432 Class 5 Slides

github.com/THOMASELOVE/432-2018

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Setup

```r
library(skimr)
library(broom)
library(modelr)
library(leaps)
library(tidyverse)

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

Today's Materials

- Review of Minute Papers after Class 04
- Discussion of Homework 1
- 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

Homework 1

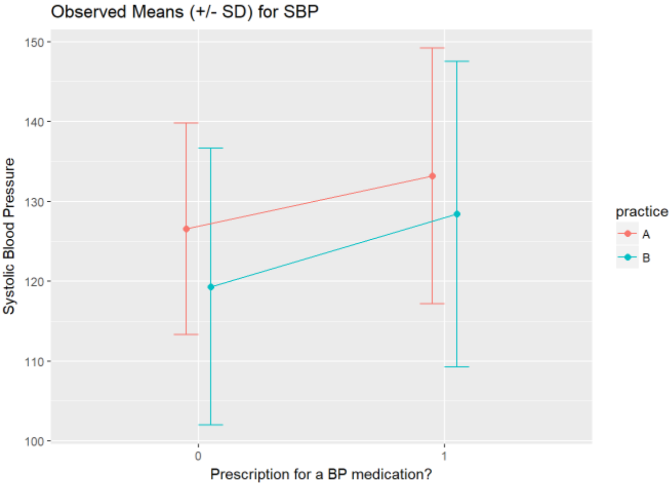
Table 1

	Stratified by practice			
	A	B	p	test
n	180	150		
age (mean (sd))	56.34 (11.17)	54.17 (11.89)	0.088	
race (%)			<0.001	
Asian/PI	0 (0.0)	10 (6.7)		
Black/AA	166 (92.7)	14 (9.4)		
Multi-Racial	4 (2.2)	3 (2.0)		
White	9 (5.0)	122 (81.9)		
eth_hisp = Yes (%)	2 (1.1)	62 (41.6)	<0.001	
sex = M (%)	61 (33.9)	66 (44.0)	0.077	
insurance (%)			0.016	
Commercial	35 (19.4)	18 (12.0)		
Medicaid	66 (36.7)	68 (45.3)		
Medicare	76 (42.2)	54 (36.0)		
Uninsured	3 (1.7)	10 (6.7)		
bmi (mean (sd))	35.20 (8.20)	34.39 (7.83)	0.365	
bmi_cat (%)			0.587	
Underweight	1 (0.6)	1 (0.7)		
Normal	11 (6.1)	14 (9.3)		
Overweight	32 (17.8)	31 (20.7)		
Obese	136 (75.6)	104 (69.3)		
sbp (mean (sd))	130.82 (15.38)	125.44 (19.00)	0.005	
dbp (mean (sd))	74.49 (11.40)	75.05 (8.58)	0.617	

Notes for Table 1:

1. There are 4 subjects missing Hispanic ethnicity status in practice A, and 1 in practice B.
2. There is 1 subject in each practice missing Race.
3. Results are shown in terms of means and standard deviations for quantitative variables, and t tests are used for comparisons, because a Normal approximation was a reasonable choice for each such variable.
4. For categorical variables, we display counts and percentages, and use Pearson chi-square tests of significance.

Question 2



I don't see much to suggest a meaningful interaction here. The lines joining the points are essentially parallel. It looks like the group with the lowest (healthiest) mean SBP are the subjects in practice B without a medication.

Question 2 ANOVA (no interaction)

```
Call:
lm(formula = sbp ~ practice + bpmed, data = hbp330)

Residuals:
    Min      1Q  Median      3Q     Max
-41.844 -11.961  -0.702   9.369  63.039

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  125.844      1.768  71.164  < 2e-16 ***
practiceB     -5.600      1.852  -3.023   0.0027 **
bpmed          7.716      1.944   3.970 8.85e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 16.75 on 327 degrees of freedom
Multiple R-squared:  0.06889,	Adjusted R-squared:  0.06319
F-statistic:  12.1 on 2 and 327 DF,  p-value: 8.548e-06
```

Since each of the two factors is binary, we can simply read off that both `practice` and `bpmed` appear to have a significant impact on SBP, with practice B having lower SBP levels, on average, and subjects without BP medications having lower SBP levels, on average.

Question 3 (ANOVA test to compare models)

```
anova(hw1_q3, hw1_q2_no_int)
```

```
Analysis of Variance Table

Model 1: sbp ~ practice + bpmed + age
Model 2: sbp ~ practice + bpmed
  Res.Df   RSS Df Sum of Sq      F  Pr(>F)
1    326 90178
2    327 91712 -1   -1534.3 5.5467 0.01911 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

It does appear that `age` adds significant predictive value to the no-interaction model.

