STAT5120, Allen Baumgarten, Building the Regression Model, Pt. I

1. In each case below, indicate whether a more flexible model (like a high-degree polynomial) would tend to perform better or worse on a test set than a more inflexible one (like a low-degree polynomial). Explain your reasoning.

(a) The number of observations n is large and the number of predictor variables is small. A flexible, higher-order polynomial model (HOPM) would perform better. One reason is that in having a smaller number of predictors we could try some higher-order terms without taxing our computing resources (if you happen to own IBM's Watson supercomputer, this would be a non-issue). Flexible models are advantageous in that they allow us to explore other possibilities for fitting the data. With smaller numbers of predictors, we can do this.

(b) There is a very large number of predictor variables, but a small number of observations n. In this case, we might opt for an Inflexible, low-degree model (ILDM) since having a larger number of predictors, and then multiplying them by adding many high-order terms, would be cumbersome at best. Better to select, or at least start with, a simpler modeling scenario.

(c) The apparent dependence of the response on the predictor variables is highly non-linear. This is (even for me) a "No-brainer:" if we detect a curvilinear trend in the response vs. predictors, we would need a HOPM with its higher-order terms to fine-tune and fit the curved response in the data better than a ILDM would.

(d) The variance of the error terms is very high. If the variance of the errors is very high, perhaps even higher than the odds of the Dolphins NOT making the Play Offs, then we would likely need a HOPM to fit this data. Polynomials could fit to the response better and reduce variance in the error terms.[1]

2. Answer the following.
(a) True or false, and explain. If a regression model has high bias, it is unlikely that collecting more data to train/build the model will increase its performance on a validation or test set (with respect to, say, SSE; MSE, or R2). TRUE. Bias happens when a model is "under-specified" due to the omission of important predictor variables. When a model lacks one or more important predictor variables, and n is already large enough, adding more observations will probably not do much more than reduce the standard errors of the terms.

Commenting on bias due to variable selection, Rawlings et al state, "Assume that the correct model involves *t* independent variables but that a subset of *p* variables (chosen randomly or on the basis of external information) is used in the regression equation. Let X_p and β_p denote submatrices of X and β that relate to the *p* selected variables. $\hat{\beta}_p$ denotes the least squares estimate of β_p obtained from the p-variate subset model. Similarly, $\hat{Y}_{pi}$, $\hat{Y}pred_{pi}$, and MS(Res_p) denote the estimated mean for the *i*th observation, the prediction for the *i*th observation, and the means squared residual, respectively, obtained from the p-variate subset model. Hocking (1976) summarizes the following properties: 1. MS(Res_p) is a *positively* biased estimate of σ^2 unless the true regression coefficients for all deleted variables are zero. 2. $\hat{\beta}_p$ is a biased estimate of β_p and $\hat{Y}_{pi}$ is a biased estimate of $\varepsilon(Y_i)$ unless the true regression coefficient for each deleted variable is zero or, in the case of $\hat{\beta}_p$, each deleted variable is orthogonal to the *p* retained variables. 3. $\hat{\beta}_p$, $\hat{Y}_{pi}$, and $\hat{Y}pred_{pi}$ are generally *less* variable than the

[1] This wouldn't help the Dolphins' post-season prospects but that's another discussion for another day.

corresponding statistics obtained from the t-variate model. 4. There are conditions under which the mean squared errors (variance plus squared bias) of $\hat{\beta}_p$, $\hat{Y}_{pi}$, and $\hat{Y}pred_{pi}$ are smaller than the variances of the estimates obtained under the t-variate model."[2]

(b) What do you think will happen to the variance of an over-fitted regression model as the size of the training set increases? Variance will be very high. This is because with an over-fitted model, the already-existing data points are highly anticipated by the model coefficients. However, when new data points which do NOT have the same values as the originals are entered into the model, the model "misses" these new points and variance occurs in the (new) errors that result.

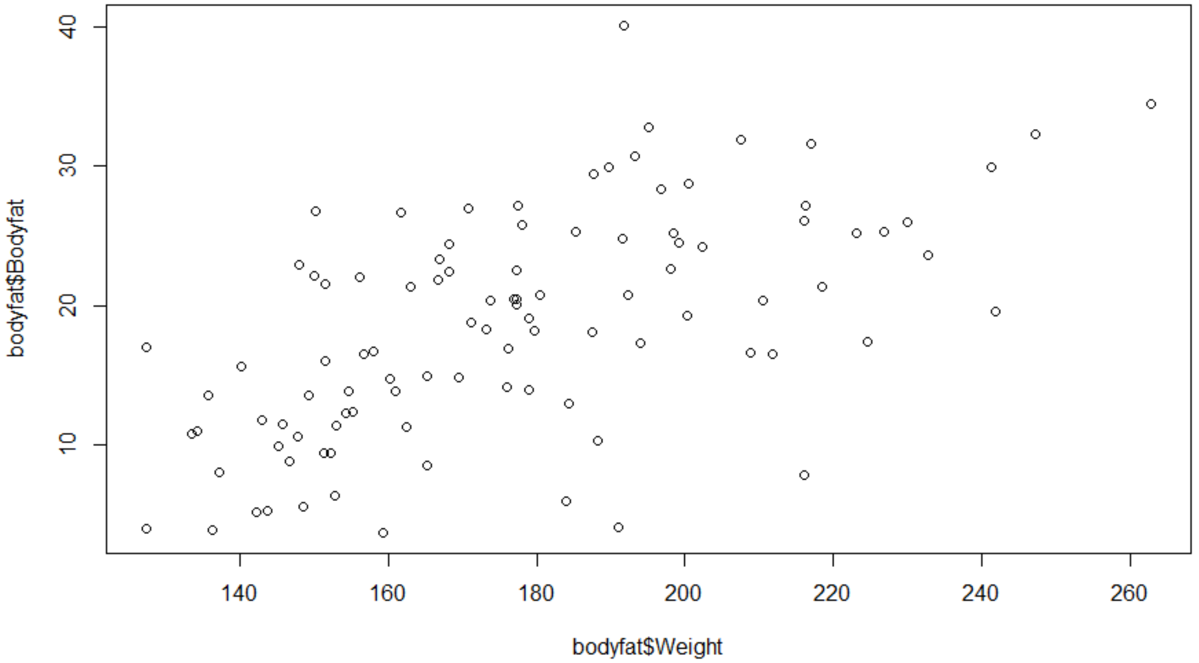
(c) Suppose you build polynomial regressions in one variable (y^ = 0 + p⍰1k=1 kxk), and you want to choose the polynomial degree by evaluating the performance of your models (using say, MSE) on a validation or test set. Once you choose the final model, would you expect the test MSE to be higher or lower than the training MSE? Why? The MSE measures the mean squared errors of the fitted response vs. the actual responses. When we train and then test a model, we used a majority of our data, say, 75% of the observations to train the model, that is, estimate our coefficients, and then use the remaining 25% to test how those estimates work. If we have estimated well and iterated some ideas for the best model fit, we would expect our MSE to be lower than the training on the training set. If MSE was higher we would simple stick with that fitted result rather than pick a final model with a higher MSE.

