432 Class 5 Slides

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Today's Materials

- Ohio County Health Rankings Data
- Variable Selection via Best Subsets
  - Adjusted R^2
  - Mallows' C_p
  - AIC after Correction for Bias
  - BIC
- Cross-Validating to Compare Two Model-Building Approaches
- Assessing Residual Diagnostic Plots

Setup

```
library(skimr); library(broom); library(car)
library(modelr); library(leaps)
library(tidyverse)

oh_count <- read.csv("data/counties2017a.csv") %>% tbl_df
```

Ohio County Health Rankings Data
http://www.countyhealthrankings.org/rankings/data/oh

Codebook (2017 County Health Rankings), I

Variable	Description
fips	FIPS code for county (an ID)
state	Ohio in all cases
county	County Name (88 counties in Ohio)
years_lost	Years of potential life lost before age 75 per 100,000 population (age-adjusted, 2012-14)
population	County population, Census Population Estimates, 2015
female	% female (Census Population Estimates, 2015)
rural	3 categories from % rural (0-20: Urban, 20.1-50: Suburban, 50.1+: Rural; Census 2015)
non_white	4 categories from 100 - % white non-hispanic: (> 20: High, 10.1-20: Medium, 5.1-10: Low, <=5: Very Low, Census 2015)

Codebook (2017 County Health Rankings), II

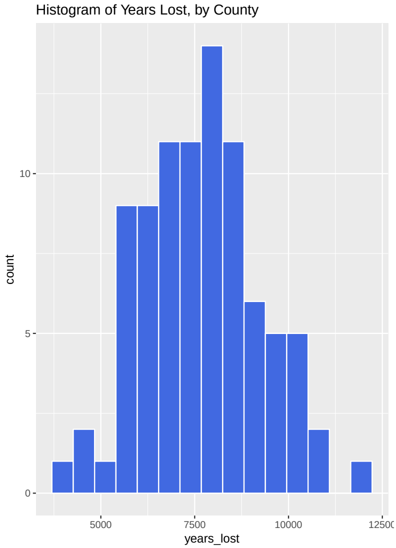
Variable	Description
sroh_fairpoor	% of adults reporting fair or poor health (age-adjusted via 2015 BRFSS)
smoker_pct	% of adults who currently smoke (2015 BRFSS)
food_envir	Food environment index (0 = worst, 10 = best) (via USDA Map the Meal 2014)
exer_access	% of population with adequate access to locations for physical activity (several sources)
income_ratio	Ratio of household income at the 80th percentile to income at the 20th percentile (ACS 2011-15)
air_pollution	Mean daily density of fine particulate matter in micrograms per cubic meter (PM2.5)
health_costs	Health Care Costs (from Dartmouth Atlas, 2014)

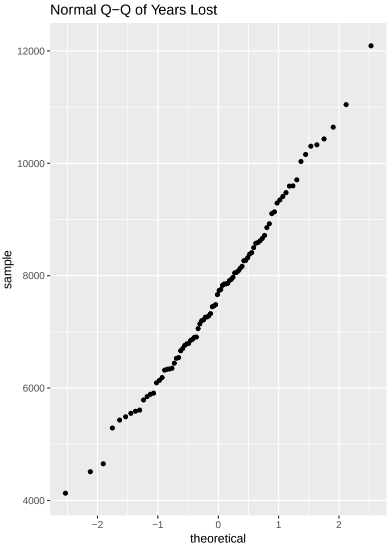
Basic Data Summaries

```r
oh_count %>% select(-fips, -state, -county) %>% skim()
```

