = c(0, 3, 3, 3, 0, 0))

g3
```

name	r.squared	adj.r.squared	sigma	AIC	BIC
mod_3	0.336	0.328	0.024	-1474	-1451

Tidied coefficients (`mod_3`)

```r
tidy(mod_3, conf.int = TRUE, conf.level = 0.95) %>%
  select(term, est = estimate, se = std.error, p = p.value,
         low95 = conf.low, high95 = conf.high) %>%
  knitr::kable(digits = c(0, 4, 4, 3, 4, 4))
```

term	est	se	p	low95	high95
(Intercept)	0.1925	0.0128	0.000	0.1674	0.2175
a1c_old	-0.0095	0.0008	0.000	-0.0111	-0.0079
age	0.0002	0.0002	0.142	-0.0001	0.0006
incomeBetween_30-50K	0.0025	0.0031	0.433	-0.0037	0.0087
incomeHigher_than_50K	-0.0002	0.0036	0.962	-0.0073	0.0070

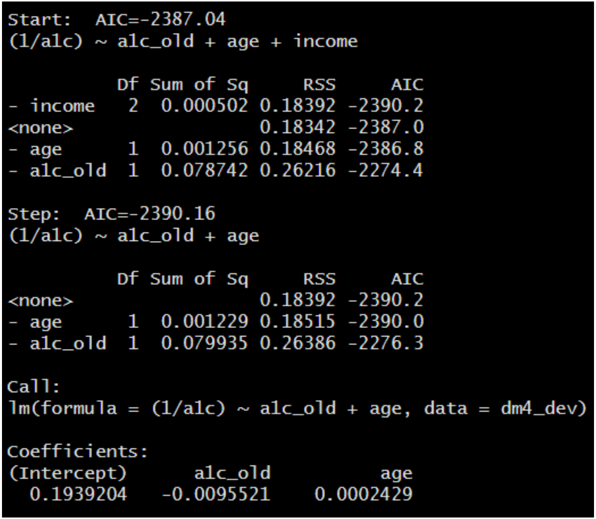
Could we have fit other predictor sets?

Perhaps an automated procedure like stepwise regression would suggest a better alternative?

- Three predictor candidates, so we could have used any of these predictor sets:
- a1c_old alone (our mod_1)
- age alone
- income alone
- a1c_old and age (our mod_2)
- a1c_old and income
- age and income
- a1c_old, age and income (our mod_3)

```
step(mod_3)
```

Stepwise Regression Results?



```
Start:  AIC=-2387.04
(1/a1c) ~ a1c_old + age + income

          Df Sum of Sq     RSS     AIC
- income   2  0.000502 0.18392 -2390.2
<none>                 0.18342 -2387.0
- age      1  0.001256 0.18468 -2386.8
- a1c_old  1  0.078742 0.26216 -2274.4

Step:  AIC=-2390.16
(1/a1c) ~ a1c_old + age

          Df Sum of Sq     RSS     AIC
<none>                 0.18392 -2390.2
- age      1  0.001229 0.18515 -2390.0
- a1c_old  1  0.079935 0.26386 -2276.3

Call:
lm(formula = (1/a1c) ~ a1c_old + age, data = dm4_dev)

Coefficients:
(Intercept)      a1c_old          age
  0.1939204   -0.0095521    0.0002429
```

Comparing Summary Measures of Fit

in the development sample…