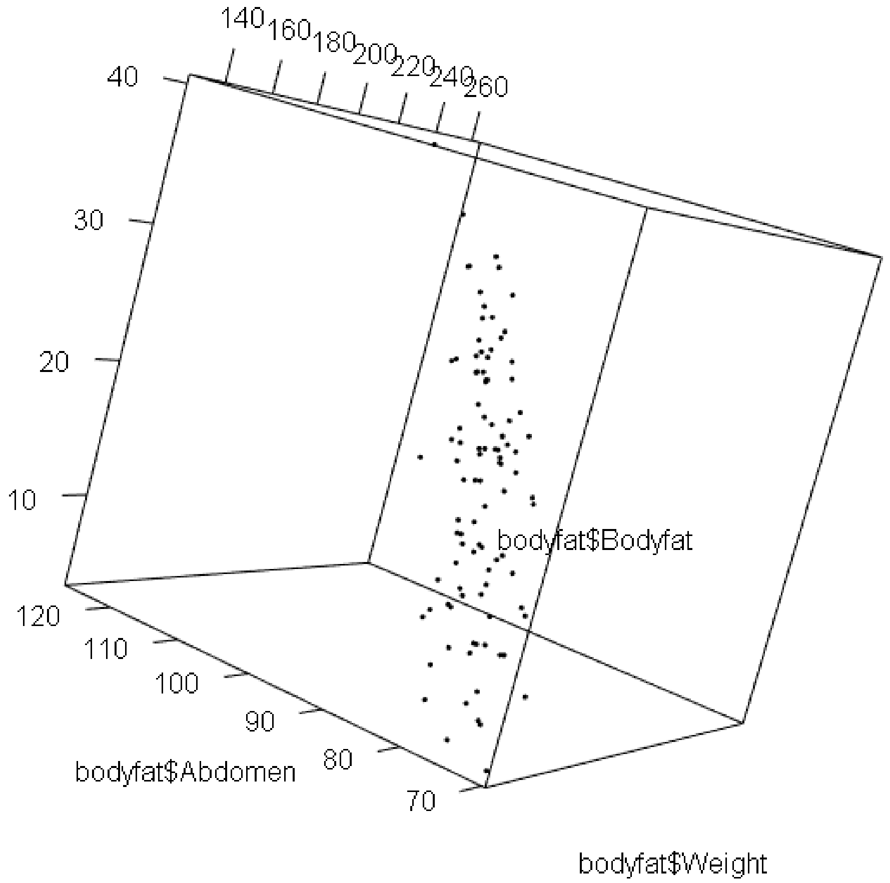
(d) Suppose when you add flexibility to your model by adding higher order terms or more predictor variables that you begin to see the test or validation error (MSE or SSE evaluated on the test or validation set) begin to increase away from the training error. What kind of a problem are your models experiencing? One possibility would be that we have a collinearity problem developing.

3. Simpson's Paradox.[3] Open the *Bodyfat* data in R and refer to the R examples at the beginning of this set of notes. Plot Bodyfat vs Weight. The plot seems to indicate body fat percentage tends to increase as weight increases. Now make a 3D plot of Bodyfat vs. Weight and Abdomen.

[2] Rawlings, John O., Sastry G. Pantula, and David A. Dickey, *Applied Regression Analysis: A Research Tool*, 2nd ed., (Springer-Verlag: New York, 1998), 208-09.

[3] This is not to be confused with "Sampson's Paradox" which goes something like, "What in the world did I ever see in that gal?" (sorry)


bodyfat$Bodyfat
10
20
30
40
140
160
180
200
220
240
260
bodyfat$Weight


140
160
180
200
220
240
260
40
30
20
10
bodyfat$Bodyfat
120
110
100
90
80
70
bodyfat$Abdomen
bodyfat$Weight

Describe how Simpson's Paradox is apparent in this context. Recall how the sign of the Weight coefficient changed when we included the Abdomen variable in the regression model. Simpson's Paradox is the phenomenon of seeing a trend in a data relationship seemingly reverse trend as other variates are considered. In the Encyclopedia Britannica we read, "Simpson's paradox, also called Yule-Simpson effect, in statistics, an effect that occurs when the marginal association between two categorical variables is qualitatively different from the partial association between the same two variables after controlling for one or more other variables. Simpson's paradox is important for three critical reasons. First, people often expect statistical relationships to be immutable. They often are not. The relationship between two variables might increase, decrease, or even change direction depending on the set of variables being controlled. Second, Simpson's paradox is not simply an obscure phenomenon of interest only to a small group of statisticians. Simpson's paradox is actually one of a large class of association paradoxes. Third, Simpson's paradox reminds researchers that causal inferences, particularly in nonexperimental studies, can be hazardous. Uncontrolled and even unobserved variables that would eliminate or reverse the association observed between two variables might exist."[4]

We see in this example set how the data seems to curve back around after we add the *abdomen* variable. Initially, as *weight* increases so, too does *bodyfat*. But almost paradoxically after the *abdomen* variable is introduced, *bodyfat* seems to curve back around.[5]

4. Open the *prostate* data from the faraway package. Model l*psa* as the response and all other variables as predictors. Implement the methods of best subsets as well as forward and backward stepwise selection to determine "best" models, comparing them based on the performance measures Cp, BIC, etc.
Rawlings et al remark that, "Alternative variable selection methods have been developed that identify good (although not necessarily the best) subset models, with considerably less computing than is required for all possible regressions. These methods are referred to as stepwise regression methods. The subset models are identified sequentially by adding or deleting, depending on the method, the one variable that has the greatest impact on the residual sum of squares. These stepwise methods are not guaranteed to find the 'best' subset for each subset size, and the results produced by different methods may not agree with each other."[6]

"Backward" elimination starts with all variables and systematically eliminates variables and testing the fit of the model with each iteration. "Forward" stepwise is the same process but in the opposite direction with one variable being added to the sequentially.[7]

[4] "Simpson's Paradox," *Encyclopedia Britannica*, accessed on 4/7/18 at: https://www.britannica.com/topic/Simpsons-paradox

[5] This same paradox can be observed in the seemingly backward trajectory of the Miami Heat's prospects for playoff standing after they introduced a great but aging Dwayne Wade back onto the roster. Great player but aging as all greats do.