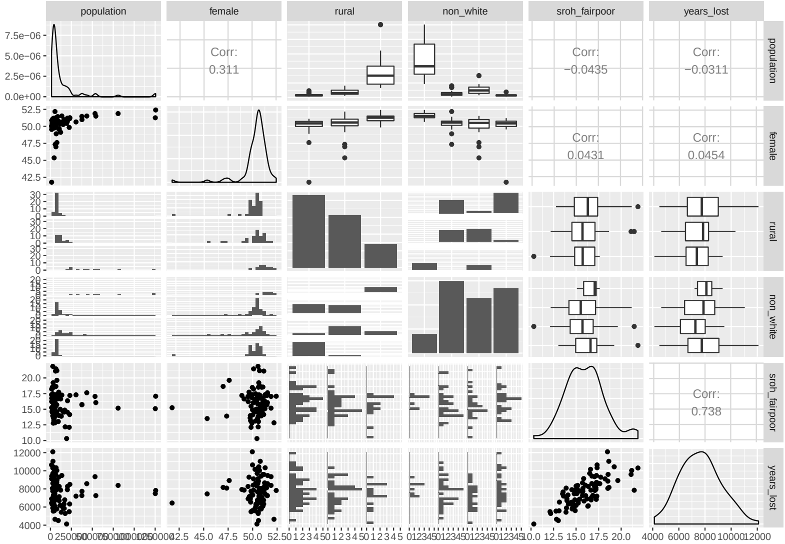
```
Skim summary statistics
 n obs: 189
 n variables: 9

Variable type: factor
 variable missing complete   n n_unique                     top_counts ordered
       ht       0      189 189        2          0: 177, 1: 12, NA: 0   FALSE
  preterm       0      189 189        2       no: 159, yes: 30, NA: 0   FALSE
   race_f       0      189 189        3 whi: 96, oth: 67, bla: 26, NA: 0   FALSE
    smoke       0      189 189        2          0: 115, 1: 74, NA: 0   FALSE
       ui       0      189 189        2          0: 161, 1: 28, NA: 0   FALSE

Variable type: integer
 variable missing complete   n    mean     sd  p0  p25 median  p75 p100     hist
      age       0      189 189   23.24    5.3  14   19     23   26   45
      bwt       0      189 189 2944.66 729.02 709 2414   2977 3475 4990
      ftv       0      189 189    0.79   1.06   0    0      0    1    6
      lwt       0      189 189  129.81  30.58  80  110    121  140  250
```

Our Outcome: Age-Adjusted Years Lost

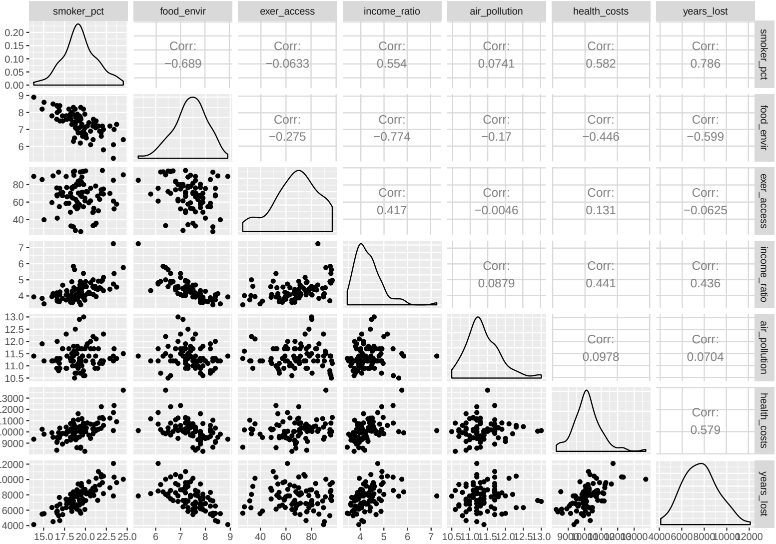




Scatterplot Matrix with `GGally`, Part I



Scatterplot Matrix with `GGally`, Part II



The "Kitchen Sink" Model?

Predict `years_lost` using 11 predictors.

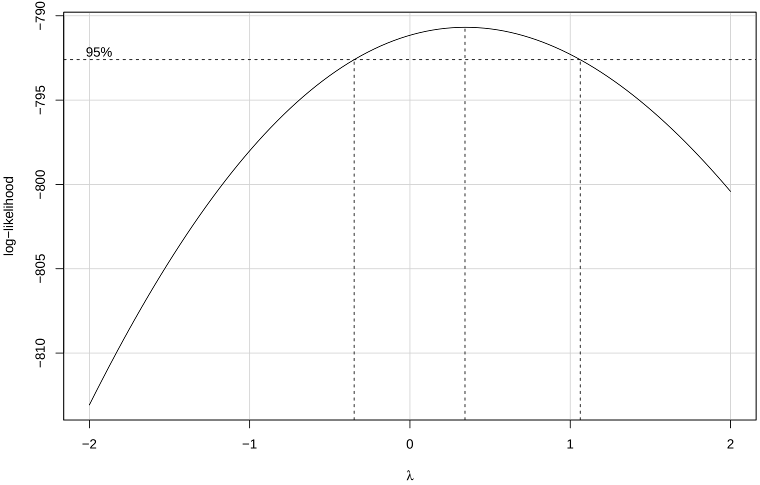
```
m_ks <- lm(years_lost ~ population + female + rural +
               non_white + sroh_fairpoor + smoker_pct +
               food_envir + exer_access + income_ratio +
               air_pollution + health_costs,
           data = oh_count)

glance(m_ks) %>% select(r.squared, adj.r.squared)
```

```
# A tibble: 1 x 2
  r.squared adj.r.squared
      <dbl>         <dbl>
1     0.689         0.630
```