Question 3 (Fit Summaries)

```
glance(hw1_q3)
```

```
  r.squared adj.r.squared    sigma statistic      p.value df    logLik
1 0.08446494    0.07603977 16.63185  10.02531 2.452493e-06  4 -1393.973
       AIC      BIC deviance df.residual
1 2797.946 2816.941  90177.6         326
```

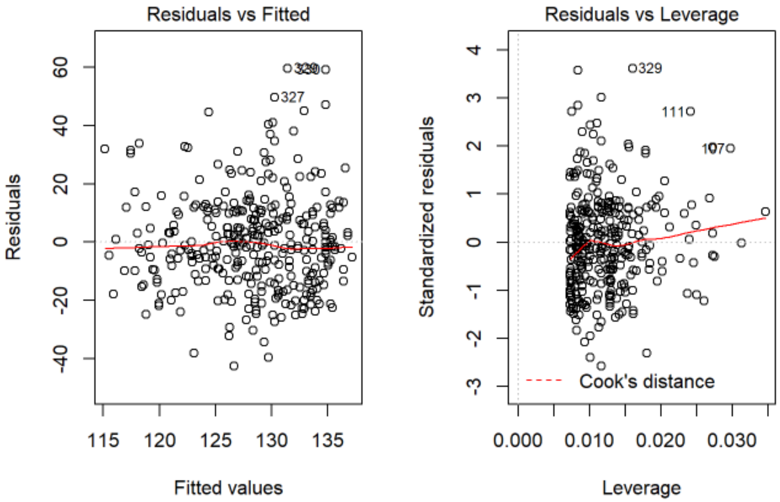
Hide

```
glance(hw1_q2_no_int)
```

```
  r.squared adj.r.squared    sigma statistic      p.value df    logLik
1 0.06888764    0.06319276 16.74708  12.09642 8.547555e-06  3 -1396.757
       AIC     BIC deviance df.residual
1 2801.513 2816.71 91711.92         327
```

The model with `age` included performs a bit better in terms of adjusted (and raw) R^2 and AIC and performs comparably in terms of BIC.

Question 3 (Residual plots)



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)