[6] Rawlings, 213.

[7] Ibid.

Backward elimination was done and resulting diagnostics examined, beginning with a full model:

```
Call:
lm(formula = prostate$lpsa ~ prostate$lcavol + prostate$lweight +
    prostate$age + prostate$lbph + prostate$svi + prostate$lcp +
    prostate$gleason + prostate$pgg45)
Residuals:
    Min      1Q  Median      3Q     Max
-1.7331 -0.3713 -0.0170  0.4141  1.6381

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)       0.669337   1.296387   0.516  0.60693
prostate$lcavol   0.587022   0.087920   6.677 2.11e-09 ***
prostate$lweight  0.454467   0.170012   2.673  0.00896 **
prostate$age     -0.019637   0.011173  -1.758  0.08229 .
prostate$lbph     0.107054   0.058449   1.832  0.07040 .
prostate$svi      0.766157   0.244309   3.136  0.00233 **
prostate$lcp     -0.105474   0.091013  -1.159  0.24964
prostate$gleason  0.045142   0.157465   0.287  0.77503
prostate$pgg45    0.004525   0.004421   1.024  0.30886
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.7084 on 88 degrees of freedom
Multiple R-squared:  0.6548,	Adjusted R-squared:  0.6234
F-statistic: 20.86 on 8 and 88 DF,  p-value: < 2.2e-16
```

```
Call:
lm(formula = prostate$lpsa ~ prostate$lcavol + prostate$lweight +
    prostate$age + prostate$lbph + prostate$svi + prostate$lcp +
    prostate$gleason)
Residuals:
     Min       1Q   Median       3Q      Max
-1.78803 -0.36933  0.00302  0.43436  1.62160

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)       0.02416    1.13313   0.021  0.98304
prostate$lcavol   0.57471    0.08712   6.597 2.92e-09 ***
prostate$lweight  0.45260    0.17005   2.662  0.00923 **
prostate$age     -0.01812    0.01108  -1.636  0.10542
prostate$lbph     0.10886    0.05844   1.863  0.06579 .
prostate$svi      0.79783    0.24241   3.291  0.00143 **
prostate$lcp     -0.07488    0.08599  -0.871  0.38619
prostate$gleason  0.14591    0.12292   1.187  0.23837
---
```

```
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.7086 on 89 degrees of freedom
Multiple R-squared:  0.6506,      Adjusted R-squared:  0.6232
F-statistic: 23.68 on 7 and 89 DF,  p-value: < 2.2e-16


Call:
lm(formula = prostate$lpsa ~ prostate$lcavol + prostate$lweight +
   prostate$age + prostate$lbph + prostate$svi + prostate$lcp)
Residuals:
     Min       1Q   Median       3Q      Max
-1.82853 -0.40741  0.01695  0.47159  1.59040

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)       0.93487    0.83577   1.119  0.26630
prostate$lcavol   0.58765    0.08663   6.783  1.2e-09 ***
prostate$lweight  0.41808    0.16792   2.490  0.01462 *
prostate$age     -0.01511    0.01081  -1.398  0.16546
prostate$lbph     0.11381    0.05842   1.948  0.05452 .
prostate$svi      0.78256    0.24261   3.226  0.00175 **
prostate$lcp     -0.04118    0.08135  -0.506  0.61392
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.7102 on 90 degrees of freedom
Multiple R-squared:  0.6451,      Adjusted R-squared:  0.6215
F-statistic: 27.27 on 6 and 90 DF,  p-value: < 2.2e-16


Call:
lm(formula = prostate$lpsa ~ prostate$lcavol + prostate$lweight +
   prostate$age + prostate$lbph + prostate$svi)
Residuals:
     Min       1Q   Median       3Q      Max
-1.83505 -0.39396  0.00414  0.46336  1.57888

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)       0.95100    0.83175   1.143 0.255882
prostate$lcavol   0.56561    0.07459   7.583 2.77e-11 ***
prostate$lweight  0.42369    0.16687   2.539 0.012814 *
prostate$age     -0.01489    0.01075  -1.385 0.169528
prostate$lbph     0.11184    0.05805   1.927 0.057160 .
prostate$svi      0.72095    0.20902   3.449 0.000854 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
Residual standard error: 0.7073 on 91 degrees of freedom
Multiple R-squared:  0.6441,	Adjusted R-squared:  0.6245
F-statistic: 32.94 on 5 and 91 DF,  p-value: < 2.2e-16


Call:
lm(formula = prostate$lpsa ~ prostate$lcavol + prostate$lweight +
    prostate$age + prostate$lbph)
Residuals:
    Min      1Q  Median      3Q     Max
-1.4885 -0.4241 -0.0001  0.4031  1.8073

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)      0.73074    0.87703   0.833   0.4069
prostate$lcavol  0.69854    0.06754  10.343   <2e-16 ***
prostate$lweight 0.45770    0.17617   2.598   0.0109 *
prostate$age    -0.01371    0.01137  -1.206   0.2309
prostate$lbph    0.08404    0.06080   1.382   0.1702
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.748 on 92 degrees of freedom
Multiple R-squared:  0.5976,	Adjusted R-squared:  0.5801
F-statistic: 34.15 on 4 and 92 DF,  p-value: < 2.2e-16


Call:
lm(formula = prostate$lpsa ~ prostate$lcavol + prostate$lweight +
    prostate$age)
Residuals:
     Min       1Q   Median       3Q      Max
-1.60894 -0.44897 -0.02805  0.45602  1.91756

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)       0.146917   0.772374   0.190  0.84956
prostate$lcavol   0.687819   0.067418  10.202  < 2e-16 ***
prostate$lweight  0.549941   0.163838   3.357  0.00114 **
prostate$age     -0.009486   0.011003  -0.862  0.39082
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.7517 on 93 degrees of freedom
Multiple R-squared:  0.5892,	Adjusted R-squared:  0.576
F-statistic: 44.47 on 3 and 93 DF,  p-value: < 2.2e-16
```

```
Call:
lm(formula = prostate$lpsa ~ prostate$lcavol + prostate$lweight)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.61965 -0.50778 -0.02095  0.52291  1.89885 

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)    
(Intercept)      -0.30262    0.56904  -0.532  0.59612    
prostate$lcavol   0.67753    0.06626  10.225  < 2e-16 ***
prostate$lweight  0.51095    0.15726   3.249  0.00161 ** 
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.7506 on 94 degrees of freedom
Multiple R-squared:  0.5859,	Adjusted R-squared:  0.5771 
F-statistic: 66.51 on 2 and 94 DF,  p-value: < 2.2e-16


> summary(regmod_1)
Call:
lm(formula = prostate$lpsa ~ prostate$lcavol)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.67625 -0.41648  0.09859  0.50709  1.89673 

Coefficients:
                Estimate Std. Error t value Pr(>|t|)    
(Intercept)      1.50730    0.12194   12.36   <2e-16 ***
prostate$lcavol  0.71932    0.06819   10.55   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.7875 on 95 degrees of freedom
Multiple R-squared:  0.5394,	Adjusted R-squared:  0.5346 
F-statistic: 111.3 on 1 and 95 DF,  p-value: < 2.2e-16
```