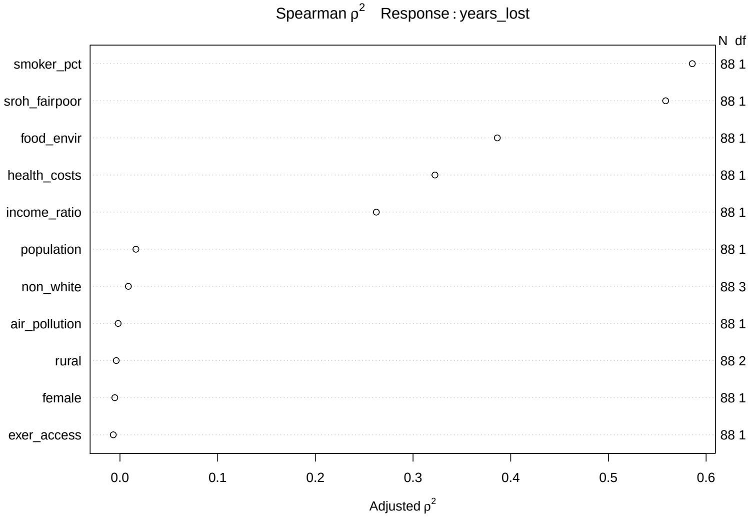
- 11 predictors with 88 observations?

Box-Cox plot: Outcome transformation?

```
boxCox(m_ks)
```



Spearman ρ^2 Plot (code in R Markdown)



Spearman ρ^2 Plot (code)

```
plot(Hmisc::spearman2(years_lost ~ population + female +
                          rural + non_white +
                          sroh_fairpoor + smoker_pct +
                          food_envir + exer_access +
                          income_ratio + air_pollution +
                          health_costs, data = oh_count))
```

Using “Best Subsets” to Select Variables

Using “Best Subsets” to Select Variables

We’ll consider models using some combination of the 11 available meaningful predictors.

```
bs_preds <- with(oh_count, cbind(population, female, rural,
                               non_white, sroh_fairpoor,
                               smoker_pct, food_envir,
                               exer_access, income_ratio,
                               air_pollution, health_costs))
```

We’ll look for models using up to 8 of those predictors.

```
bs_subs <- regsubsets(bs_preds,
                      y = oh_count$years_lost,
                      nvmax = 8)
bs_mods <- summary(bs_subs)
```

Looking at `bs_mods`

```r
bs_mods
```

```
> lbw_win
# A tibble: 8 x 16
      k    r2  adjr2    cp aic.c    bic `(Intercept)` lwt   age   race_fblack race_fother smoke1 ftv   ht1   ui1   pretermyes
  <int> <dbl>  <dbl> <dbl> <dbl>  <dbl> <lgl>         <lgl> <lgl> <lgl>       <lgl>       <lgl>  <lgl> <lgl> <lgl> <lgl>
1     2 0.101 0.0915 31.8   2475 - 4.43 T             T     F     F           F           F      F     F     T     F
2     3 0.148 0.134  22.7   2467 - 9.22 T             T     F     F           F           F      F     T     T     F
3     4 0.174 0.156  18.4   2463 - 9.94 T             T     F     T           F           F      F     T     T     F
4     5 0.204 0.183  13.1   2458 -11.8  T             T     F     T           T           T      F     F     T     F
5     6 0.240 0.215   6.56  2451 -15.2  T             T     F     T           T           T      F     T     T     F
6     7 0.250 0.221   6.15  2451 -12.5  T             T     F     T           T           T      F     T     T     T
7     8 0.251 0.218   8.04  2453 - 7.40 T             T     F     T           T           T      T     T     T     T
8     9 0.251 0.213  10.0   2455 - 2.20 T             T     T     T           T           T      T     T     T     T
```

