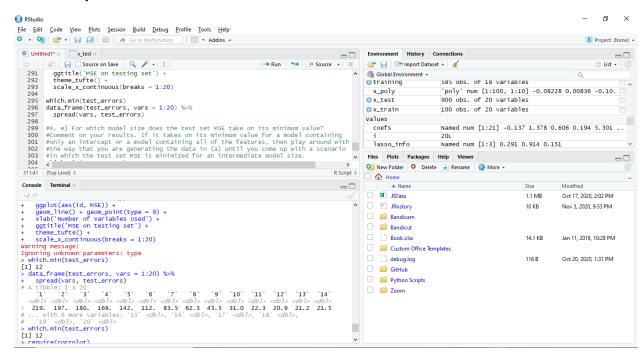
### **Introduction to Statistical Learning Lab5**

Name: Sandeep Reddy Salkuti

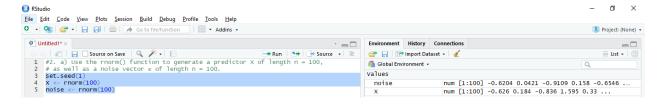
Student id: 16296868

Email: sswf7@umsystem.edu

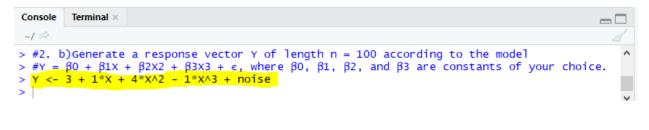
1. You may download the R Code for Labs and the Data Sets to use from the textbook website.

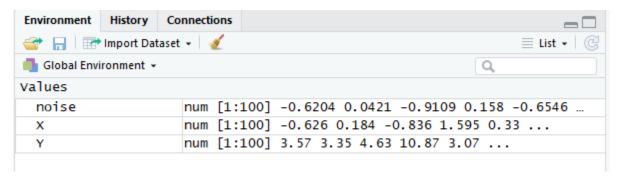


- 2. (30 points total) In this exercise, we will generate simulated data, and will then use this data to perform best subset selection.
- (a) (5 points) Use the rnorm() function to generate a predictor X of length n = 100, as well as a noise vector  $\epsilon$  of length n = 100.



(b) (5 points) Generate a response vector Y of length n = 100 according to the model Y =  $\beta$ 0 +  $\beta$ 1X +  $\beta$ 2X 2 +  $\beta$ 3X 3 +  $\epsilon$ , where  $\beta$ 0,  $\beta$ 1,  $\beta$ 2, and  $\beta$ 3 are constants of your choice.





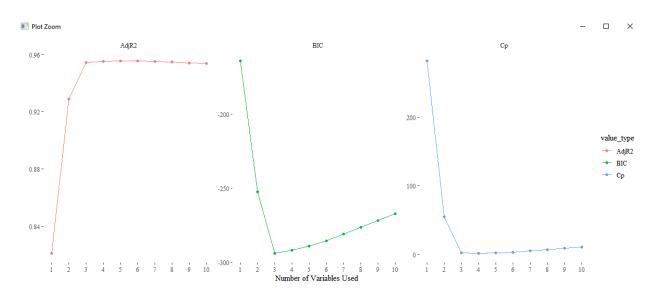
(c) (5 points) Use the regsubsets() function to perform best subset selection in order to choose the best model containing the predictors X, X2,..., X10. What is the best model obtained according to Cp, BIC, and adjusted R2? Show some plots to provide evidence for your answer, and report the coefficients of the best model obtained. Note you will need to use the data.frame() function to create a single data set containing both X and Y.

```
Console Terminal ×
 > require(leaps)
> df <- data.frame(Y, X)
> fit <- regsubsets(Y ~ poly(X, 10), data = df, nvmax = 10)
> fit_summary <- summary(fit)</pre>
  > require(tidyverse); require(ggplot2); require(ggthemes);
 Loading required package: tidyverse
 -- Attaching packages ----
                                                                                                                  ----- tidyverse 1.3.0 --
v tibble 3.0.4
v tidyr 1.1.2
v readr 1.3.1
                                             v dplyr 1.0.2
v stringr 1.4.0
                                              v forcats 0.4.0
 v purrr
                       0.3.4
  -- Conflicts --
                                                                                                 ----- tidyverse_conflicts() --
 x dplyr::filter() masks stats::filter()
x dplyr::lag() masks stats::lag()
warning messages:
1: package 'tidyverse' was built under R version 3.6.3
2: package 'tibble' was built under R version 3.6.3
3: package 'tidyr' was built under R version 3.6.3
4: package 'purrr' was built under R version 3.6.3
5: package 'dplyr' was built under R version 3.6.3
Loading required package: ggthemes
 x dplyr::lag()
                                        masks stats::lag()
Loading required package: ggthemes
Warning message:
package 'ggthemes' was built under R version 3.6.3
> data_frame(cp = fit_summary$cp,
+ BIC = fit_summary$bic,
+ AdjR2 = fit_summary$adjr2) %>%
+ mutate(id = row_number()) %>%
         mutate(id = row_number()) %>%
gather(value_type, value, -id) %>%
ggplot(aes(id, value, col = value_type)) +
geom_line() + geom_point() + ylab('') + xlab('Number of Variables Used') +
facet_wrap(~ value_type, scales = 'free') +
theme_tufte() + scale_x_continuous(breaks = 1:10)
'data_frame()' is deprecated as of tibble 1.1.0.

Please use `tibble()' instead.

This warning is displayed once every 8 hours.

Call `lifecycle::last_warnings()' to see where this warning was generated.
```



