# Homework 8 Key

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#### 10.1

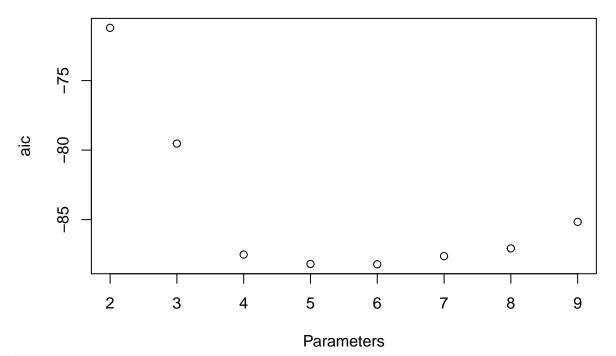
## lweight

(a) The best model from the backward selection approach is the model including the predictors lcavol, lweight, and, svi.

```
library(faraway)
data(prostate, package = 'faraway')
lmod <- lm(lpsa ~., data = prostate)</pre>
sumary(lmod)
##
                Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.6693367 1.2963875 0.5163
                                           0.606934
## lcavol
               ## lweight
                         0.1700124 2.6731
               0.4544674
                                           0.008955
              -0.0196372
                         0.0111727 -1.7576
## age
                                           0.082293
## lbph
               0.1070540 0.0584492 1.8316
                                           0.070398
## svi
              0.7661573 0.2443091 3.1360
                                           0.002329
## lcp
              -0.1054743 0.0910135 -1.1589
                                           0.249638
## gleason
               0.0451416
                        0.1574645 0.2867
                                           0.775033
               0.0045252 0.0044212 1.0235 0.308860
## pgg45
##
## n = 97, p = 9, Residual SE = 0.70842, R-Squared = 0.65
lmod <- update(lmod, .~. -gleason)</pre>
sumary(lmod)
##
                Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.9539260 0.8294393 1.1501 0.253190
## lcavol
               ## lweight
               0.4482924
                         0.1677706 2.6721
                                           0.008965
              -0.0193365
                        0.0110659 -1.7474
## age
                                           0.084018
## lbph
               0.1076711
                         0.0581076 1.8530
                                           0.067202
## svi
               0.7577335
                         0.2412818 3.1405
                                           0.002290
## lcp
              -0.1044823
                         0.0904775 -1.1548
                                           0.251269
               0.0053177 0.0034326 1.5492 0.124884
## pgg45
##
## n = 97, p = 8, Residual SE = 0.70475, R-Squared = 0.65
lmod <- update(lmod, .~. -lcp)</pre>
sumary(lmod)
                Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.9800848 0.8306648 1.1799 0.241157
## lcavol
               0.5457697  0.0764313  7.1407  2.312e-10
```

0.4494499 0.1680782 2.6741 0.008900

```
## age
            -0.0174699 0.0109674 -1.5929 0.114692
            0.1057551 0.0581914 1.8174 0.072489
## lbph
             0.6416661 0.2197567 2.9199 0.004424
## svi
## pgg45
             0.0035276 0.0030683 1.1497 0.253309
## n = 97, p = 7, Residual SE = 0.70606, R-Squared = 0.65
lmod <- update(lmod, .~. -age)</pre>
sumary(lmod)
##
             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.0664614 0.6059095 0.1097 0.912898
## lcavol
            ## lweight
            ## lbph
            ## svi
            0.6537607 0.2214728 2.9519 0.004017
## pgg45
            0.0025285 0.0030288 0.8348 0.405992
## n = 97, p = 6, Residual SE = 0.71200, R-Squared = 0.64
lmod <- update(lmod, .~. -pgg45)</pre>
sumary(lmod)
            Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.145541 0.597473 0.2436 0.808088
## lcavol
            ## lweight
            ## lbph
## svi
            ##
## n = 97, p = 5, Residual SE = 0.71082, R-Squared = 0.64
lmod <- update(lmod, .~. -lbph)</pre>
sumary(lmod)
##
             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.268093   0.543500 -0.4933   0.622984
## lcavol
             0.551638
                      0.074668 7.3879 6.304e-11
## lweight
             0.508541
                      0.150170 3.3864 0.001039
             0.666158
                      0.209777 3.1756 0.002029
## svi
##
## n = 97, p = 4, Residual SE = 0.71681, R-Squared = 0.63
(b) According to the AIC criterion, the best model has the predictors lcavol, lweight, age, lbph, and
    svi.
library(leaps)
rc <- regsubsets(lpsa ~ ., data = prostate)</pre>
rcs <- summary(rc)</pre>
aic <- rcs$bic - 2:9*log(nobs(lmod)) + 2:9*2
plot(aic ~ I(2:9), xlab = 'Parameters')
```