Look at the models that "win"

```
bs_mods$which
```

```
> bs_mods$which
  (Intercept) population female rural non_white sroh_fairpoor smoker_pct food_envir exer_access income_ratio air_pollution health_costs
1        TRUE      FALSE  FALSE FALSE     FALSE         FALSE       TRUE      FALSE       FALSE        FALSE         FALSE        FALSE
2        TRUE      FALSE  FALSE FALSE     FALSE         FALSE       TRUE      FALSE       FALSE        FALSE         FALSE         TRUE
3        TRUE      FALSE  FALSE FALSE     FALSE          TRUE       TRUE      FALSE       FALSE        FALSE         FALSE         TRUE
4        TRUE      FALSE  FALSE FALSE     FALSE         FALSE       TRUE       TRUE       FALSE         TRUE         FALSE         TRUE
5        TRUE      FALSE   TRUE FALSE     FALSE         FALSE       TRUE       TRUE       FALSE         TRUE         FALSE         TRUE
6        TRUE      FALSE   TRUE FALSE     FALSE         FALSE       TRUE       TRUE        TRUE         TRUE         FALSE         TRUE
7        TRUE      FALSE   TRUE FALSE     FALSE          TRUE       TRUE       TRUE        TRUE         TRUE         FALSE         TRUE
8        TRUE      FALSE   TRUE FALSE      TRUE          TRUE       TRUE       TRUE        TRUE         TRUE         FALSE         TRUE
```

Sometimes easier to transpose this...

```r
t(bs_mods$which)
```

```
> t(bs_mods$which)
                   1     2     3     4     5     6     7     8
(Intercept)     TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
population     FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
female         FALSE FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE
rural          FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
non_white      FALSE FALSE FALSE FALSE FALSE FALSE FALSE  TRUE
sroh_fairpoor  FALSE FALSE  TRUE FALSE FALSE FALSE  TRUE  TRUE
smoker_pct      TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
food_envir     FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE
exer_access    FALSE FALSE FALSE FALSE FALSE  TRUE  TRUE  TRUE
income_ratio   FALSE FALSE FALSE  TRUE  TRUE  TRUE  TRUE  TRUE
air_pollution  FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
health_costs   FALSE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
```

Look at the R-square values for each "winning" model

```
bs_mods$rsq
```

```
[1] 0.6172471 0.6397030 0.6460605 0.6530869 0.6649312
[6] 0.6730306 0.6783975 0.6802613
```

```
bs_mods$adjr2
```

```
[1] 0.6127964 0.6312255 0.6334198 0.6363682 0.6445001
[6] 0.6488107 0.6502573 0.6478827
```

Place winning results in bs_winners

```
bs_winners <- tbl_df(bs_mods$which)
bs_winners$k <- 2:9 ## in general, this is 2:(nvmax + 1)
bs_winners$r2 <- bs_mods$rsq
bs_winners$adjr2 <- bs_mods$adjr2
bs_winners$cp <- bs_mods$cp
bs_winners$bic <- bs_mods$bic
```

Calculate Bias-Corrected AIC from Residual Sum of Squares

This requires specifying the sample size (`temp.n`) and the number of inputs that you'll look at in your largest subset (here, we limited the number of variables to 8 with `nvmax` and so that's 9 inputs, including the intercept term.)

```
temp.n <- nrow(oh_count)
temp.inputs <- 9 ## nvmax + 1

bs_mods$aic.corr <- temp.n*log(bs_mods$rss / temp.n) +
    2*(2:temp.inputs) +
    (2 * (2:temp.inputs) * ((2:temp.inputs)+1) /
         (temp.n - (2:temp.inputs) - 1))

bs_winners$aic.corr <- bs_mods$aic.corr
```

Detailed Breakdown: `bs_winners`

Inputs	Predictors	Raw r^2	Adj. r^2	C_p	BIC	AIC_c
2	`smoker_pct`	.617	.613	8.0	-75.6	1213.0
3	+ `health_costs`	.640	.631	4.6	**-76.4**	**1209.9**
4	+ `sroh_fairpoor`	.646	.633	5.1	-73.5	1210.5
5	(*see below*)	.653	.636	**5.4**	-70.8	1211.0
6	+ `female`	.665	.645	4.5	-69.4	1210.2
7	+ `exer_access`	.673	.649	4.6	-67.0	1210.4
8	+ `sroh_fairpoor`	.678	**.650**	5.3	-64.0	1211.4
9	+ `non_white`	.680	.648	6.9	-60.0	1213.4

- The "best" model with 5 inputs includes `smoker_pct`, `health_costs`, `food_envir` and `income_ratio`.
- That model forms the basis for the "best" models with 6-9 inputs.