```
bind_rows(glance(mod_1), glance(mod_2), glance(mod_3)) %>%
  mutate(name = c("mod_1", "mod_2", "mod_3")) %>%
  select(name, r2 = r.squared, adj_r2 = adj.r.squared,
         sigma, AIC, BIC, df, df_resid = df.residual) %>%
  knitr::kable(digits = c(0, 4, 4, 4, 1, 0, 0, 0))
```

name	r2	adj_r2	sigma	AIC	BIC	df	df_resid
mod_1	0.3297	0.3276	0.0241	-1477.1	-1466	2	319
mod_2	0.3341	0.3299	0.0240	-1477.2	-1462	3	318
mod_3	0.3359	0.3275	0.0241	-1474.1	-1451	5	316

OK. What do we think?

Section 7

Check adherence to regression assumptions in the development sample.

Checking Regression Assumptions

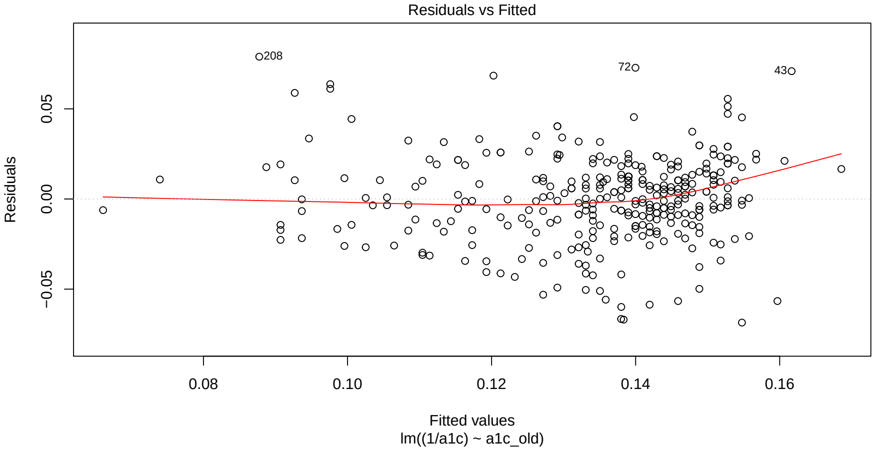
Four key assumptions we need to think about:

1. Linearity
2. Constant Variance (Homoscedasticity)
3. Normality
4. Independence

How do we assess 1, 2, and 3? Residual plots.

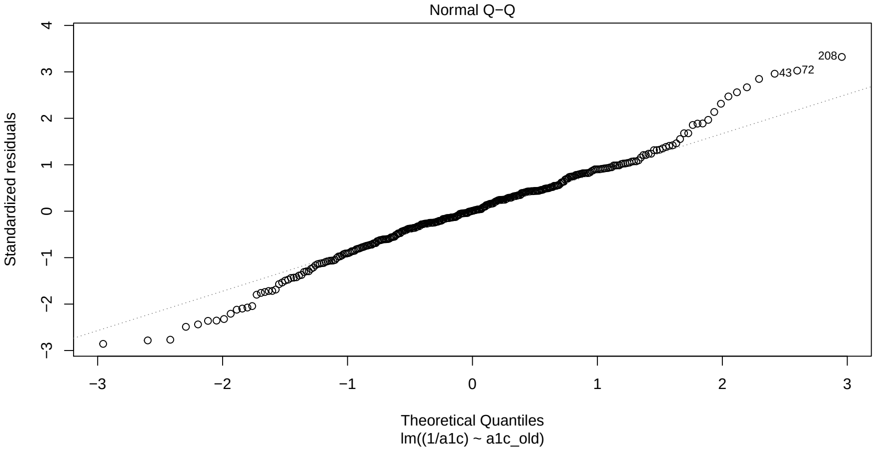
Residuals vs. Fitted Values Plot (Model `mod_1`)

```r
plot(mod_1, which = 1)
```



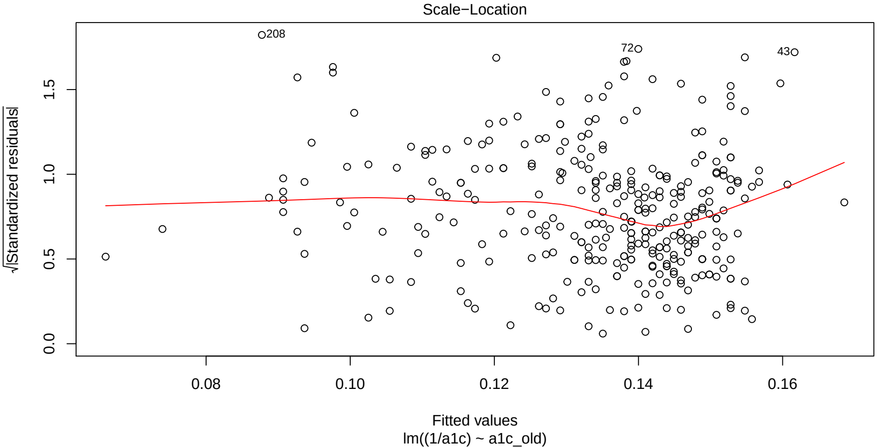
Normal Q-Q of Standardized Residuals (mod_1)