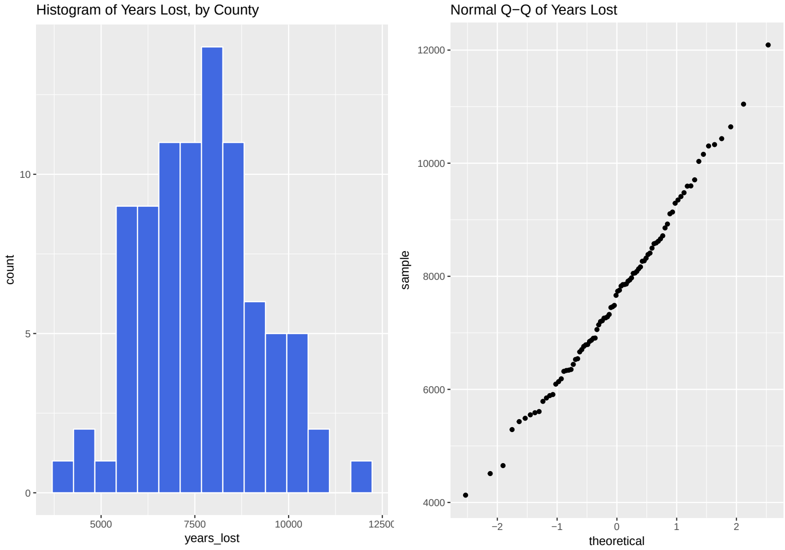
Basic Data Summaries

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

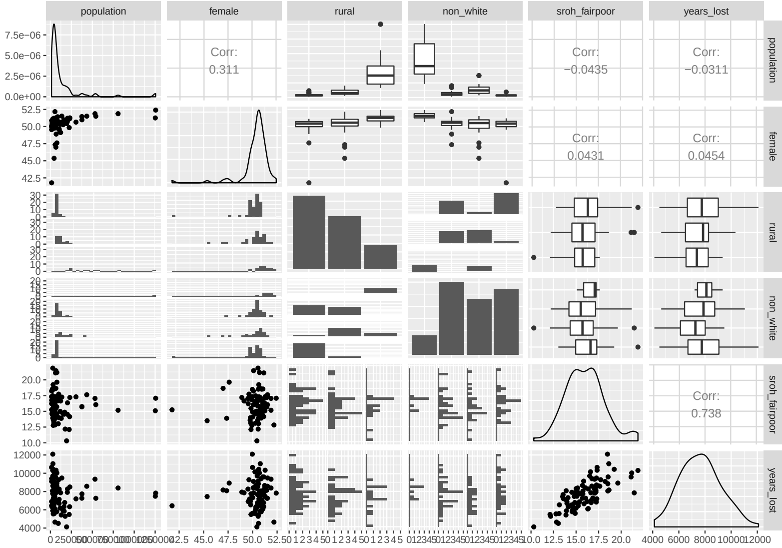
```
Skim summary statistics
 n obs: 88
 n variables: 12

Variable type: factor
  variable missing complete  n n_unique                        top_counts ordered
 non_white       0       88 88        4 Low: 30, Ver: 27, Med: 23, Hig: 8   FALSE
    rural2       0       88 88        3  Rur: 43, Sub: 31, Urb: 14, NA: 0   FALSE

Variable type: integer
   variable missing complete  n      mean        sd    p0      p25  median       p75    p100     hist
 population       0       88 88 131970.72 216261.12 13048 36982.25 57733.5 123712.75 1255921
 years_lost       0       88 88   7659.12   1563.34  4129  6538.75  7700      8597.5    12091
```

```
Variable type: numeric
       variable missing complete  n     mean     sd      p0     p25   median      p75     p100     hist
  air_pollution       0       88 88    11.38   0.47    10.5    11.1     11.3     11.7       13
    exer_access       0       88 88    68.19  17.43    26.2   58.18    69.73    80.09    96.23
         female       0       88 88    50.34   1.38   41.78   50.05    50.58    50.96    52.41
     food_envir       0       88 88      7.4   0.67     5.3       7     7.45      7.8      8.9
   health_costs       0       88 88 10158.06 859.43 8274.48  9650.2 10093.36 10577.49 13702.91
   income_ratio       0       88 88     4.33    0.6    3.45    3.94     4.21     4.57     7.24
     smoker_pct       0       88 88    19.33   2.05   13.82   18.23    19.28    20.61    24.53
   sroh_fairpoor      0       88 88    15.99   2.14   10.31   14.58    15.86    17.21    21.86
```