Regsubsets chooses three as the optimal number of parameters, just like we declared the Y variable.

# (d) (5 points) Repeat (c), using forward stepwise selection and also using backwards stepwise selection. How does your answer compare to the results in (c)?

```
Terminal ×
Console
                                                                                       -\Box
~/ @
The downloaded binary packages are in
        C:\Users\SandeepReddy\AppData\Local\Temp\Rtmpgx3Hdg\downloaded_packages
> require(caret)
Loading required package: caret
Loading required package: lattice
Attaching package: 'caret'
The following object is masked from 'package:purrr':
    1ift
Warning messages:
1: package 'caret' was built under R version 3.6.3
2: package 'lattice' was built under R version 3.6.3
> model_back <- train(Y ~ poly(X, 10), data = df,</pre>
                      method = 'glmStepAIC', direction = 'backward',
                      trace = 0,
                      trControl = trainControl(method = 'none', verboseIter = FALSE))
> postResample(predict(model_back, df), df$Y)
     RMSE Rsquared
0.9314956 0.9569843 0.7488821
> |
```

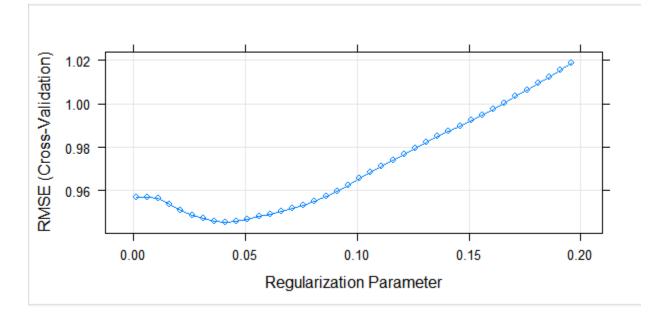
```
Console
       Terminal ×
~/ @
> summary(model_back$finalModel)
call:
NULL
Deviance Residuals:
   Min
         1Q Median
                              3Q
                                      Max
-1.8914 -0.5860 -0.1516
                          0.5892
                                   2.1794
Coefficients:
               Estimate Std. Error t value Pr(>|t|)
                6.10265 0.09557 63.856 < 2e-16 ***
(Intercept)
                          0.95569 -7.526 2.96e-11 ***
poly(x, 10)1
              -7.19295
             40.74405
 poly(x, 10)2
                           0.95569 42.633 < 2e-16 ***
poly(X, 10)3 -14.70908
                         0.95569 -15.391 < 2e-16 ***
`poly(x, 10)5`
               1.48019
                         0.95569 1.549
                                             0.125
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for gaussian family taken to be 0.9133516)
    Null deviance: 2017.132 on 99 degrees of freedom
Residual deviance:
                  86.768 on 95 degrees of freedom
AIC: 281.59
Number of Fisher Scoring iterations: 2
> |
```

From above backward stepwise model agrees with the best subsets model.