```r
plot(mod_1, which = 2)
```



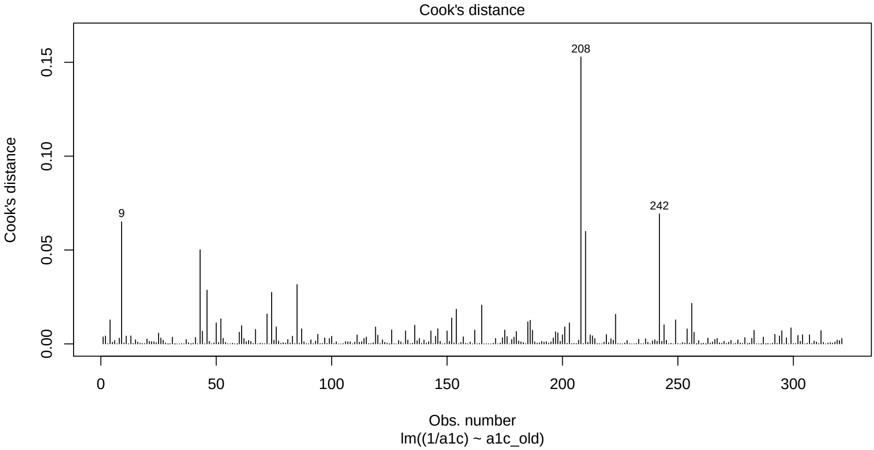
Scale-Location: Non-constant variance check (`mod_1`)

```
plot(mod_1, which = 3)
```



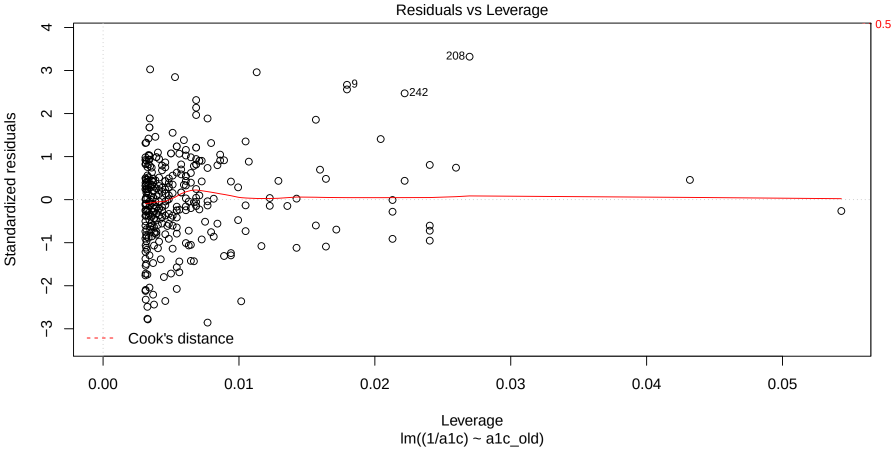
Index plot of Cook's distance for influence (`mod_1`)

```
plot(mod_1, which = 4)
```



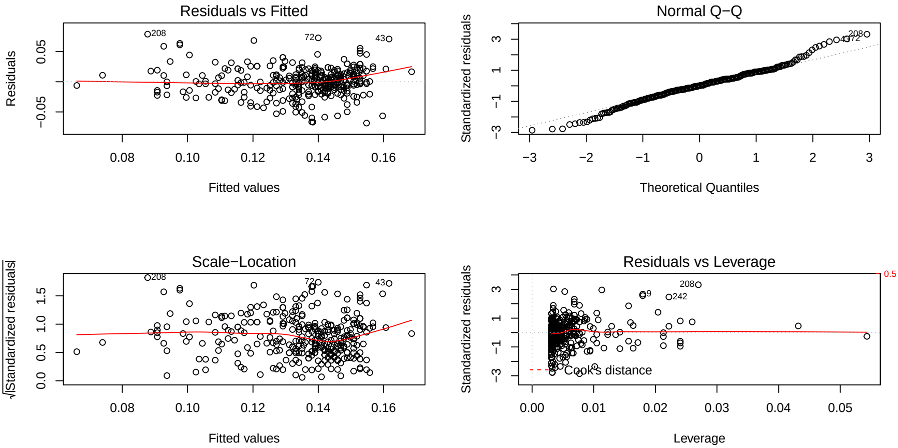
Residuals, Leverage and Influence plot (`mod_1`)