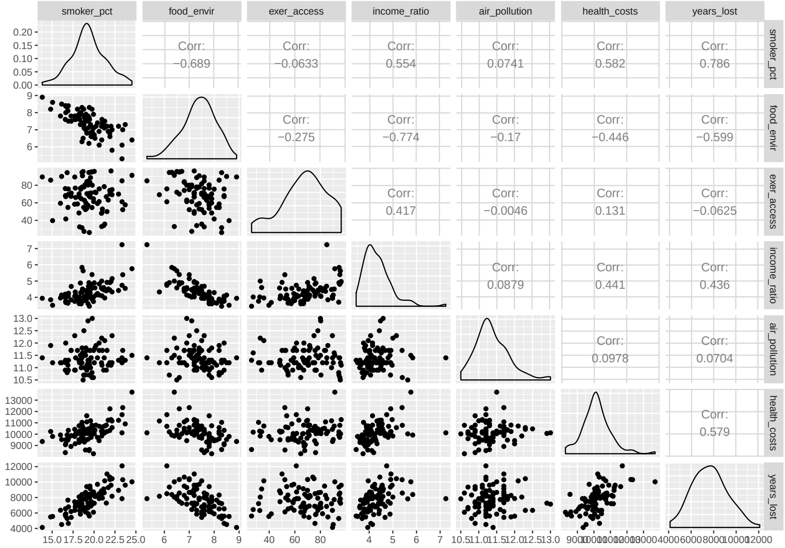
Our Outcome: Age-Adjusted Years Lost



Scatterplot Matrix with `GGally`, Part I



Scatterplot Matrix with `GGally`, Part II



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

```
bs_mods
```

```
> bs_mods
Subset selection object
11 Variables  (and intercept)
              Forced in Forced out
sroh_fairpoor     FALSE      FALSE
smoker_pct        FALSE      FALSE
exer_access       FALSE      FALSE
food_env          FALSE      FALSE
income_ratio      FALSE      FALSE
food_insecure     FALSE      FALSE
health_costs      FALSE      FALSE
population        FALSE      FALSE
female            FALSE      FALSE
rural2            FALSE      FALSE
race_mix          FALSE      FALSE
1 subsets of each size up to 8
Selection Algorithm: exhaustive
         sroh_fairpoor smoker_pct exer_access food_env income_ratio food_insecure health_costs population female rural2 race_mix
1  ( 1 ) " "           " "        "*"         " "      " "          " "           " "          " "        " "    " "    " "
2  ( 1 ) " "           " "        "*"         " "      " "          " "           " "          " "        " "    " "    "*"
3  ( 1 ) " "           " "        "*"         " "      " "          " "           " "          "*"        " "    " "    "*"
4  ( 1 ) " "           " "        "*"         " "      " "          "*"           " "          "*"        " "    " "    "*"
5  ( 1 ) "*"           " "        "*"         " "      " "          "*"           " "          "*"        " "    " "    "*"
6  ( 1 ) "*"           " "        "*"         " "      " "          "*"           " "          "*"        " "    "*"    "*"
7  ( 1 ) "*"           " "        "*"         " "      " "          "*"           "*"          "*"        " "    "*"    "*"
8  ( 1 ) "*"           " "        "*"         " "      " "          "*"           "*"          "*"        "*"    "*"    "*"
```

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...

```
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

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

```
# A tibble: 2 x 18
  `(Intercept)` population female rural non_white
  <lgl>         <lgl>      <lgl>  <lgl> <lgl>
1 T             F          F      F     F
2 T             F          F      F     F
# ... 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:

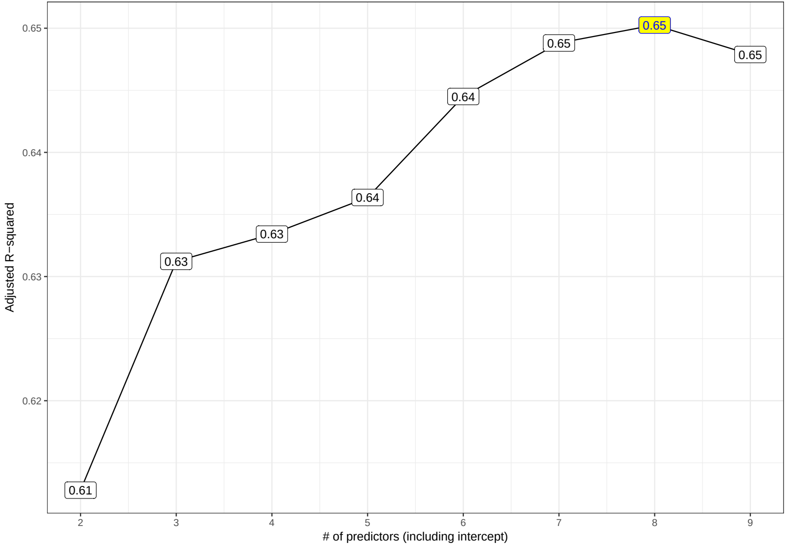
- `smoker_pct`, `health_costs`, `food_envir`, `income_ratio`, `female`, and `exer_access`
- also known as what "best subsets" chose for its model 7.

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")
```

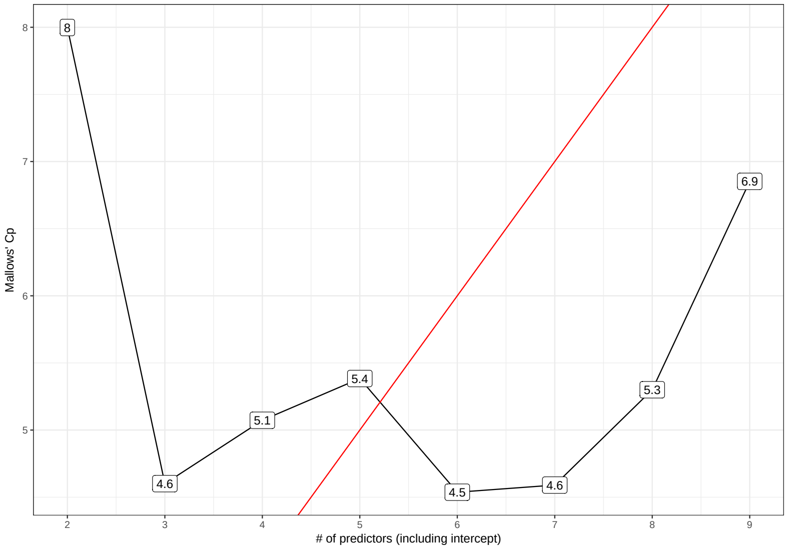
Adjusted R-square plot using `ggplot2`



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")
```