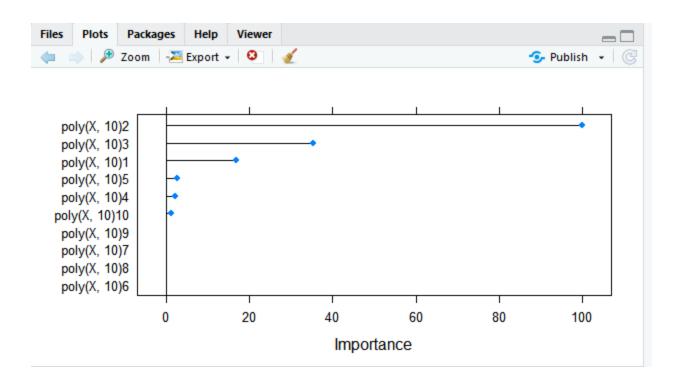
```
> summary(model_forw$finalModel)
call:
NULL
Deviance Residuals:
   Min
                               3Q
             1Q Median
                                      Max
-1.8914 -0.5860 -0.1516 0.5892
                                   2.1794
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)
            6.10265
                     0.09557 63.856 < 2e-16 ***
poly2
            40.74405
                        0.95569 42.633 < 2e-16 ***
poly3
           -14.70908
                       0.95569 -15.391 < 2e-16 ***
            -7.19295
                       0.95569 -7.526 2.96e-11 ***
poly1
            1.48019
                        0.95569 1.549
                                          0.125
poly5
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for gaussian family taken to be 0.9133516)
    Null deviance: 2017.132 on 99
                                   degrees of freedom
Residual deviance:
                    86.768 on 95
                                   degrees of freedom
AIC: 281.59
Number of Fisher Scoring iterations: 2
> |
```

From above it is clear that forward stepwise model also agrees.

(e) (5 points) Now fit a lasso model to the simulated data, again using X, X2,..., X10 as predictors. Use cross-validation to select the optimal value of  $\lambda$ . Create plots of the cross-validation error as a function of  $\lambda$ . Report the resulting coefficient estimates, and discuss the results obtained.



```
> plot(varImp(lasso_model))
> |
```

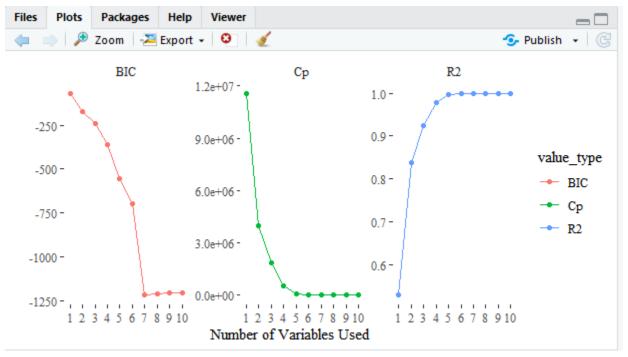


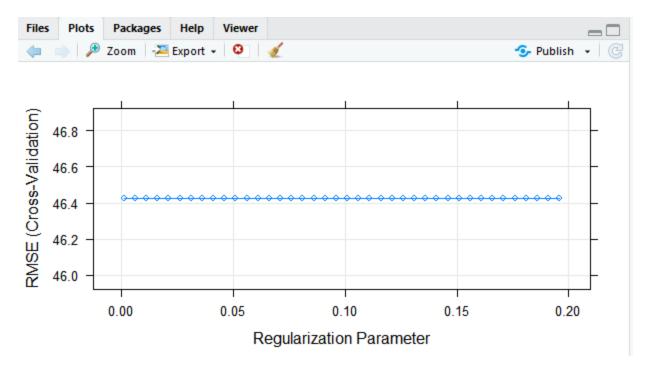
```
> coef(lasso_model$finalModel, lasso_model$bestTune$lambda)
11 x 1 sparse Matrix of class "dgCMatrix"
(Intercept)
                6.1026472
poly(X, 10)1
               -6.7829512
poly(X, 10)2
               40.3340466
poly(X, 10)3
              -14.2990830
poly(X, 10)4
                0.8470950
poly(X, 10)5
                1.0701884
poly(x, 10)6
poly(x, 10)7
poly(x, 10)8
poly(X, 10)9
poly(X, 10)10
              -0.5412295
```

```
> postResample(predict(lasso_model, df), df$Y)
        RMSE Rsquared MAE
0.9235360 0.9578972 0.7511252
> |
```