```
plot(mod_1, which = 5)
```

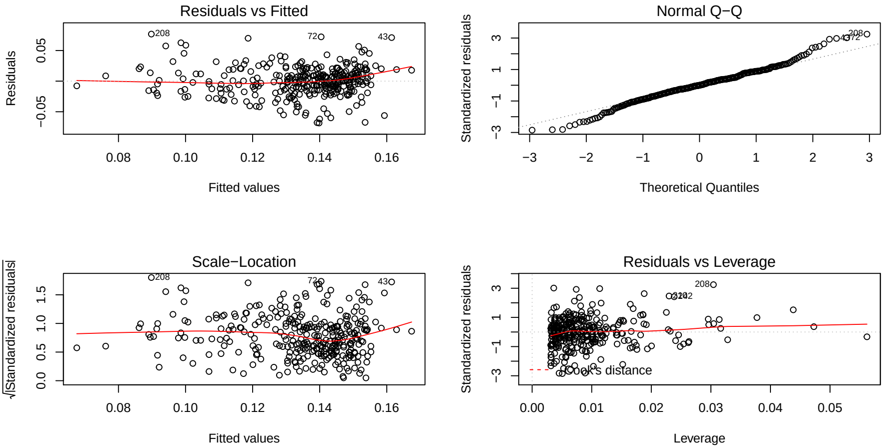


Residual Plots for Model `mod_1`

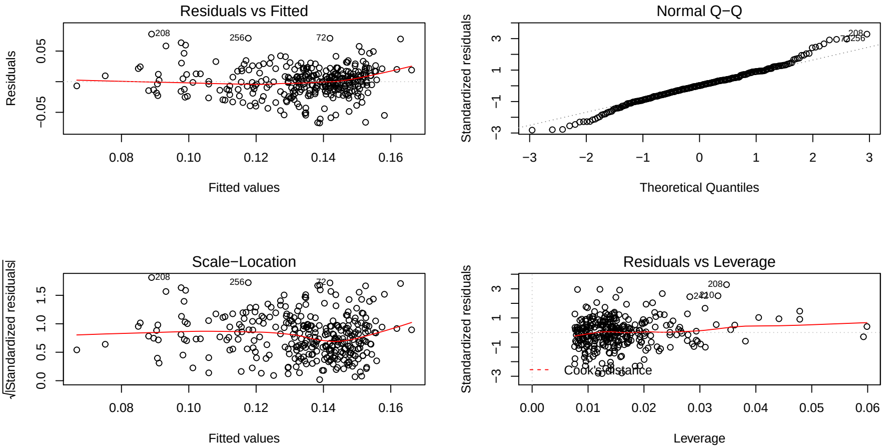
```r
par(mfrow = c(2,2)); plot(mod_1); par(mfrow = c(1,1))
```



Residual Plots for Model `mod_2`



Residual Plots for Model `mod_3`



Conclusions so far?

1. In-sample model predictions are about equally accurate for each of the three models. It's not clear yet that we need anything more than the simple regression on `a1c_old`.
2. Residual plots look similarly reasonable for linearity, Normality and constant variance in all three models.
3. Probably worth considering all three models further, but it would depend on the context.

Section 8

When you have candidates, assess them based on the accuracy of the predictions they make for the data held out (and thus not used in building the models.)

Calculate prediction errors for mod_1 in test sample

The augment function in the broom package will create predictions within our new sample, but we want to back-transform these predictions so that they are on the original scale (a1c, rather than our transformed regression outcome 1/a1c). Since the way to back out of the inverse transformation is to take the inverse again, we will take the inverse of the fitted values provided by augment and then calculate residuals on the original scale, as follows. . .

```
test_m1 <- augment(mod_1, newdata = dm4_test) %>%
  mutate(name = "mod_1", fit_a1c = 1 / .fitted,
         res_a1c = a1c - fit_a1c)
```

What does `test_m1` now include?