Examining these models, we can ascertain that by including and excluding individual variables, the model using cavol, a variable commonly seen to have a significant p-value in all iterations, has the lowest R^2_{adj} of all of them. This model might be the best choice.

5. Open the *divusa* data from the faraway package. Model *divorce* as the response and all other variables as predictors. Implement the methods of best subsets as well as forward and backward stepwise selection to determine “best" models, comparing them based on the performance measures Cp, BIC, etc.

Opened and loaded the divusa dataset and used the glm() function to generate the AIC statistics besides the R^{2adj} and SSE:

```
Call:
glm(formula = divusa$divorce ~ divusa$year + divusa$unemployed + divusa$femlab + divusa$marriage +
divusa$birth + divusa$military)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.9087  -0.9212  -0.0935   0.7447   3.4689

Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
(Intercept)         380.14761   99.20371   3.832 0.000274 ***
divusa$year          -0.20312    0.05333  -3.809 0.000297 ***
divusa$unemployed    -0.04933    0.05378  -0.917 0.362171
divusa$femlab         0.80793    0.11487   7.033 1.09e-09 ***
divusa$marriage       0.14977    0.02382   6.287 2.42e-08 ***
divusa$birth         -0.11695    0.01470  -7.957 2.19e-11 ***
divusa$military      -0.04276    0.01372  -3.117 0.002652 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 2.288535)

Null deviance:      2442.5  on 76  degrees of freedom
Residual deviance:  160.2  on 70  degrees of freedom
AIC: 290.93

Number of Fisher Scoring iterations: 2


Call:
glm(formula = divusa$divorce ~ divusa$year + divusa$unemployed + divusa$femlab + divusa$marriage +
divusa$birth)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.3483  -0.9429   0.0430   0.8912   3.8625

Coefficients:
                    Estimate Std. Error t value Pr(>|t|)
(Intercept)        285.53474  100.07330   2.853  0.00567 **
divusa$year         -0.15213    0.05378  -2.829  0.00607 **
divusa$unemployed   -0.02846    0.05654  -0.503  0.61626
```

```
divusa$femlab          0.69620    0.11564   6.021 6.92e-08 ***
divusa$marriage        0.12832    0.02416   5.310 1.20e-06 ***
divusa$birth          -0.11711    0.01557  -7.520 1.29e-10 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 2.56942)

Null deviance:        2442.53  on 76  degrees of freedom
Residual deviance:  182.43  on 71  degrees of freedom
AIC: 298.93

Number of Fisher Scoring iterations: 2


Call:
glm(formula = divusa$divorce ~ divusa$year + divusa$unemployed + divusa$femlab + divusa$marriage)
Deviance Residuals: 
    Min       1Q   Median       3Q      Max  
-3.2553  -1.5614  -0.6785   1.2788   4.9885  

Coefficients:
                        Estimate Std. Error t value Pr(>|t|)    
(Intercept)            454.99121  129.77695   3.506 0.000787 ***
divusa$year           -0.25045    0.06944  -3.607 0.000568 ***
divusa$unemployed   0.18883    0.06468   2.919 0.004681 ** 
divusa$femlab          1.01139    0.14345   7.051 8.91e-10 ***
divusa$marriage        0.11355    0.03206   3.542 0.000700 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 4.551885)

    Null deviance:     2442.53  on 76  degrees of freedom
Residual deviance:  327.74  on 72  degrees of freedom
AIC: 342.04

Number of Fisher Scoring iterations: 2


Call:
glm(formula = divusa$divorce ~ divusa$year + divusa$unemployed + divusa$femlab)
Deviance Residuals: 
    Min       1Q   Median       3Q      Max  
-3.2112  -1.6888  -0.0618   1.0481   8.6792  

Coefficients:
                          Estimate Std. Error t value Pr(>|t|)    
```

```
(Intercept)            324.83352  133.95070   2.425   0.0178 *
divusa$year            -0.17447    0.07107  -2.455   0.0165 *
divusa$unemployed   0.04437    0.05404   0.821   0.4143
divusa$femlab          0.77071    0.13596   5.669  2.7e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 5.27198)

Null deviance:         2442.53  on 76  degrees of freedom
Residual deviance:  384.85  on 73  degrees of freedom
AIC: 352.41

Number of Fisher Scoring iterations: 2


Call:
glm(formula = divusa$divorce ~ divusa$year + divusa$unemployed)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-4.7892  -1.8315   0.1415   1.5944   7.2843

Coefficients:
                                 Estimate Std. Error t value Pr(>|t|)
(Intercept)              -4.224e+02  2.838e+01 -14.886   <2e-16 ***
divusa$year               2.225e-01  1.443e-02  15.416   <2e-16 ***
divusa$unemployed   -5.241e-03  6.356e-02  -0.082    0.935
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 7.489987)

Null deviance:         2442.53  on 76  degrees of freedom
Residual deviance:  554.26  on 74  degrees of freedom
AIC: 378.5

Number of Fisher Scoring iterations: 2


Call:
glm(formula = divusa$divorce ~ divusa$year)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-4.7828  -1.8092   0.1592   1.6292   7.3048

Coefficients:
                    Estimate Std. Error t value Pr(>|t|)
(Intercept)    -422.97530   27.29465  -15.50   <2e-16 ***
```

```
divusa$year    0.22280    0.01394   15.98   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 7.3908)

Null deviance:         2442.53  on 76  degrees of freedom
Residual deviance:  554.31  on 75  degrees of freedom
AIC: 376.51

Number of Fisher Scoring iterations: 2
```