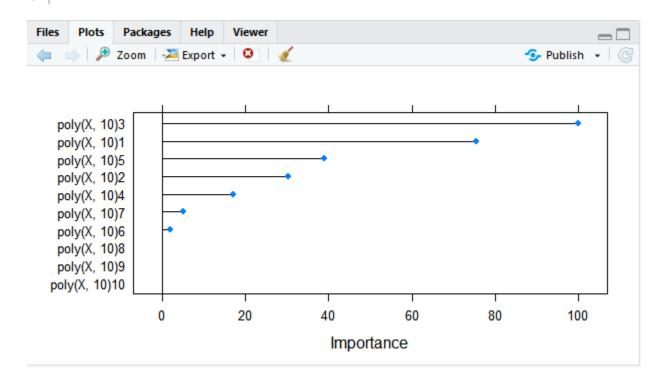
The Lasso model overestimates the number of predictors needed. This might be expected since we used only RSS to select the optimal model but not the Bayesian Inference Criterion and Adjusted R2R2 as regsubsets does or the Aikake Information Criterion as the stepwise selection does.

(f) (5 points)Now generate a response vector Y according to the model Y =  $\beta$ 0 +  $\beta$ 7X 7 +  $\epsilon$ , and perform best subset selection and the lasso. Discuss the results obtained.





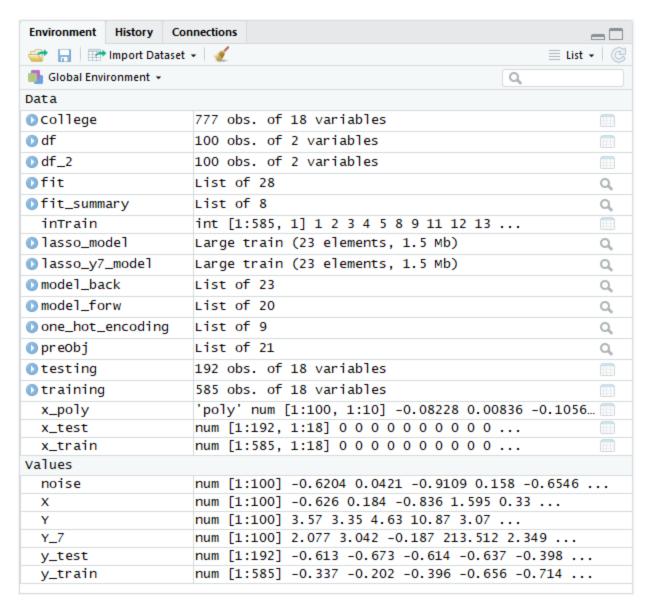
> plot(varImp(lasso\_y7\_model))



```
> coef(lasso_y7_model$finalModel, lasso_y7_model$bestTune$lambda)
11 x 1 sparse Matrix of class "dgCMatrix"
                36.72505
(Intercept)
poly(x, 10)1 2630.24239
poly(x, 10)2 1059.42846
poly(x, 10)3 3491.14380
poly(X, 10)4
              597.14287
poly(x, 10)5 1363.96802
poly(x, 10)6
               70.93052
poly(x, 10)7
              177.79560
poly(X, 10)8
poly(X, 10)9
poly(X, 10)10
>
> postResample(predict(lasso_y7_model, df_2), df_2$Y_7)
             Rsquared
      RMSE
                             MAE
14.2854376 0.9996164 4.9531386
>
```

- 3. (35 points total) In this exercise, we will predict the number of applications received using the other variables in the College data set.
- (a) (5 points) Split the data set into a training set and a test set.