Resulting `bs_winners` tibble

```
head(bs_winners, 2)
```

```
# A tibble: 2 x 18
  `(Intercept)` population female rural non_white
  <lgl>         <lgl>      <lgl>  <lgl> <lgl>
1 TRUE          FALSE      FALSE  FALSE FALSE
2 TRUE          FALSE      FALSE  FALSE FALSE
# ... with 13 more variables: sroh_fairpoor <lgl>,
#   smoker_pct <lgl>, food_envir <lgl>, exer_access <lgl>,
#   income_ratio <lgl>, air_pollution <lgl>,
#   health_costs <lgl>, k <int>, r2 <dbl>, adjr2 <dbl>,
#   cp <dbl>, bic <dbl>, aic.corr <dbl>
```

If You're Curious: A Stepwise Fit

```
step(lm(years_lost ~ population + female + rural +
            non_white + sroh_fairpoor + smoker_pct +
            food_envir + exer_access + income_ratio +
            air_pollution + health_costs, data = oh_count))
```

using backwards elimination produces the model containing:

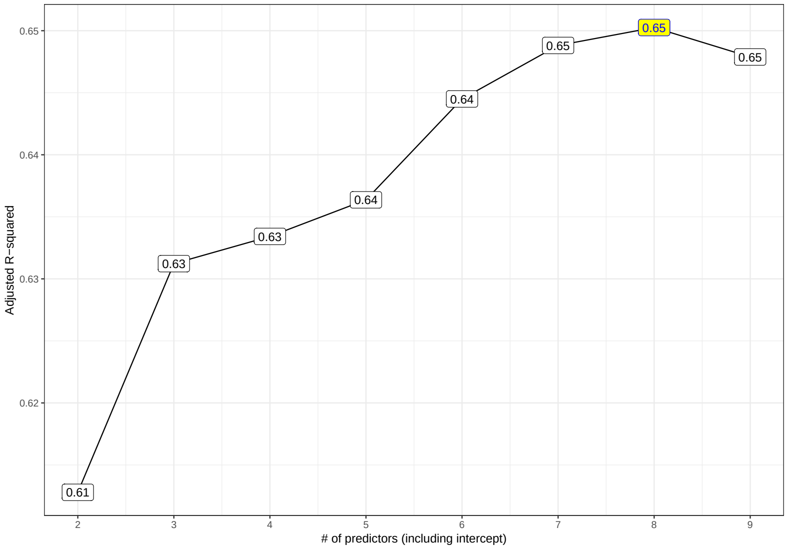
- `smoker_pct`, `health_costs`, `food_envir`, `income_ratio`, `female`, and `exer_access`
- also known as what "best subsets" chose for its model 7.

Building the "Best Subsets" Plots

Adjusted R-square plot using ggplot2

```
p1 <- ggplot(bs_winners, aes(x = k, y = adjr2,
                        label = round(adjr2,2))) +
    geom_line() +
    geom_label() +
    geom_label(data = subset(bs_winners,
                          adjr2 == max(adjr2)),
               aes(x = k, y = adjr2, label = round(adjr2,2)),
               fill = "yellow", col = "blue") +
    theme_bw() +
    scale_x_continuous(breaks = 2:9) +
    labs(x = "# of predictors (including intercept)",
         y = "Adjusted R-squared")
```

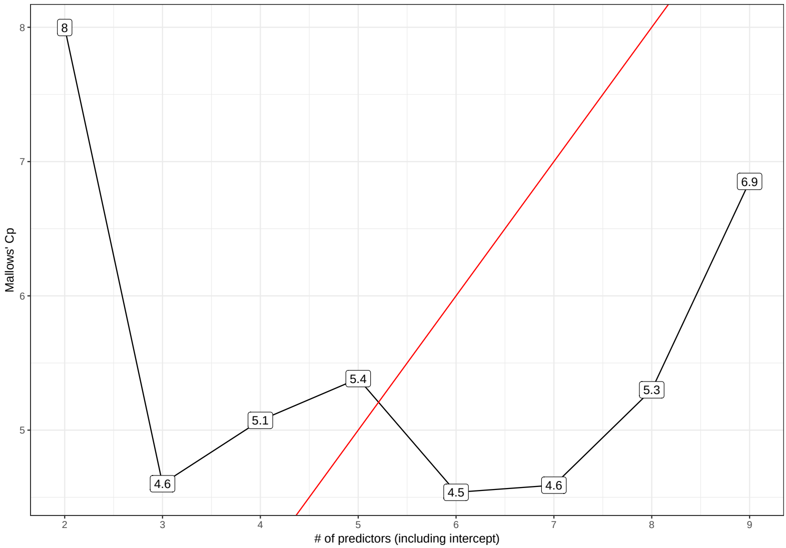
Adjusted R-square plot using `ggplot2`



Mallows' C_p plot using ggplot2

```
p2 <- ggplot(bs_winners, aes(x = k, y = cp,
                             label = round(cp,1))) +
    geom_line() +
    geom_label() +
    geom_abline(intercept = 0, slope = 1,
                col = "red") +
    theme_bw() +
    scale_x_continuous(breaks = 2:9) +
    labs(x = "# of predictors (including intercept)",
         y = "Mallows' Cp")
```