Keeping year and femlab results in a comparably high AIC score along with an R^2_{adj} = .8367. This iteration avoids including the insignificant variables while maintaining a nice AIC score and R^2_{adj}

```
> summary(regmod_2b <-glm(divusa$divorce ~ divusa$year+divusa$femlab))

Call:
glm(formula = divusa$divorce ~ divusa$year + divusa$femlab)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.2545  -1.6205  -0.0812   0.9239   8.4775

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   312.1191   132.7594   2.351   0.0214 *
divusa$year    -0.1675     0.0704  -2.379   0.0200 *
divusa$femlab   0.7526     0.1339   5.622 3.16e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 5.248768)

Null deviance:         2442.53  on 76  degrees of freedom
Residual deviance:  388.41  on 74  degrees of freedom
AIC: 351.12

Number of Fisher Scoring iterations: 2
```

6. Load and read the documentation for the *Boston* data set from the MASS package. We want to build a model to predict the per capita crime rate. Implement the methods of (1) best subsets, (2) forward and (3) backward stepwise selection, (4) LOOCV, and (5) k-fold cross validation to build models (use k = 10). Compare and discus the models.

Loaded the Boston dataset and ran iterations of models to find the best fit. Begain with a full model to find statistically significant variables:

```
Residuals:
    Min      1Q  Median      3Q     Max 
-10.129  -2.031  -0.438   1.000  74.887 

Coefficients:
                  Estimate   Std. Error  t value   Pr(>|t|)    
(Intercept)       21.845372   6.645791    3.287   0.00108 ** 
Boston$zn          0.048614   0.018631    2.609   0.00935 ** 
Boston$indus      -0.053696   0.083334   -0.644   0.51965    
Boston$chas       -0.742473   1.182266   -0.628   0.53029    
Boston$nox       -10.599854   5.282238   -2.007   0.04533 *  
Boston$rm          0.137741   0.588242    0.234   0.81496    
Boston$age         0.010751   0.017065    0.630   0.52897    
Boston$dis        -1.040772   0.280481   -3.711   0.00023 ***
Boston$rad         0.609621   0.087264    6.986   9.21e-12 ***
Boston$tax        -0.004453   0.005149   -0.865   0.38756    
Boston$ptratio    -0.301584   0.185884   -1.622   0.10535    
Boston$black      -0.008034   0.003668   -2.190   0.02897 *  
Boston$medv       -0.243237   0.054450   -4.467   9.84e-06 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 6.451 on 493 degrees of freedom
Multiple R-squared:  0.4509,	Adjusted R-squared:  0.4376 
F-statistic: 33.74 on 12 and 493 DF,  p-value: < 2.2e-16
```

Six variables were seen to have statistical significance in relation to the predictor. A reduced model was run to see how these variables alone would fair, using a backward elimination approach:

```
Call:
lm(formula = Boston$crim ~ Boston$zn + Boston$nox + Boston$dis + 
    Boston$rad + Boston$black + Boston$medv)

Residuals:
    Min      1Q  Median      3Q     Max 
-10.240  -1.915  -0.376   0.852  75.438 
```

```
Coefficients:
                Estimate     Std. Error   t value    Pr(>|t|)
(Intercept)     14.642639    3.709443     3.947      9.04e-05 ***
Boston$zn        0.053963    0.017305     3.118      0.001923 **
Boston$nox      -9.238768    4.477580    -2.063      0.039597 *
Boston$dis      -0.992811    0.255075    -3.892      0.000113 ***
Boston$rad       0.499838    0.044036    11.351     < 2e-16 ***
Boston$black    -0.008711    0.003612    -2.412      0.016237 *
Boston$medv     -0.195990    0.037685    -5.201      2.90e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 6.452 on 499 degrees of freedom
Multiple R-squared:  0.444,	Adjusted R-squared:  0.4373
F-statistic: 66.42 on 6 and 499 DF,  p-value: < 2.2e-16
```

It was found that these six variables didn’t result in a stronger model than even the full one but did nevertheless provide at least some explanatory power.

APPENDIX: R SCRIPTS IMPLEMENTED

Question 3:

```
> library(readxl)
> bodyfat <- read_excel("c:/Users/baumgaral/Data/bodyfat.xlsx")
> head(bodyfat)
# A tibble: 6 x 10
  Bodyfat   Age Weight Height  Neck Chest Abdomen Ankle Biceps Wrist
    <dbl> <dbl>  <dbl>  <dbl> <dbl> <dbl>   <dbl> <dbl>  <dbl> <dbl>
1    32.3   41.   247.   73.5  42.1 117.    116.   26.3   37.3  19.7
2    22.5   31.   177.   71.5  36.2 101.     92.4  24.6   30.1  18.2
3    22.0   42.   156.   69.0  35.5  97.8    86.0  24.0   31.2  17.4
4    12.3   23.   154.   67.8  36.2  93.1    85.2  21.9   32.0  17.1
5    20.5   46.   177.   70.0  37.2  99.7    95.6  22.5   29.1  17.7
> plot(bodyfat$Bodyfat ~ bodyfat$Weight)
> library(scatterplot3d)
> library(readxl)
> plot3d(bodyfat$Weight, bodyfat$Abdomen, bodyfat$Bodyfat)
```

