431 Class 23

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Agenda for Today

- 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

In today's class, we started with slide 20, and ended on slide 47.

Our R Setup

```
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()
```

Things discussed in Class 22

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?

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

```
[1] 431
```

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

```
[1] 430
```

```r
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

```r
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
```

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

Focus on Four Variables (+ Subject)

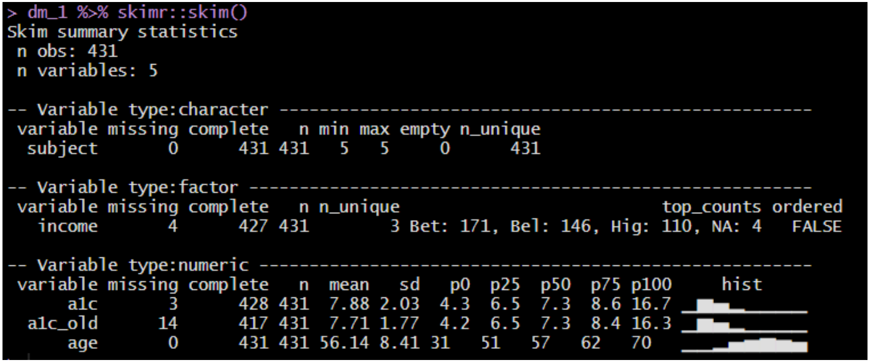
```r
dm431 <- readRDS(here("data", "dm431_fixed.Rds"))

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

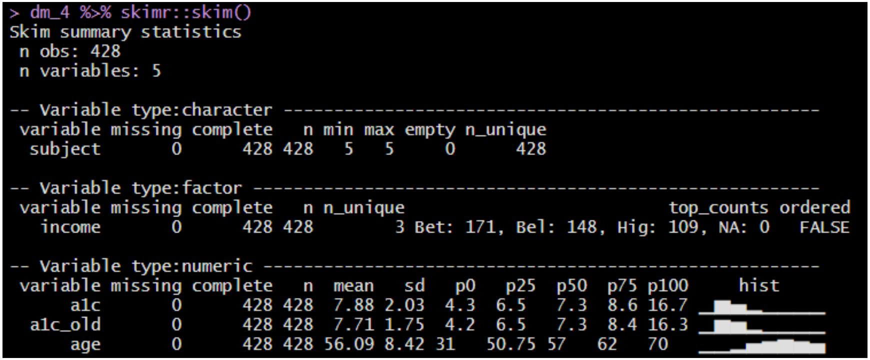
Or we could put all of our imputations together in a chain. I encourage you to try `rlm` for quantitative variables, and `cart` for categorical variables, for now.

```
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?

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.

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

```
set.seed(20191114)

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

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

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

```
[1] 428

[1] 321

[1] 107
```

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)...

```r
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()
```

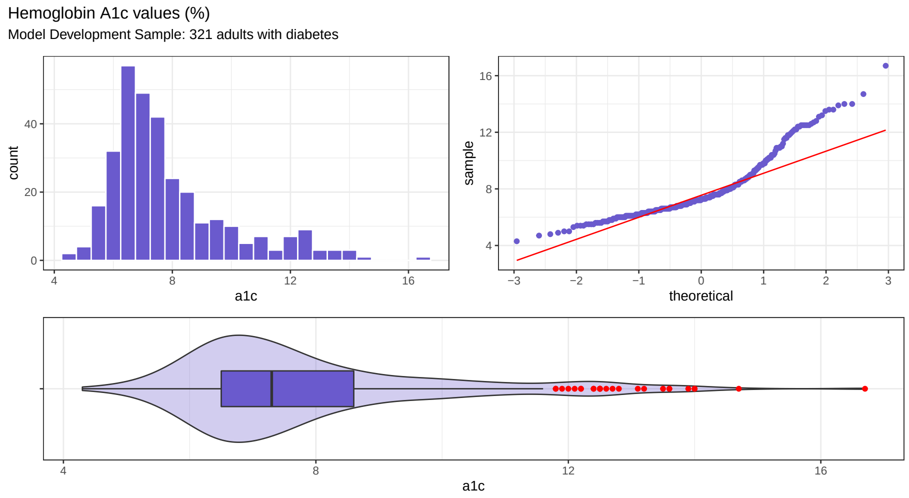
A look at the outcome (a1c) distribution

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?