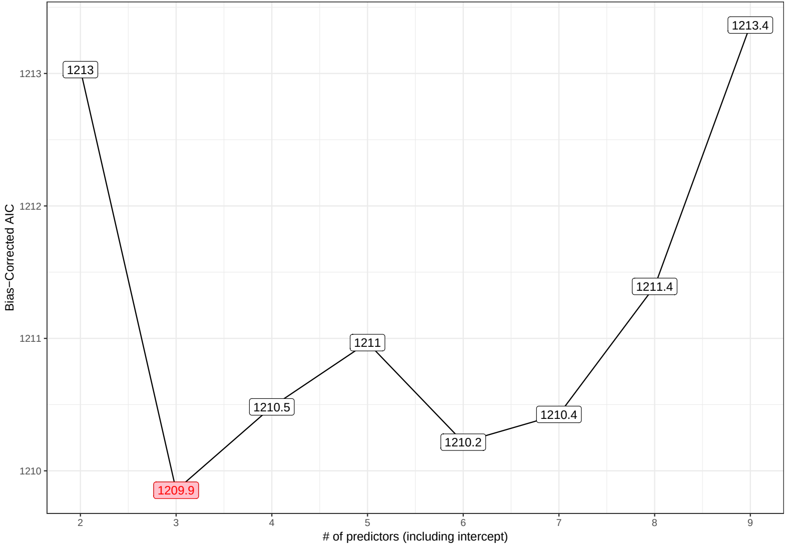
Mallows' C_p plot using ggplot2



Corrected AIC plot using ggplot2

```
p3 <- ggplot(bs_winners, aes(x = k, y = aic.corr,
                             label = round(aic.corr,1))) +
    geom_line() +
    geom_label() +
    geom_label(data = subset(bs_winners,
                             aic.corr == min(aic.corr)),
               aes(x = k, y = aic.corr),
               fill = "pink", col = "red") +
    theme_bw() +
    scale_x_continuous(breaks = 2:9) +
    labs(x = "# of predictors (including intercept)",
         y = "Bias-Corrected AIC")
```