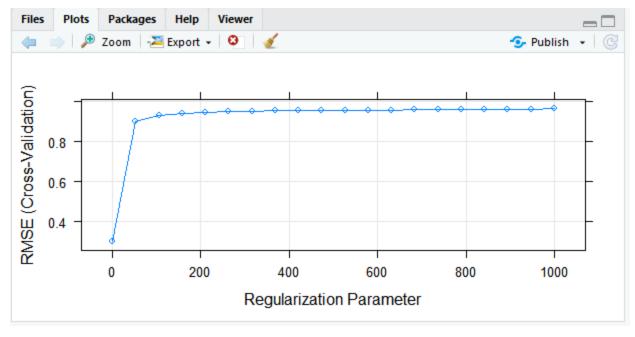
```
Console
       Terminal ×
~/ @
> require(ISLR)
Loading required package: ISLR
Warning message:
package 'ISLR' was built under R version 3.6.3
> require(caret)
> require(tidyverse)
> data('College')
> set.seed(1)
> inTrain <- createDataPartition(College$Apps, p = 0.75, list = FALSE)</pre>
> training <- College[inTrain,]
> testing <- College[-inTrain,]
> preObj <- preProcess(training, method = c('center', 'scale'))</pre>
> training <- predict(preObj, training)</pre>
> testing <- predict(preObj, testing)
> y_train <- training$Apps
> y_test <- testing$Apps
> one_hot_encoding <- dummyVars(Apps ~ ., data = training)
> x_train <- predict(one_hot_encoding, training)</pre>
> x_test <- predict(one_hot_encoding, testing)</pre>
```



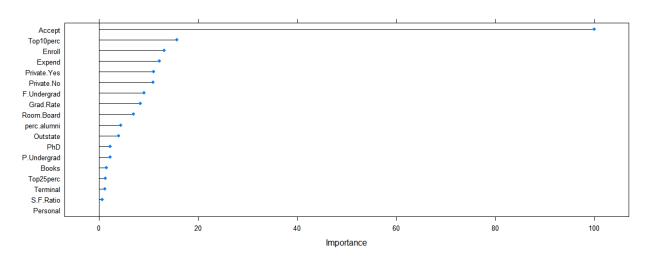
## (b) (5 points) Fit a linear model using least squares on the training set, and report the test error obtained.

(c) (5 points) Fit a ridge regression model on the training set, with  $\lambda$  chosen by cross-validation. Report the test error obtained.

```
> ridge_fit <- train(x = x_train, y = y_train,
                   method = 'glmnet',
                   trControl = trainControl(method = 'cv', number = 10).
+
                   tuneGrid = expand.grid(alpha = 0,
                                         lambda = seq(0, 10e2, length.out = 20)))
Warning message:
In nominalTrainWorkflow(x = x, y = y, wts = weights, info = trainInfo, :
 There were missing values in resampled performance measures.
> (ridge_info <- postResample(predict(ridge_fit, x_test), y_test))</pre>
     RMSE Rsquared
                       MAE
0.2853247 0.9211286 0.1645806
> coef(ridge_fit$finalModel, ridge_fit$bestTune$lambda)
19 x 1 sparse Matrix of class "dgCMatrix"
(Intercept) 0.034871314
Private.No
             0.075423210
Private.Yes -0.076037580
Accept
             0.665628733
Enroll
             0.090243372
Top10perc
             0.107160248
Top25perc
             0.011628030
F.Undergrad 0.063308801
P.Undergrad 0.017427317
          -0.028995432
Outstate
Room.Board 0.048720533
Books
            0.012799145
Personal
            -0.002894430
            -0.017989250
PhD
            -0.010434665
Terminal
S.F.Ratio
             0.006920126
perc.alumni -0.031683867
Expend
             0.083525070
Grad.Rate
             0.058131023
> |
> plot(ridge_fit)
```