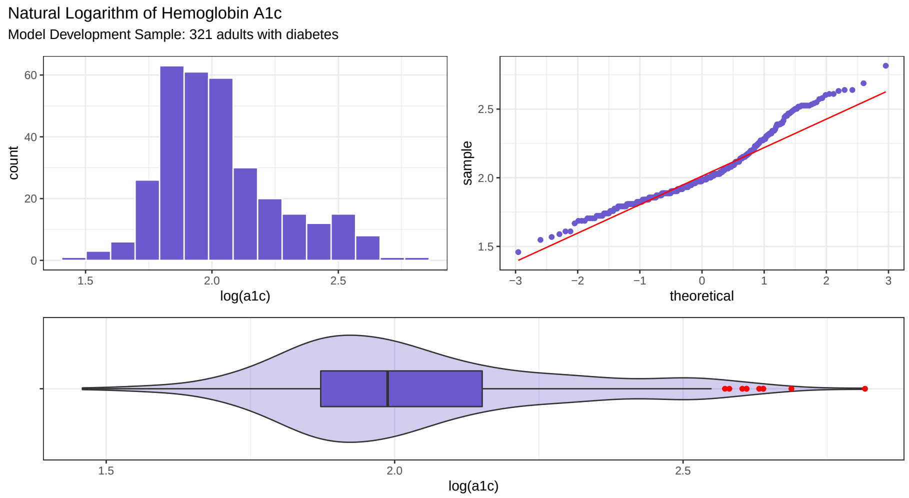
We want to try to identify a good transformation for the conditional distribution of the outcome, given the predictors, in an attempt to make the linear regression assumptions of linearity, Normality and constant variance more appropriate.

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

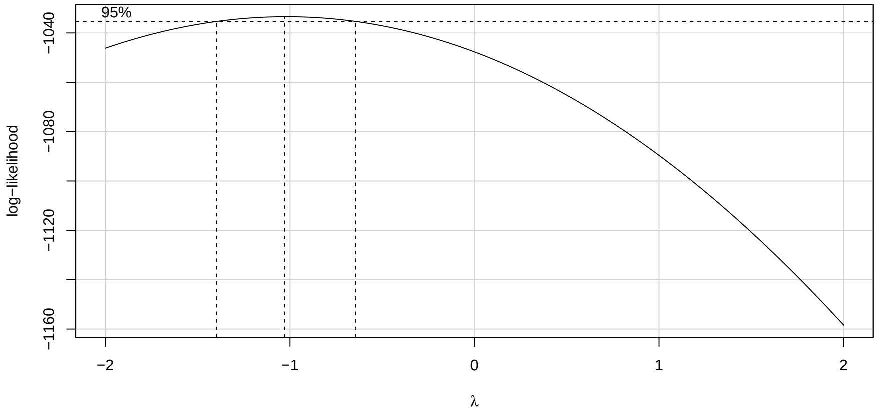
- We see some sign of right skew in the `a1c` data. Let's try a log transformation.

Consider a log transformation?



Using Box-Cox to help select a transformation?