```
test_m1 %>%
  select(subject, a1c, fit_a1c, res_a1c, a1c_old,
         age, income) %>%
  head() %>%
  knitr::kable(digits = c(0, 1, 2, 2, 1, 0, 0))
```

subject	a1c	fit_a1c	res_a1c	a1c_old	age	income
S-002	11.0	20.28	-9.28	16.3	54	Between_30-50K
S-005	6.7	6.76	-0.06	6.3	64	Between_30-50K
S-006	5.8	6.85	-1.05	6.5	48	Below_30K
S-009	12.9	7.46	5.44	7.7	55	Below_30K
S-013	8.1	6.95	1.15	6.7	55	Higher_than_50K
S-016	8.4	7.46	0.94	7.7	44	Between_30-50K

Gather test-sample prediction errors for models 2, 3

```
test_m2 <- augment(mod_2, newdata = dm4_test) %>%
  mutate(name = "mod_2", fit_a1c = 1 / .fitted,
         res_a1c = a1c - fit_a1c)

test_m3 <- augment(mod_3, newdata = dm4_test) %>%
  mutate(name = "mod_3", fit_a1c = 1 / .fitted,
         res_a1c = a1c - fit_a1c)
```

Combine test sample results from the three models

```r
test_comp <- bind_rows(test_m1, test_m2, test_m3) %>%
  arrange(subject, name)

test_comp %>% select(name, subject, a1c, fit_a1c, res_a1c,
                     a1c_old, age, income) %>%
  slice(1:3, 7:9) %>%
  knitr::kable(digits = c(0, 0, 1, 2, 2, 1, 0, 0))
```

name	subject	a1c	fit_a1c	res_a1c	a1c_old	age	income
mod_1	S-002	11.0	20.28	-9.28	16.3	54	Between_30-5
mod_2	S-002	11.0	19.48	-8.48	16.3	54	Between_30-5
mod_3	S-002	11.0	18.87	-7.87	16.3	54	Between_30-5
mod_1	S-006	5.8	6.85	-1.05	6.5	48	Below_30K
mod_2	S-006	5.8	6.97	-1.17	6.5	48	Below_30K
mod_3	S-006	5.8	7.02	-1.22	6.5	48	Below_30K

What do we do to compare the test-sample errors?

Given this tibble, including predictions and residuals from the three models on our test data, we can now:

1. Visualize the prediction errors from each model.
2. Summarize those errors across each model.
3. Identify the "worst fitting" subject for each model in the test sample.

Visualize the prediction errors

```
ggplot(test_comp, aes(x = res_a1c, fill = name)) +
  geom_histogram(bins = 20, col = "white") +
  facet_grid (name ~ .) + guides(fill = FALSE)
```

or maybe

```
ggplot(test_comp, aes(x = name, y = res_a1c, fill = name)) +
  geom_violin(alpha = 0.3) +
  geom_boxplot(width = 0.3, outlier.shape = NA) +
  geom_jitter(height = 0, width = 0.1) +
  guides(fill = FALSE)
```

Test-Sample Prediction Errors

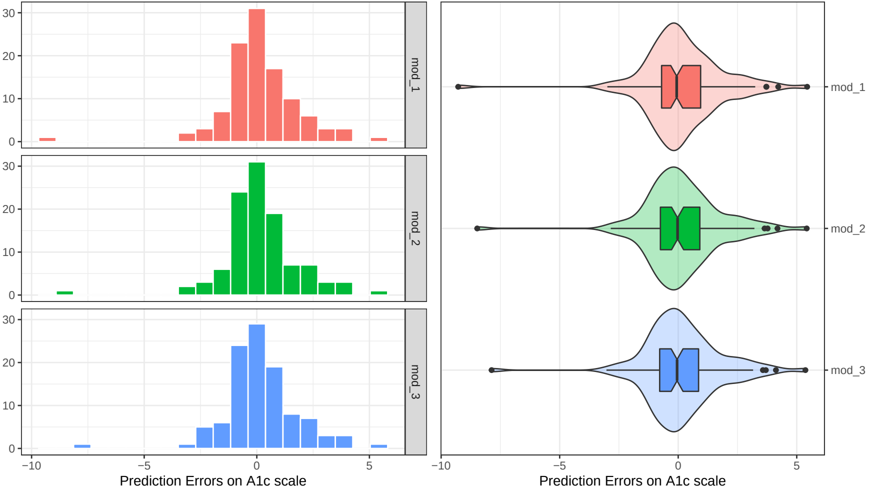


Table Comparing Model Prediction Errors

Calculate the mean absolute prediction error (MAPE), the mean squared prediction error (MSPE) and the maximum absolute error across the predictions made by each model.