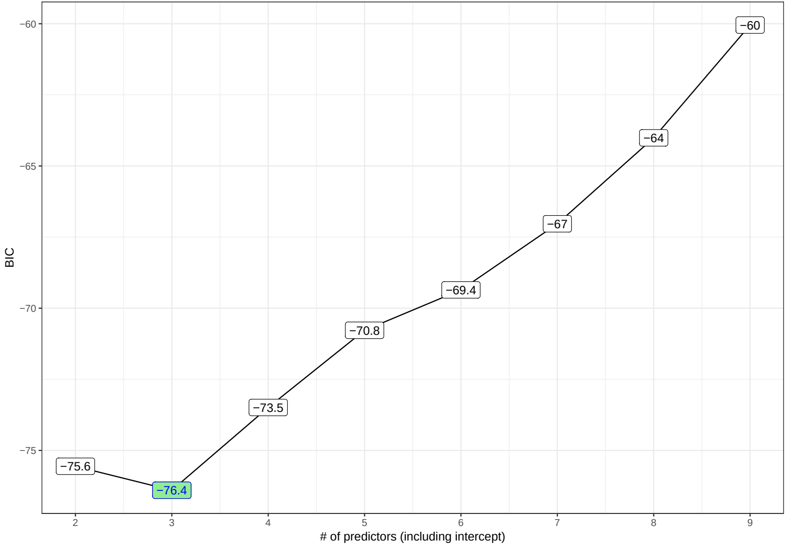
Corrected AIC plot using ggplot2



BIC plot using ggplot2

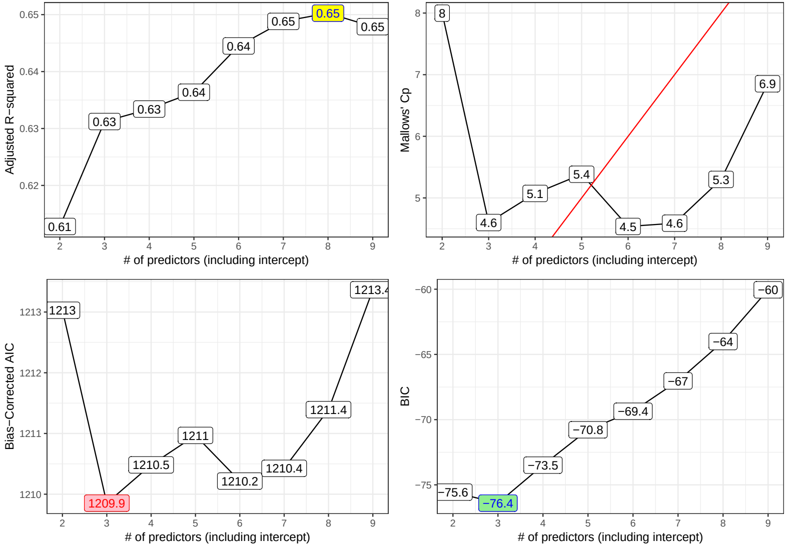
```
p4 <- ggplot(bs_winners, aes(x = k, y = bic,
                             label = round(bic,1))) +
    geom_line() +
    geom_label() +
    geom_label(data = subset(bs_winners, bic == min(bic)),
               aes(x = k, y = bic),
               fill = "lightgreen", col = "blue") +
    theme_bw() +
    scale_x_continuous(breaks = 2:9) +
    labs(x = "# of predictors (including intercept)",
         y = "BIC")
```

BIC plot using `ggplot2`



All Four Plots Together

```
gridExtra::grid.arrange(p1, p2, p3, p4, nrow = 2)
```



Candidate Models include

Inputs	Raw r^2	Adj. r^2	C_p	BIC	AIC_c
3	.640	.631	4.6	**-76.4**	**1209.9**
5	.653	.636	**5.4**	-70.8	1211.0
8	.678	**.650**	5.3	-64.0	1211.4

- 3: `smoker_pct` + `health_costs`
- 5: Model 3 + `food_envir` + `income_ratio`
- 8: Model 5 + `female` + `exer_access` + `sroh_fairpoor`

Comparing our Candidate Models in our Training Sample

In-Sample Comparisons of our Candidate Models

```
m3 <- lm(years_lost ~ smoker_pct + health_costs,
         data = oh_count)
m5 <- lm(years_lost ~ smoker_pct + health_costs +
             food_envir + income_ratio, data=oh_count)
m8 <- lm(years_lost ~ smoker_pct + health_costs +
              food_envir + income_ratio + female +
             exer_access + sroh_fairpoor, data=oh_count)
```

Models are **nested** so comparisons within samples are straightforward.

Comparisons in-sample with anova

```
anova(m3, m5, m8)
```

```
Analysis of Variance Table

Model 1: years_lost ~ smoker_pct + health_costs
Model 2: years_lost ~ smoker_pct + health_costs + food_envir +
Model 3: years_lost ~ smoker_pct + health_costs + food_envir +
    female + exer_access + sroh_fairpoor
  Res.Df      RSS Df Sum of Sq      F Pr(>F)
1     85 76610187
2     83 73764357  2   2845831 1.6647 0.1957
3     80 68382551  3   5381806 2.0987 0.1069
```

Comparisons in-sample with AIC

```
a <- AIC(m3, m5, m8)
b <- BIC(m3, m5, m8); b$model <- row.names(b)
left_join(a, b)
```

```
Joining, by = "df"
```

```
  df      AIC      BIC model
1  4 1461.301 1471.210    m3
2  6 1461.970 1476.834    m5
3  9 1461.303 1483.599    m8
```

What if the models you're comparing aren't nested?

What if you're comparing:

- Model A: `lm(y = x1 + x2 + x3, data = dataset)`
- Model B: `lm(y = x1 + x4 + x5, data = dataset)`

Then ...

- default *p* values from the ANOVA table comparing Model A to Model B aren't reasonable
- AIC and BIC are OK, can also used adjusted R^2 to help make a decision within the model building sample
- Still useful to think about out-of-sample prediction and cross-validation

Comparing out-of-sample predictive ability of our Candidate Models with cross-validation

10-fold Cross-Validation for Model 3

```
set.seed(432012)

cv_3 <- oh_count %>%
  crossv_kfold(k = 10) %>%
  mutate(model = map(train, ~ lm(years_lost ~
                     smoker_pct + health_costs, data = .)))

cv3_pred <- cv_3 %>%
  unnest(map2(model, test, ~ augment(.x, newdata = .y)))

cv3_res <- cv3_pred %>%
  summarize(Model = "3",
            RMSE = sqrt(mean((years_lost - .fitted) ^2)),
            MAE = mean(abs(years_lost - .fitted)))
```