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

boxCox(mod_0)
```

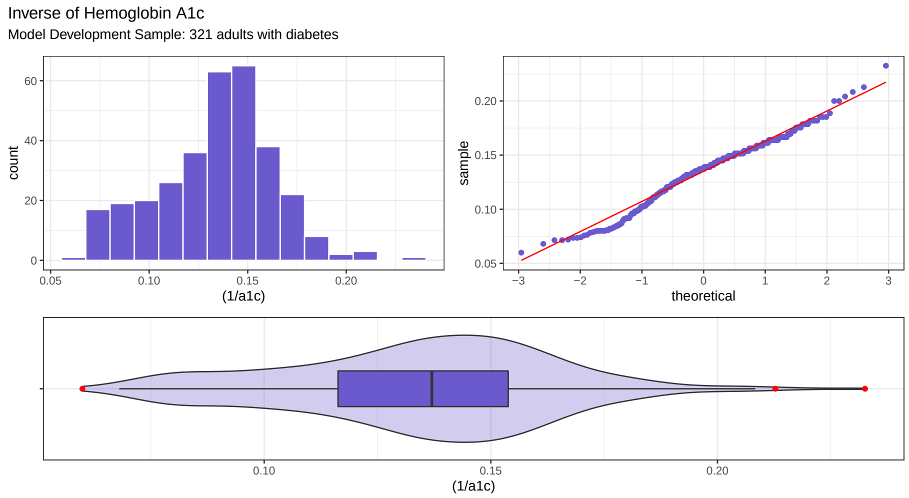


Using Box-Cox to help select a transformation?

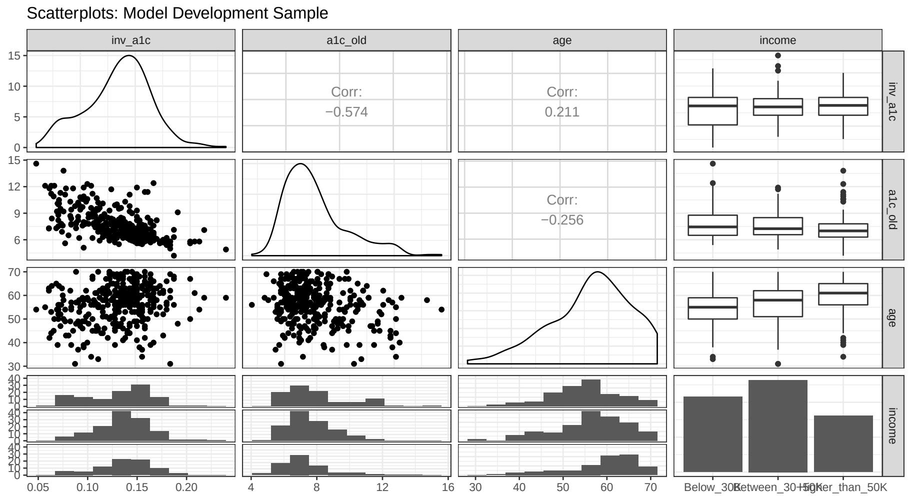
```r
summary(powerTransform(mod_0))
```

```
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 Developmen
          lower = list(combo = wrap("facethist", bins = 10)))
```

Note that ggpairs comes from the GGally package.

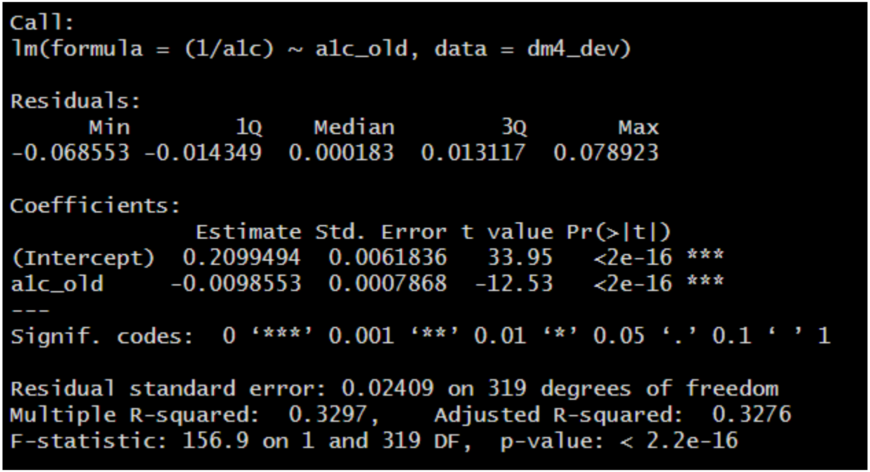
Three Regression Models We'll Fit

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)
```