Question 4:

```
> library(faraway)
> head(prostate)
      lcavol lweight age      lbph svi      lcp gleason pgg45     lpsa
1 -0.5798185  2.7695  50 -1.386294   0 -1.38629       6     0 -0.43078
2 -0.9942523  3.3196  58 -1.386294   0 -1.38629       6     0 -0.16252
3 -0.5108256  2.6912  74 -1.386294   0 -1.38629       7    20 -0.16252
4 -1.2039728  3.2828  58 -1.386294   0 -1.38629       6     0 -0.16252
5  0.7514161  3.4324  62 -1.386294   0 -1.38629       6     0  0.37156
6 -1.0498221  3.2288  50 -1.386294   0 -1.38629       6     0  0.76547

> regmod1_full <- lm(prostate$lpsa ~ prostate$lcavol+prostate$lweight+prostate$age+prostate$lbph+prostate$svi+prostate$lcp+prostate$gleason+prostate$pgg45)
> regmod1_6 <- lm(prostate$lpsa ~ prostate$lcavol+prostate$lweight+prostate$age+prostate$lbph+prostate$svi+prostate$lcp+prostate$gleason)
> regmod1_5 <- lm(prostate$lpsa ~ prostate$lcavol+prostate$lweight+prostate$age+prostate$lbph+prostate$svi+prostate$lcp)
> regmod1_4 <- lm(prostate$lpsa ~ prostate$lcavol+prostate$lweight+prostate$age+prostate$lbph+prostate$svi)
> regmod1_3 <- lm(prostate$lpsa ~ prostate$lcavol+prostate$lweight+prostate$age+prostate$lbph)
> regmod_7 <- regmod1_6
> regmod_6 <- regmod1_5
> regmod_5 <- regmod1_4
> regmod_4 <- regmod1_3
> regmod_3 <- lm(prostate$lpsa ~ prostate$lcavol+prostate$lweight+prostate$age)
> regmod_2 <- lm(prostate$lpsa ~ prostate$lcavol+prostate$lweight)
> regmod_1 <- lm(prostate$lpsa ~ prostate$lcavol)
> summary(regmod1_full)
Call:
lm(formula = prostate$lpsa ~ prostate$lcavol + prostate$lweight +
    prostate$age + prostate$lbph + prostate$svi + prostate$lcp +
    prostate$gleason + prostate$pgg45)

Residuals:
    Min      1Q  Median      3Q     Max
-1.7331 -0.3713 -0.0170  0.4141  1.6381

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)       0.669337   1.296387   0.516  0.60693
prostate$lcavol   0.587022   0.087920   6.677 2.11e-09 ***
prostate$lweight  0.454467   0.170012   2.673  0.00896 **
prostate$age     -0.019637   0.011173  -1.758  0.08229 .
prostate$lbph     0.107054   0.058449   1.832  0.07040 .
prostate$svi      0.766157   0.244309   3.136  0.00233 **
prostate$lcp     -0.105474   0.091013  -1.159  0.24964
prostate$gleason  0.045142   0.157465   0.287  0.77503
prostate$pgg45    0.004525   0.004421   1.024  0.30886
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.7084 on 88 degrees of freedom
Multiple R-squared:  0.6548,	Adjusted R-squared:  0.6234
F-statistic: 20.86 on 8 and 88 DF,  p-value: < 2.2e-16

> summary(regmod_7)
Call:
lm(formula = prostate$lpsa ~ prostate$lcavol + prostate$lweight +
    prostate$age + prostate$lbph + prostate$svi + prostate$lcp +
    prostate$gleason)

Residuals:
     Min       1Q   Median       3Q      Max
-1.78803 -0.36933  0.00302  0.43436  1.62160

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)       0.02416    1.13313   0.021  0.98304
prostate$lcavol   0.57471    0.08712   6.597 2.92e-09 ***
prostate$lweight  0.45260    0.17005   2.662  0.00923 **
prostate$age     -0.01812    0.01108  -1.636  0.10542
prostate$lbph     0.10886    0.05844   1.863  0.06579 .
prostate$svi      0.79783    0.24241   3.291  0.00143 **
prostate$lcp     -0.07488    0.08599  -0.871  0.38619
```

```
prostate$gleason  0.14591    0.12292   1.187  0.23837
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.7086 on 89 degrees of freedom
Multiple R-squared:  0.6506,      Adjusted R-squared:  0.6232
F-statistic: 23.68 on 7 and 89 DF,  p-value: < 2.2e-16

> summary(regmod_6)
Call:
lm(formula = prostate$lpsa ~ prostate$lcavol + prostate$lweight +
    prostate$age + prostate$lbph + prostate$svi + prostate$lcp)

Residuals:
     Min       1Q   Median       3Q      Max
-1.82853 -0.40741  0.01695  0.47159  1.59040

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)       0.93487    0.83577   1.119  0.26630
prostate$lcavol   0.58765    0.08663   6.783  1.2e-09 ***
prostate$lweight  0.41808    0.16792   2.490  0.01462 *
prostate$age     -0.01511    0.01081  -1.398  0.16546
prostate$lbph     0.11381    0.05842   1.948  0.05452 .
prostate$svi      0.78256    0.24261   3.226  0.00175 **
prostate$lcp     -0.04118    0.08135  -0.506  0.61392
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.7102 on 90 degrees of freedom
Multiple R-squared:  0.6451,      Adjusted R-squared:  0.6215
F-statistic: 27.27 on 6 and 90 DF,  p-value: < 2.2e-16

> summary(regmod_5)
Call:
lm(formula = prostate$lpsa ~ prostate$lcavol + prostate$lweight +
    prostate$age + prostate$lbph + prostate$svi)

Residuals:
     Min       1Q   Median       3Q      Max
-1.83505 -0.39396  0.00414  0.46336  1.57888

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)       0.95100    0.83175   1.143 0.255882
prostate$lcavol   0.56561    0.07459   7.583 2.77e-11 ***
prostate$lweight  0.42369    0.16687   2.539 0.012814 *
prostate$age     -0.01489    0.01075  -1.385 0.169528
```

```
prostate$lbph     0.11184    0.05805   1.927 0.057160 .
prostate$svi      0.72095    0.20902   3.449 0.000854 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.7073 on 91 degrees of freedom
Multiple R-squared:  0.6441,      Adjusted R-squared:  0.6245
F-statistic: 32.94 on 5 and 91 DF,  p-value: < 2.2e-16

> summary(regmod_4)
Call:
lm(formula = prostate$lpsa ~ prostate$lcavol + prostate$lweight +
    prostate$age + prostate$lbph)

Residuals:
    Min      1Q  Median      3Q     Max
-1.4885 -0.4241 -0.0001  0.4031  1.8073

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)       0.73074    0.87703   0.833   0.4069
prostate$lcavol   0.69854    0.06754  10.343   <2e-16 ***
prostate$lweight  0.45770    0.17617   2.598   0.0109 *
prostate$age     -0.01371    0.01137  -1.206   0.2309
prostate$lbph     0.08404    0.06080   1.382   0.1702
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.748 on 92 degrees of freedom
Multiple R-squared:  0.5976,      Adjusted R-squared:  0.5801
F-statistic: 34.15 on 4 and 92 DF,  p-value: < 2.2e-16

> summary(regmod_3)
Call:
lm(formula = prostate$lpsa ~ prostate$lcavol + prostate$lweight +
    prostate$age)

Residuals:
     Min       1Q   Median       3Q      Max
-1.60894 -0.44897 -0.02805  0.45602  1.91756

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)       0.146917   0.772374   0.190  0.84956
prostate$lcavol   0.687819   0.067418  10.202  < 2e-16 ***
prostate$lweight  0.549941   0.163838   3.357  0.00114 **
prostate$age     -0.009486   0.011003  -0.862  0.39082
---
```

```
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.7517 on 93 degrees of freedom
Multiple R-squared:  0.5892,	Adjusted R-squared:  0.576 
F-statistic: 44.47 on 3 and 93 DF,  p-value: < 2.2e-16

> summary(regmod_2)
Call:
lm(formula = prostate$lpsa ~ prostate$lcavol + prostate$lweight)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.61965 -0.50778 -0.02095  0.52291  1.89885 

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)    
(Intercept)      -0.30262    0.56904  -0.532  0.59612    
prostate$lcavol   0.67753    0.06626  10.225  < 2e-16 ***
prostate$lweight  0.51095    0.15726   3.249  0.00161 ** 
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.7506 on 94 degrees of freedom
Multiple R-squared:  0.5859,	Adjusted R-squared:  0.5771 
F-statistic: 66.51 on 2 and 94 DF,  p-value: < 2.2e-16

> summary(regmod_1)
Call:
lm(formula = prostate$lpsa ~ prostate$lcavol)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.67625 -0.41648  0.09859  0.50709  1.89673 

Coefficients:
                Estimate Std. Error t value Pr(>|t|)    
(Intercept)      1.50730    0.12194   12.36   <2e-16 ***
prostate$lcavol  0.71932    0.06819   10.55   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.7875 on 95 degrees of freedom
Multiple R-squared:  0.5394,	Adjusted R-squared:  0.5346 
F-statistic: 111.3 on 1 and 95 DF,  p-value: < 2.2e-16
```