## rcs\$which[which.min(aic),]

##	(Intercept) TRUE	lcavol	lweight	age	lbph	svi
##		TRUE	TRUE	TRUE	TRUE	TRUE
##	lcp FALSE	gleason FALSE	pgg45 FALSE			

(c) According to the adjusted r-squared criterion, the best model includes all predictors except gleason.

## rcs\$which[which.max(rcs\$adjr2),]

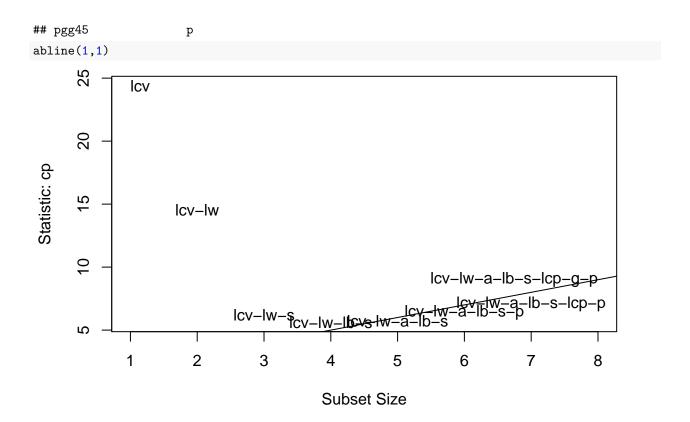
```
## (Intercept)
                      lcavol
                                  lweight
                                                    age
                                                                lbph
                                                                              svi
##
           TRUE
                        TRUE
                                     TRUE
                                                   TRUE
                                                                TRUE
                                                                             TRUE
##
            lcp
                     gleason
                                    pgg45
##
           TRUE
                       FALSE
                                     TRUE
```

(d) According to Mallow's  $C_p$  criterion, the best model has the predictors lcavol, lweight, age, lbph, and svi.

```
car::subsets(rc, statistic = 'cp', legend = F)
```

```
## Registered S3 methods overwritten by 'car':
## method from
## influence.merMod lme4
## cooks.distance.influence.merMod lme4
## dfbeta.influence.merMod lme4
## dfbetas.influence.merMod lme4
```

##		Abbreviation
##	lcavol	lcv
##	lweight	lw
##	age	a
##	lbph	1b
##	svi	s
##	lcp	lcp
##	${\tt gleason}$	g



#### 10.4

Comparing the second-order model to the first-order model (using the F-test, AIC, BIC, and adjusted  $R^2$  criteria), the second-order model is preferred. We shouldn't simplify the model.

```
data(trees)
lmod1 = lm(log(Volume) ~ Girth + Height, data = trees)
lmod2 = lm(log(Volume) ~ Girth + Height + I(Girth^2) + I(Height^2) + Girth:Height, data = trees)
anova(lmod1, lmod2)
## Analysis of Variance Table
##
## Model 1: log(Volume) ~ Girth + Height
## Model 2: log(Volume) ~ Girth + Height + I(Girth^2) + I(Height^2) + Girth:Height
               RSS Df Sum of Sq
                                     F Pr(>F)
## 1
         28 0.26214
         25 0.17932 3 0.082817 3.8486 0.02156 *
## 2
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
comp = data.frame(AIC = c(AIC(lmod1),AIC(lmod2)), BIC = c(BIC(lmod1),BIC(lmod2)),
                 AR2 = c(summary(lmod1)$adj, summary(lmod2)$adj))
row.names(comp) = c('Linear','Quadratic')
knitr::kable(comp)
```

	AIC	BIC	AR2
Linear	-51.98466	-46.24871	0.9661964
Quadratic	-57.75516	-47.71725	0.9741010