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)

```r
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
```

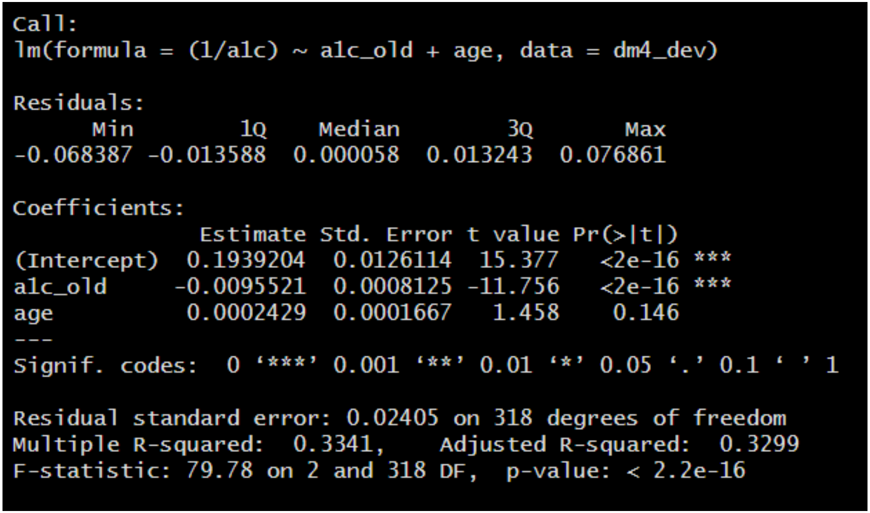
name	r.squared	adj.r.squared	sigma	AIC	BIC
mod_1	0.33	0.328	0.024	-1477	-1466

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)

```r
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
```

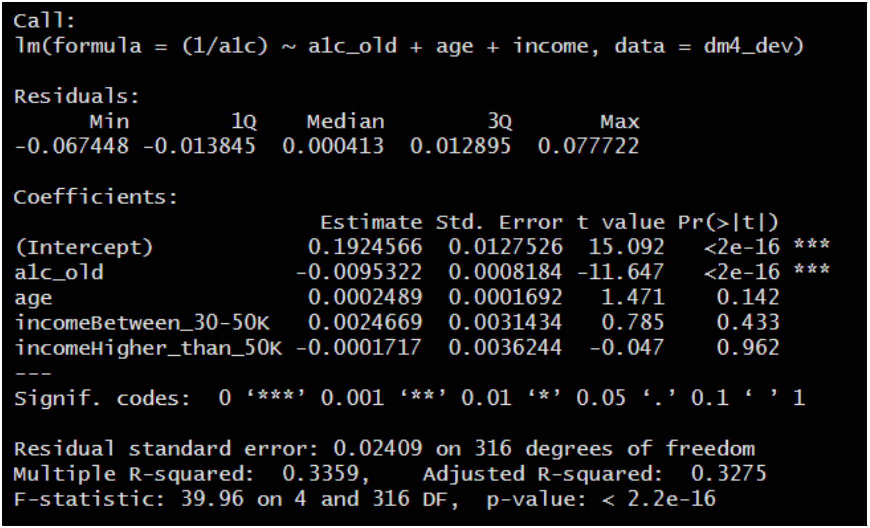
name	r.squared	adj.r.squared	sigma	AIC	BIC
mod_2	0.334	0.33	0.024	-1477	-1462

Tidied coefficients (mod_2)

```
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)

```r
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

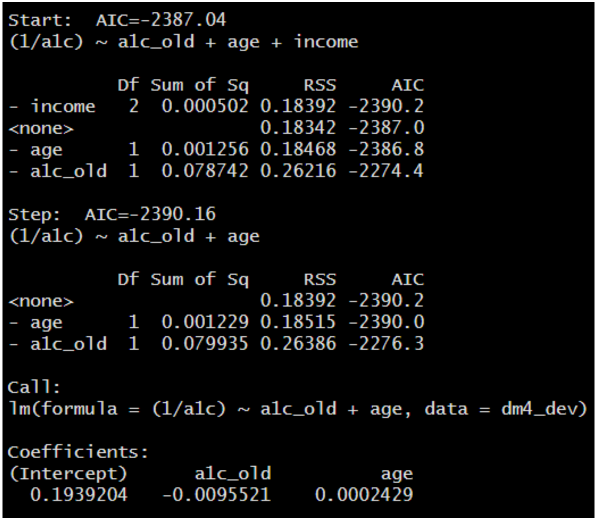
Could we have fit other predictor sets?