Question 5:

```
> summary(regmod_full)
```

```
Call:
glm(formula = divusa$divorce ~ divusa$year + divusa$unemployed + divusa$femlab + divusa$marriage +
divusa$birth + divusa$military)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.9087  -0.9212  -0.0935   0.7447   3.4689

Coefficients:
                    Estimate Std. Error t value Pr(>|t|)
(Intercept)        380.14761   99.20371   3.832 0.000274 ***
divusa$year         -0.20312    0.05333  -3.809 0.000297 ***
divusa$unemployed   -0.04933    0.05378  -0.917 0.362171
divusa$femlab        0.80793    0.11487   7.033 1.09e-09 ***
divusa$marriage      0.14977    0.02382   6.287 2.42e-08 ***
divusa$birth        -0.11695    0.01470  -7.957 2.19e-11 ***
divusa$military     -0.04276    0.01372  -3.117 0.002652 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 2.288535)

Null deviance: 2442.5  on 76  degrees of freedom
Residual deviance:  160.2  on 70  degrees of freedom
AIC: 290.93

Number of Fisher Scoring iterations: 2

> summary(regmod_5)
Call:
glm(formula = divusa$divorce ~ divusa$year + divusa$unemployed + divusa$femlab + divusa$marriage +
divusa$birth)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.3483  -0.9429   0.0430   0.8912   3.8625

Coefficients:
                    Estimate Std. Error t value Pr(>|t|)
(Intercept)        285.53474  100.07330   2.853  0.00567 **
divusa$year         -0.15213    0.05378  -2.829  0.00607 **
divusa$unemployed   -0.02846    0.05654  -0.503  0.61626
divusa$femlab        0.69620    0.11564   6.021 6.92e-08 ***
divusa$marriage      0.12832    0.02416   5.310 1.20e-06 ***
divusa$birth        -0.11711    0.01557  -7.520 1.29e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 2.56942)
```

```
Null deviance: 2442.53  on 76  degrees of freedom
Residual deviance:  182.43  on 71  degrees of freedom
AIC: 298.93

Number of Fisher Scoring iterations: 2

> summary(regmod_4)
Call:
glm(formula = divusa$divorce ~ divusa$year + divusa$unemployed + divusa$femlab + divusa$marriage)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.2553  -1.5614  -0.6785   1.2788   4.9885

Coefficients:
                      Estimate Std. Error t value Pr(>|t|)
(Intercept)           454.99121  129.77695   3.506 0.000787 ***
divusa$year            -0.25045    0.06944  -3.607 0.000568 ***
divusa$unemployed   0.18883    0.06468   2.919 0.004681 **
divusa$femlab         1.01139    0.14345   7.051 8.91e-10 ***
divusa$marriage       0.11355    0.03206   3.542 0.000700 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 4.551885)

    Null deviance: 2442.53  on 76  degrees of freedom
Residual deviance:  327.74  on 72  degrees of freedom
AIC: 342.04

Number of Fisher Scoring iterations: 2

> summary(regmod_3)
Call:
glm(formula = divusa$divorce ~ divusa$year + divusa$unemployed + divusa$femlab)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.2112  -1.6888  -0.0618   1.0481   8.6792

Coefficients:
                      Estimate Std. Error t value Pr(>|t|)
(Intercept)           324.83352  133.95070   2.425   0.0178 *
divusa$year            -0.17447    0.07107  -2.455   0.0165 *
divusa$unemployed   0.04437    0.05404   0.821   0.4143
divusa$femlab         0.77071    0.13596   5.669  2.7e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 5.27198)
```

```
Null deviance: 2442.53  on 76  degrees of freedom
Residual deviance:  384.85  on 73  degrees of freedom
AIC: 352.41

Number of Fisher Scoring iterations: 2

> summary(regmod_2)
Call:
glm(formula = divusa$divorce ~ divusa$year + divusa$unemployed)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-4.7892  -1.8315   0.1415   1.5944   7.2843

Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
(Intercept)         -4.224e+02  2.838e+01 -14.886   <2e-16 ***
divusa$year          2.225e-01  1.443e-02  15.416   <2e-16 ***
divusa$unemployed   -5.241e-03  6.356e-02  -0.082    0.935
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 7.489987)

Null deviance: 2442.53  on 76  degrees of freedom
Residual deviance:  554.26  on 74  degrees of freedom
AIC: 378.5

Number of Fisher Scoring iterations: 2

> summary(regmod_1)
Call:
glm(formula = divusa$divorce ~ divusa$year)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-4.7828  -1.8092   0.1592   1.6292   7.3048

Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)    -422.97530   27.29465  -15.50   <2e-16 ***
divusa$year      0.22280    0.01394   15.98   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 7.3908)

Null deviance: 2442.53  on 76  degrees of freedom
Residual deviance:  554.31  on 75  degrees of freedom
```

```
AIC: 376.51

Number of Fisher Scoring iterations: 2

> summary(regmod_2b <-glm(divusa$divorce ~ divusa$year+divusa$femlab))

Call:
glm(formula = divusa$divorce ~ divusa$year + divusa$femlab)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.2545  -1.6205  -0.0812   0.9239   8.4775

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)   312.1191   132.7594   2.351   0.0214 *
divusa$year    -0.1675     0.0704  -2.379   0.0200 *
divusa$femlab   0.7526     0.1339   5.622 3.16e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 5.248768)

    Null deviance: 2442.53  on 76  degrees of freedom
Residual deviance:  388.41  on 74  degrees of freedom
AIC: 351.12

Number of Fisher Scoring iterations: 2

> summary(regmod_2b <-lm(divusa$divorce ~ divusa$year+divusa$femlab))

Call:
lm(formula = divusa$divorce ~ divusa$year + divusa$femlab)

Residuals:
    Min      1Q  Median      3Q     Max
-3.2545 -1.6205 -0.0812  0.9239  8.4775

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)   312.1191   132.7594   2.351   0.0214 *
divusa$year    -0.1675     0.0704  -2.379   0.0200 *
divusa$femlab   0.7526     0.1339   5.622 3.16e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.291 on 74 degrees of freedom
Multiple R-squared:  0.841,	Adjusted R-squared:  0.8367
```

```
F-statistic: 195.7 on 2 and 74 DF,  p-value: < 2.2e-16
```