10-fold Cross-Validation for Model 5

```
set.seed(432013)

cv_5 <- oh_count %>%
  crossv_kfold(k = 10) %>%
  mutate(model = map(train, ~ lm(years_lost ~
                        smoker_pct + health_costs +
                        food_envir + income_ratio, data = .)))

cv5_pred <- cv_5 %>%
  unnest(map2(model, test, ~ augment(.x, newdata = .y)))

cv5_res <- cv5_pred %>%
  summarize(Model = "5",
            RMSE = sqrt(mean((years_lost - .fitted) ^2)),
            MAE = mean(abs(years_lost - .fitted)))
```

10-fold Cross-Validation for Model 8

```
set.seed(432014)

cv_8 <- oh_count %>%
  crossv_kfold(k = 10) %>%
  mutate(model = map(train, ~ lm(years_lost ~
                          smoker_pct + health_costs +
                          food_envir + income_ratio +
                          female + exer_access +
                          sroh_fairpoor, data = .)))

cv8_pred <- cv_8 %>%
  unnest(map2(model, test, ~ augment(.x, newdata = .y)))

cv8_res <- cv8_pred %>%
  summarize(Model = "8",
            RMSE = sqrt(mean((years_lost - .fitted) ^2)),
            MAE = mean(abs(years_lost - .fitted)))
```

Cross-Validation Results

```
bind_rows(cv3_res, cv5_res, cv8_res)
```

```
# A tibble: 3 x 3
  Model  RMSE   MAE
  <chr> <dbl> <dbl>
1 3      975.  785.
2 5      976.  797.
3 8     1004.  809.
```

Fitting the Chosen Model

Fitting the Chosen Model

```r
m3 <- lm(years_lost ~ smoker_pct + health_costs,
         data = oh_count)

arm::display(m3)
```

```
lm(formula = years_lost ~ smoker_pct + health_costs, data = oh
             coef.est coef.se
(Intercept)  -5749.51  1248.81
smoker_pct     517.62    61.10
health_costs     0.34     0.15
---
n = 88, k = 3
residual sd = 949.37, R-Squared = 0.64
```

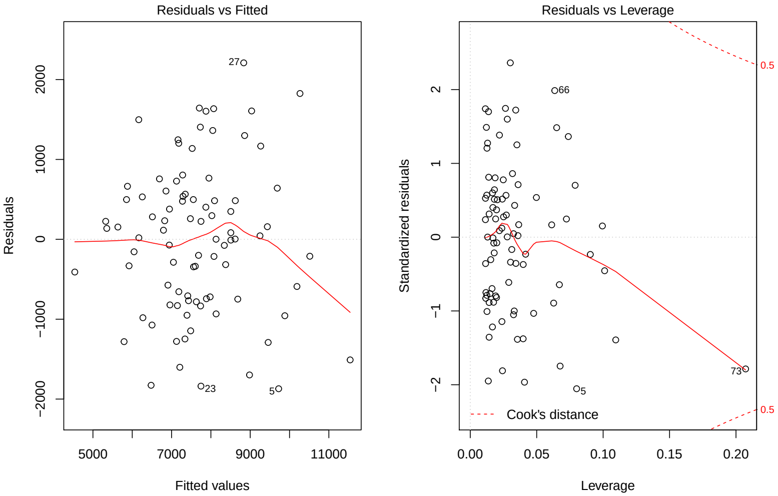
Fitting the Chosen Model

```r
glance(m3) %>% print.data.frame
```

```
  r.squared adj.r.squared    sigma statistic      p.value
1  0.639703     0.6312255 949.3663  75.45825 1.439049e-19
  df    logLik      AIC     BIC deviance df.residual
1  3 -726.6504 1461.301 1471.21 76610187          85
```

Residual Plots for the Chosen Model

```r
par(mfrow = c(1,2)); plot(m3, which = c(1, 5))
```



Coming Up

- Another Example: Low Birth Weight
- More on Cross-Validation of Linear Regression Models
- Limitations of Best Subsets
- More on the Spearman ρ^2 Plot
  - Spending Degrees of Freedom on Non-Linearity
- Building Non-Linear Predictors with
  - Polynomial Functions
  - Product Terms
  - Splines, specifically Restricted Cubic Splines
- Building a Nomogram for a Linear Regression

not to mention . . .

- Logistic Regression