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?

Check adherence to regression assumptions in the development sample.

Checking Regression Assumptions

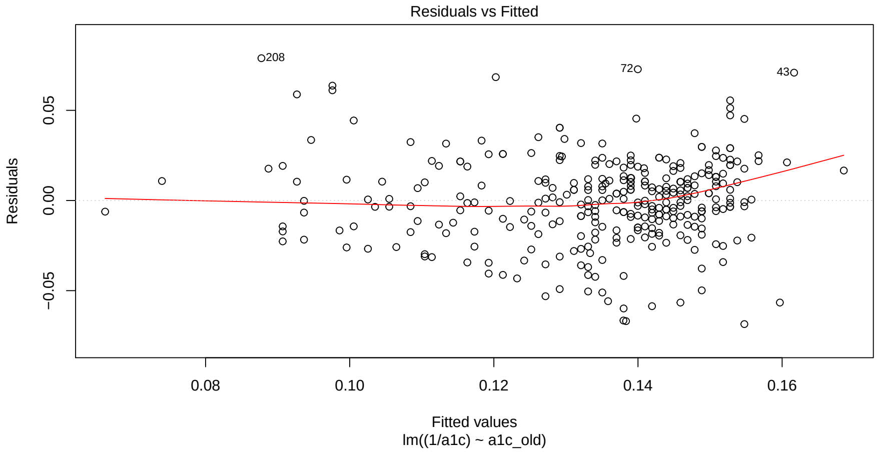
Four key assumptions we need to think about:

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

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

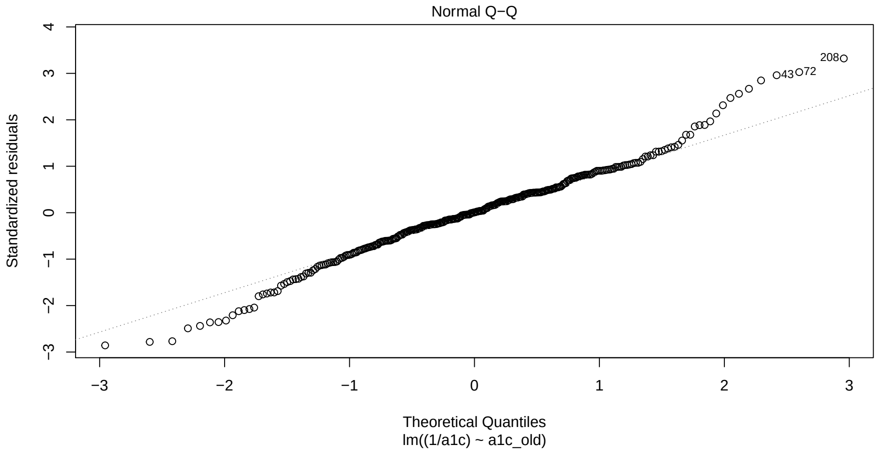
Residuals vs. Fitted Values Plot (Model `mod_1`)