Question 6:

```
> library(MASS)
> head(Boston)
     crim      zn  indus  chas   nox    rm  age    dis rad tax ptratio  black lstat medv
1 0.00632  18  2.31    0 0.538 6.575 65.2 4.0900   1 296    15.3 396.90  4.98 24.0
2 0.02731   0   7.07    0 0.469 6.421 78.9 4.9671   2 242    17.8 396.90  9.14 21.6
3 0.02729   0   7.07    0 0.469 7.185 61.1 4.9671   2 242    17.8 392.83  4.03 34.7
4 0.03237   0   2.18    0 0.458 6.998 45.8 6.0622   3 222    18.7 394.63  2.94 33.4
5 0.06905   0   2.18    0 0.458 7.147 54.2 6.0622   3 222    18.7 396.90  5.33 36.2
6 0.02985   0   2.18    0 0.458 6.430 58.7 6.0622   3 222    18.7 394.12  5.21 28.7

> regmod_full <- lm(Boston$crim ~ Boston$zn + Boston$indus + Boston$chas + Boston$nox + Boston$rm
+ Boston$age + Boston$dis + Boston$dis + Boston$rad + Boston$tax + Boston$ptratio + Boston$black +
Boston$black + Boston$medv)
> summary(regmod_full)

Call:
lm(formula = Boston$crim ~ Boston$zn + Boston$indus + Boston$chas +
    Boston$nox + Boston$rm + Boston$age + Boston$dis + Boston$dis +
    Boston$rad + Boston$tax + Boston$ptratio + Boston$black +
    Boston$black + Boston$medv)

Residuals:
    Min      1Q  Median      3Q     Max
-10.129  -2.031  -0.438   1.000  74.887

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)     21.845372   6.645791   3.287  0.00108 **
Boston$zn        0.048614   0.018631   2.609  0.00935 **
Boston$indus    -0.053696   0.083334  -0.644  0.51965
Boston$chas     -0.742473   1.182266  -0.628  0.53029
Boston$nox     -10.599854   5.282238  -2.007  0.04533 *
Boston$rm        0.137741   0.588242   0.234  0.81496
Boston$age       0.010751   0.017065   0.630  0.52897
Boston$dis      -1.040772   0.280481  -3.711  0.00023 ***
Boston$rad       0.609621   0.087264   6.986 9.21e-12 ***
Boston$tax      -0.004453   0.005149  -0.865  0.38756
Boston$ptratio  -0.301584   0.185884  -1.622  0.10535
Boston$black    -0.008034   0.003668  -2.190  0.02897 *
Boston$medv     -0.243237   0.054450  -4.467 9.84e-06 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 6.451 on 493 degrees of freedom
Multiple R-squared:  0.4509,       Adjusted R-squared:  0.4376
```

```
F-statistic: 33.74 on 12 and 493 DF,  p-value: < 2.2e-16

> regmod_reduced <- lm(Boston$crim ~ Boston$zn + Boston$nox + Boston$dis + Boston$rad +
Boston$black + Boston$medv)
> summary(regmod_reduced)

Call:
lm(formula = Boston$crim ~ Boston$zn + Boston$nox + Boston$dis +
    Boston$rad + Boston$black + Boston$medv)

Residuals:
    Min      1Q  Median      3Q     Max
-10.240  -1.915  -0.376   0.852  75.438

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  14.642639   3.709443   3.947 9.04e-05 ***
Boston$zn     0.053963   0.017305   3.118 0.001923 **
Boston$nox   -9.238768   4.477580  -2.063 0.039597 *
Boston$dis   -0.992811   0.255075  -3.892 0.000113 ***
Boston$rad    0.499838   0.044036  11.351  < 2e-16 ***
Boston$black -0.008711   0.003612  -2.412 0.016237 *
Boston$medv  -0.195990   0.037685  -5.201 2.90e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 6.452 on 499 degrees of freedom
Multiple R-squared:  0.444,	Adjusted R-squared:  0.4373
F-statistic: 66.42 on 6 and 499 DF,  p-value: < 2.2e-16
```