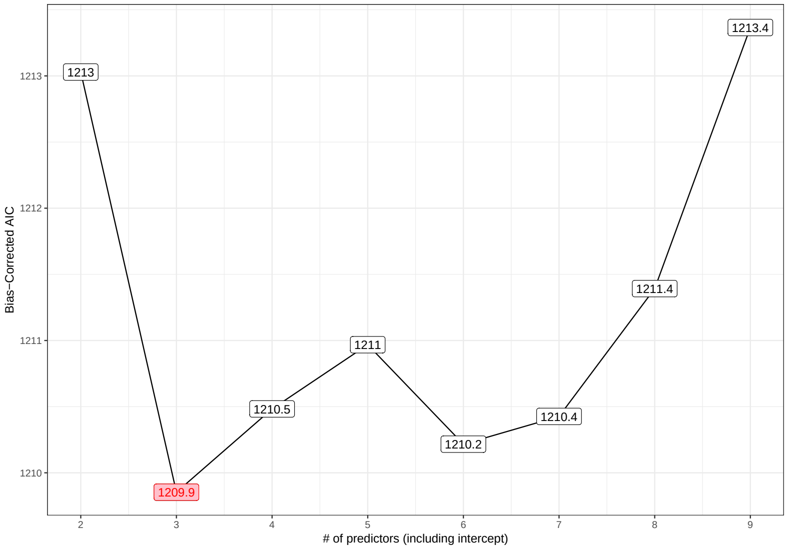
Mallows' C_p plot using `ggplot2`



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")
```

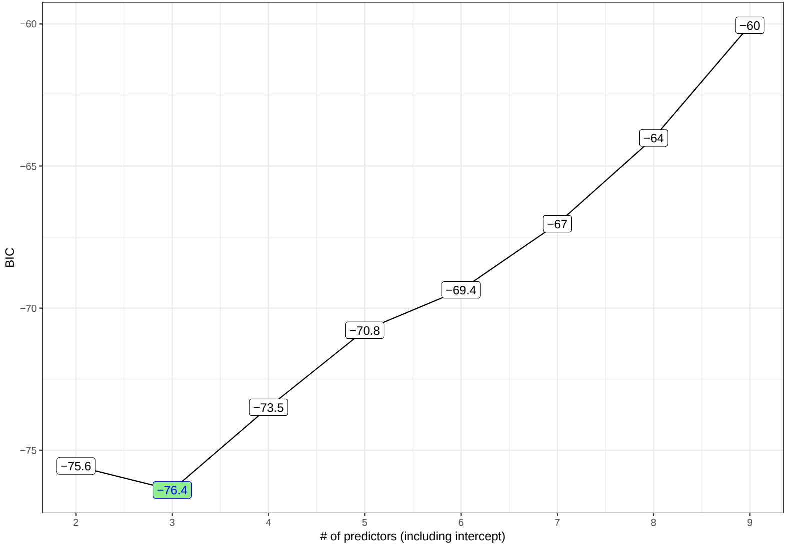
Corrected AIC plot using `ggplot2`



BIC plot using ggplot2

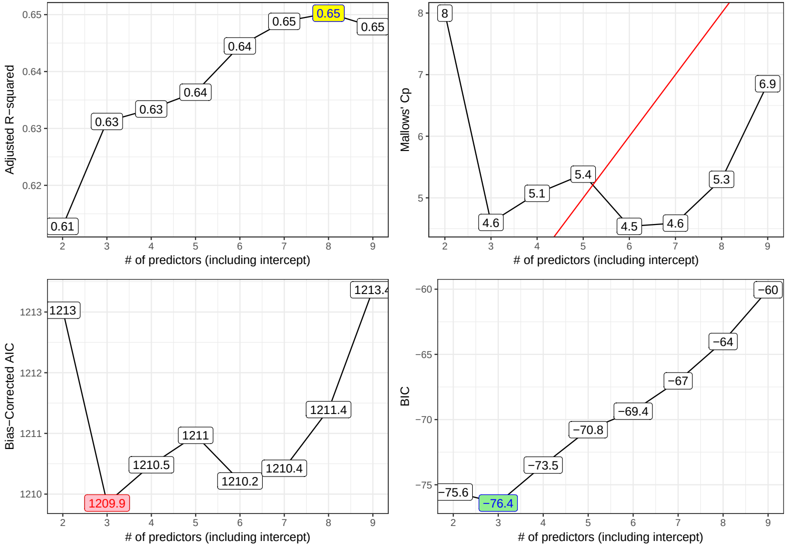
```
p4 <- ggplot(bs_winners, aes(x = k, y = bic,
                             label = round(bic,1))) +
    geom_line() +
    geom_label() +
    geom_label(data = subset(bs_winners, bic == min(bic)),
               aes(x = k, y = bic),
               fill = "lightgreen", col = "blue") +
    theme_bw()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