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



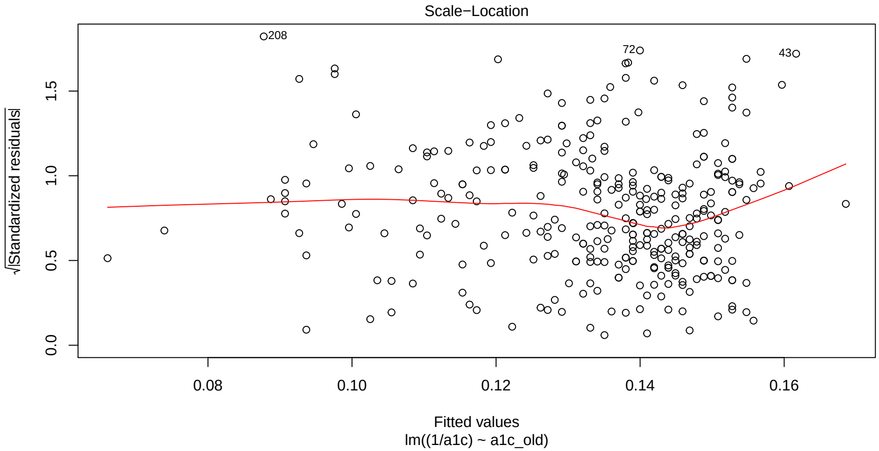
Normal Q-Q of Standardized Residuals (`mod_1`)

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



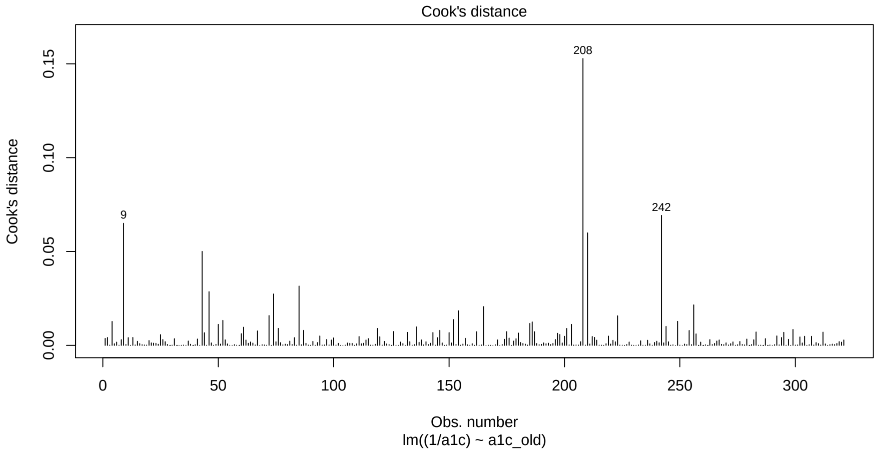
Scale-Location: Non-constant variance check (`mod_1`)

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



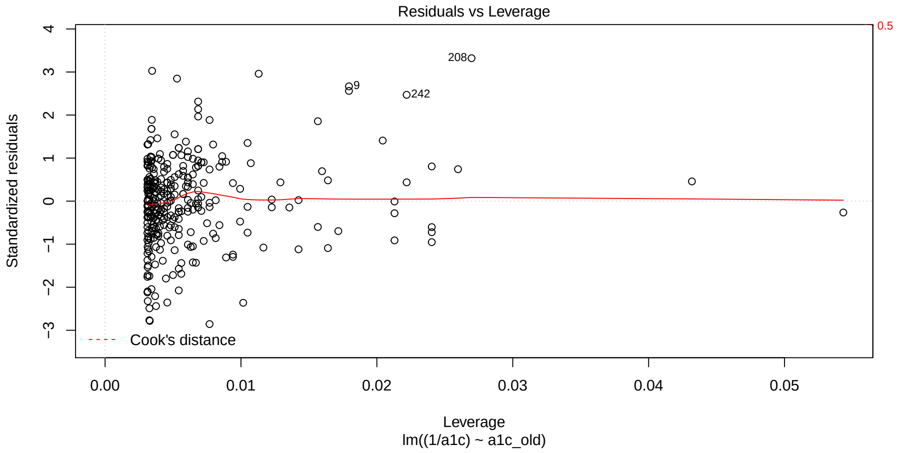
Index plot of Cook's distance for influence (`mod_1`)