```
test_comp %>%
  group_by(name) %>%
  summarize(n = n(),
            MAPE = mean(abs(res_a1c)),
            MSPE = mean(res_a1c^2),
            max_error = max(abs(res_a1c)))
```

```
# A tibble: 3 x 5
  name        n  MAPE  MSPE max_error
  <chr> <int> <dbl> <dbl>     <dbl>
1 mod_1   107  1.15  2.99      9.28
2 mod_2   107  1.14  2.83      8.48
3 mod_3   107  1.13  2.71      7.87
```

Identify the largest errors

Identify the subject(s) where that maximum prediction error was made by each model, and the observed and model-fitted values of `a1c` in each case.

```r
temp1 <- test_m1 %>%
  filter(abs(res_a1c) == max(abs(res_a1c)))

temp2 <- test_m2 %>%
  filter(abs(res_a1c) == max(abs(res_a1c)))

temp3 <- test_m3 %>%
  filter(abs(res_a1c) == max(abs(res_a1c)))
```

Identify the largest errors (Results)

Identify the subject(s) where that maximum prediction error was made by each model, and the observed and model-fitted values of a1c in each case.

```r
bind_rows(temp1, temp2, temp3) %>%
  select(subject, a1c, fit_a1c, res_a1c)
```

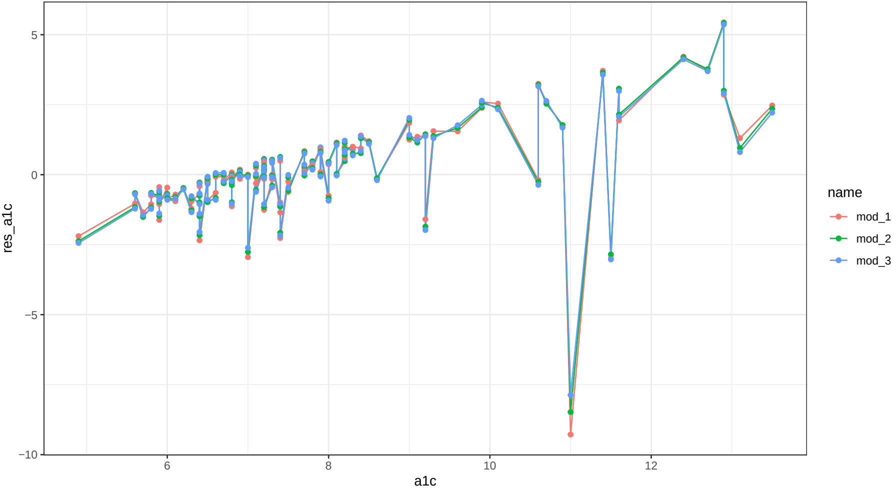
```
# A tibble: 3 x 4
  subject   a1c fit_a1c res_a1c
  <chr>   <dbl>   <dbl>   <dbl>
1 S-002      11    20.3   -9.28
2 S-002      11    19.5   -8.48
3 S-002      11    18.9   -7.87
```

Line Plot of the Errors?

Compare the errors that are made at each level of observed A1c?

```
ggplot(test_comp, aes(x = a1c, y = res_a1c,
                      group = name)) +
  geom_line(aes(col = name)) +
  geom_point(aes(col = name))
```

Line Plot of the Errors?



What if we ignored S-002 for a moment?

All three miss this subject substantially, but without S-002, we have:

```r
test_comp %>% filter(subject != "S-002") %>%
  group_by(name) %>%
  summarize(n = n(),
            MAPE = mean(abs(res_a1c)),
            MSPE = mean(res_a1c^2),
            max_error = max(abs(res_a1c)))
```

```
# A tibble: 3 x 5
  name      n  MAPE  MSPE max_error
  <chr> <int> <dbl> <dbl>     <dbl>
1 mod_1   106  1.07  2.21      5.44
2 mod_2   106  1.07  2.18      5.42
3 mod_3   106  1.07  2.16      5.37
```

With the exception of subject S-002, the three models seem to make very similar errors in the test sample. ## Conclusions now?

Repeating our 431 Strategy

Which model is "most useful" in a prediction context?

1. Split the data into a model development (training) sample of about 70-80% of the observations, and a model test (holdout) sample, containing the remaining observations.
2. Develop candidate models using the development sample.
3. Assess the quality of fit for candidate models within the development sample.
4. Check adherence to regression assumptions in the development sample.
5. When you have candidates, assess them based on the accuracy of the predictions they make for the data held out (and thus not used in building the models.)
6. Select a "final" model for use based on the evidence in steps 3, 4 and especially 5.