BIC plot using `ggplot2`

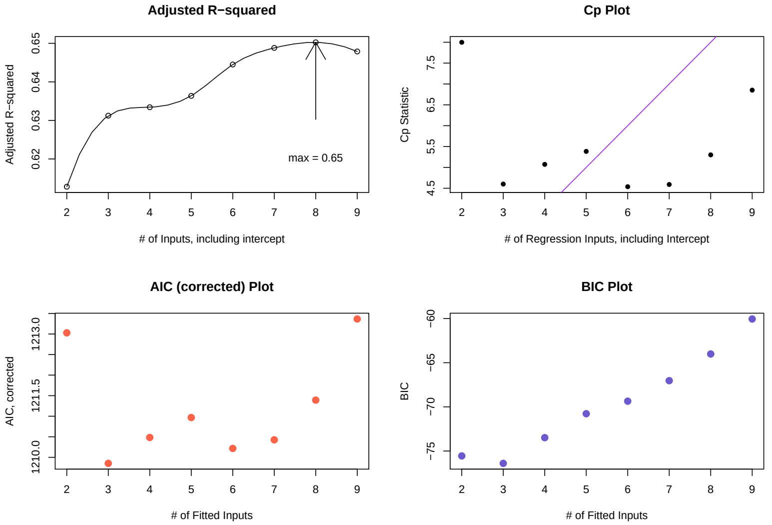


All Four Plots Together

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



The Four Plots (using Base R plotting)



Cross-Validation to Choose Between Options

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

```r
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

```r
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
```

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

10-fold Cross-Validation for Model 3

```r
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
```

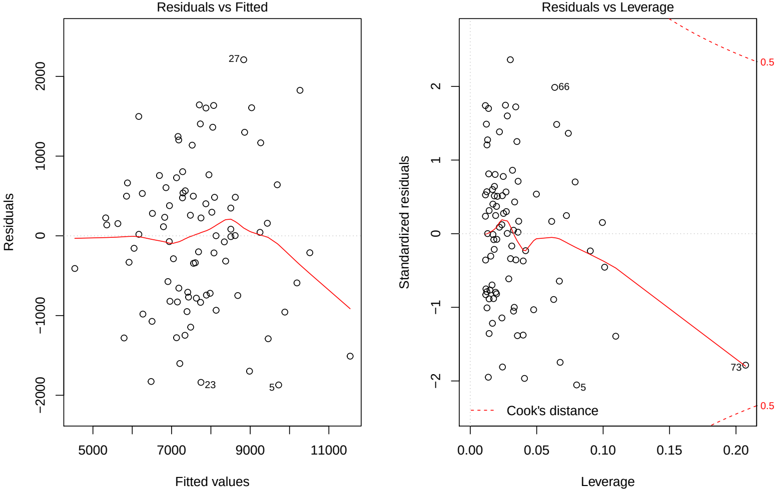
Fitting the Chosen Model

```r
glance(m3)
```

```
  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

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



Next Time

- Best Subsets (more)
- Stepwise Regression and the Allen-Cady Procedure
- (soon) Making Decisions about Non-Linearity in Y or the Xs