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



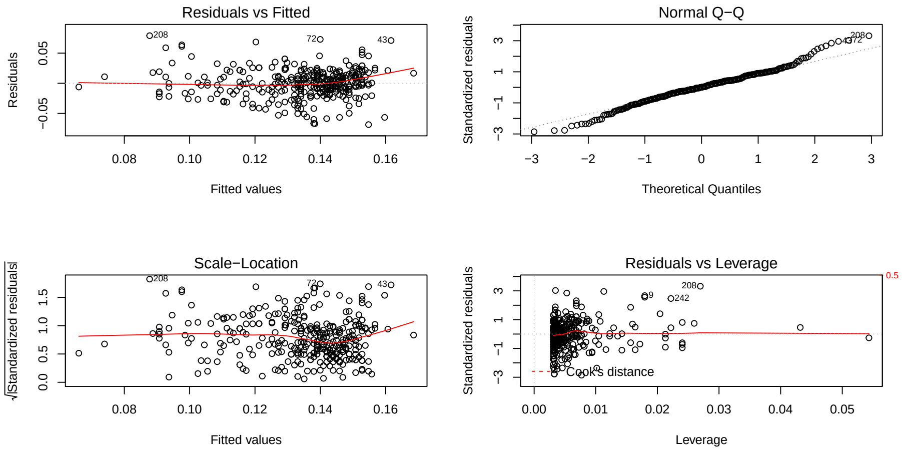
Residuals, Leverage and Influence plot (`mod_1`)

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

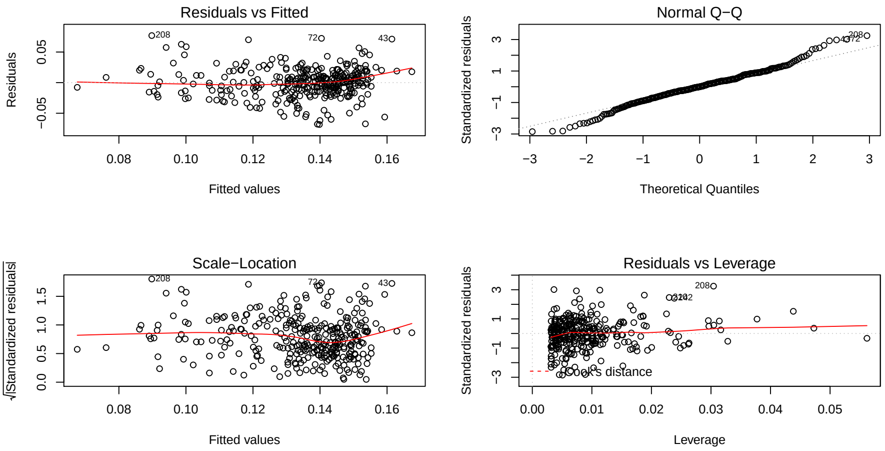


Residual Plots for Model `mod_1`

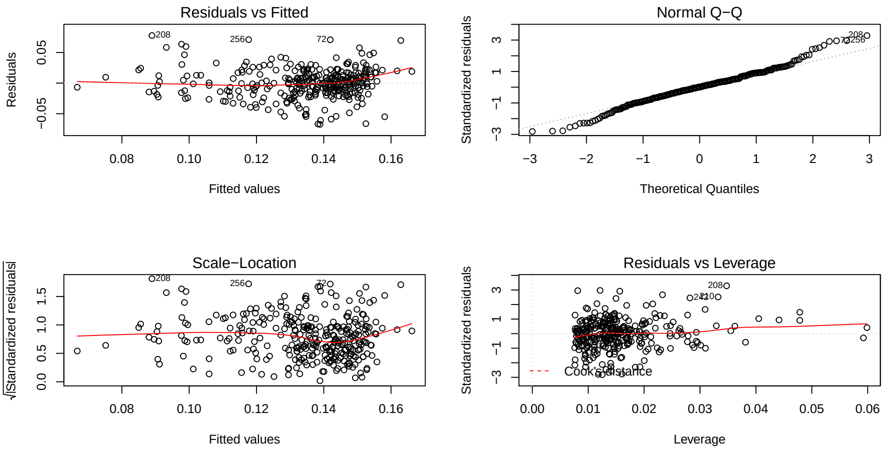
```r
par(mfrow = c(2,2)); plot(mod_1); par(mfrow = c(1,1))
```



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.

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...

```r
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

```r
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

```
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.

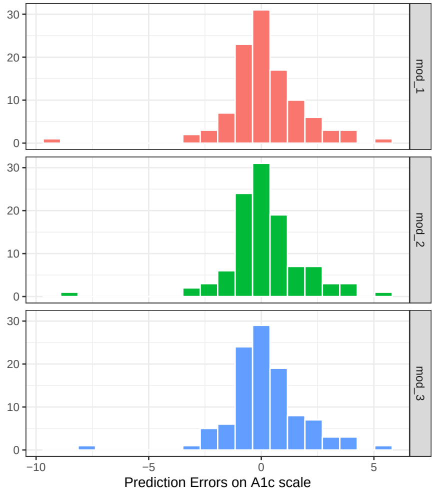
Visualize the prediction errors

```
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



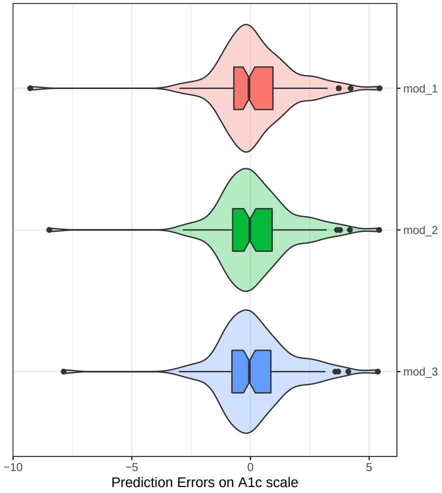


Table Comparing Model Prediction Errors

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.

```
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.

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

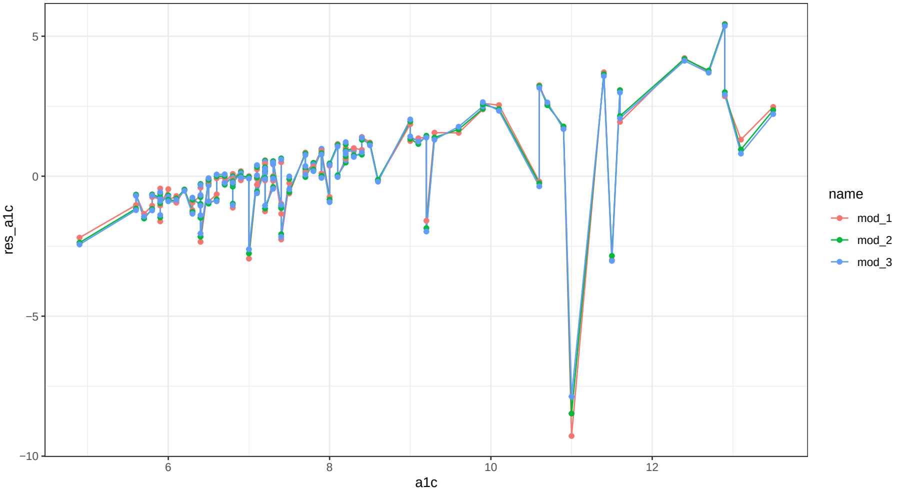
```
# A tibble: 3 x 4
  subject   a1c fit_a1c res_a1c
  <chr>   <dbl>   <dbl>   <dbl>
1 S-002      11    20.3   -9.28
2 S-002      11    19.5   -8.48
3 S-002      11    18.9   -7.87
```

Line Plot of the Errors?

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

```r
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:

```
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?

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`. The addition of the other two predictors doesn't add predictive value that is statistically detectable.
2. Residual plots look similarly reasonable for linearity, Normality and constant variance in all three models.
3. Excluding a bad miss on one subject in the test sample, all three models do about equally well, with perhaps `mod_3` very slightly better according to all three metrics (MAPE, MSPE and max_error) in the test sample.

So, what should our "most useful" model be?

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.