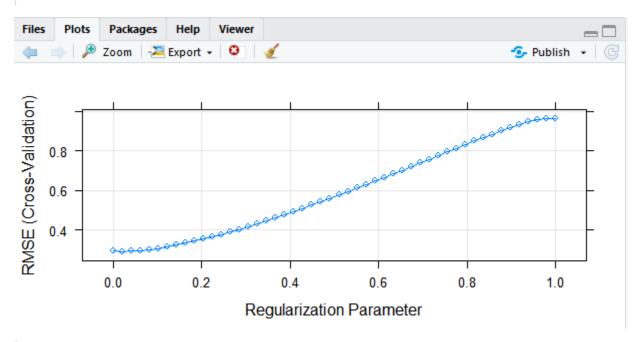


```
> plot(varImp(ridge_fit))
> |
```

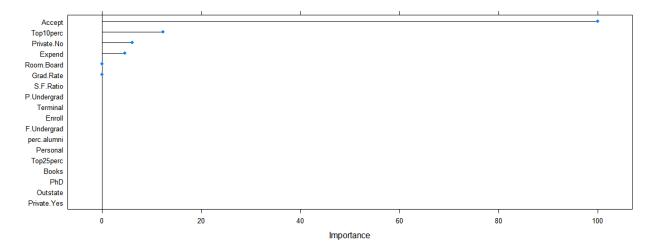


(d) (5 points) Fit a lasso model on the training set, with  $\lambda$  chosen by cross validation. Report the test error obtained, along with the number of non-zero coefficient estimates.

```
> coef(lasso_fit$finalModel, lasso_fit$bestTune$lambda)
19 x 1 sparse Matrix of class "dgCMatrix"
(Intercept) -1.470609e-02
Private.No
             5.410732e-02
Private.Yes
Accept
             8.883839e-01
Enroll
Top10perc
             1.092201e-01
Top25perc
F. Undergrad
P. Undergrad
Outstate
Room.Board
             1.483337e-04
Books
Personal
PhD
Terminal
S.F.Ratio
perc.alumni
Expend
             4.067011e-02
Grad.Rate
             4.062721e-06
> plot(lasso_fit)
```



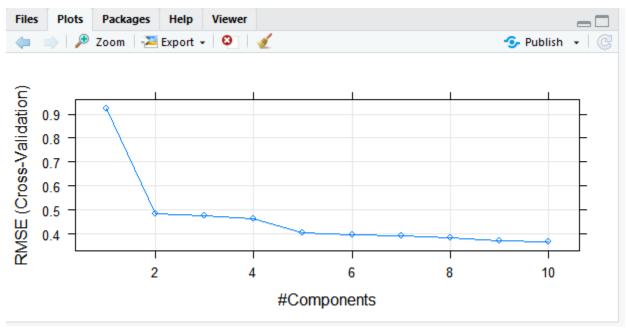
```
> plot(varImp(lasso_fit))
> |
```



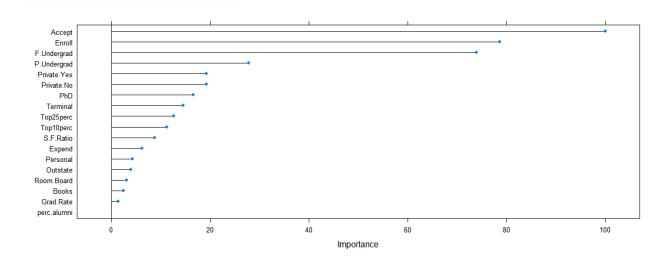
(e) (5 points) Fit a PCR model on the training set, with M chosen by cross validation. Report the test error obtained, along with the value of M selected by cross validation.

```
> pcr_model <- train(x = x_train, y = y_train,
                      method = 'pcr'
+
                      trControl = trainControl(method = 'cv', number = 10),
+
                      tuneGrid = expand.grid(ncomp = 1:10))
  (pcr_info <- postResample(predict(pcr_model, x_test), y_test))</pre>
     RMSE Rsquared
                           MAE
0.3231292 0.8916531 0.1986075
> |
> coef(pcr_model$finalModel)
, , 10 comps
                .outcome
Private.No
             0.031985972
Private.Yes -0.031985972
Accept
             0.343576750
Enroll
             0.305359773
Top10perc
             0.042630417
Top25perc
             0.027790893
F.Undergrad 0.273818439
P.Undergrad -0.049487667
Outstate
             0.038573119
Room. Board
             0.070607615
Books
             0.016433593
Personal
            -0.023529455
PhD
            -0.023992433
Terminal
            -0.024182230
S.F.Ratio
             0.003741623
perc.alumni -0.070567887
Expend
             0.090126298
             0.071302714
Grad.Rate
```

#### > plot(pcr\_model)

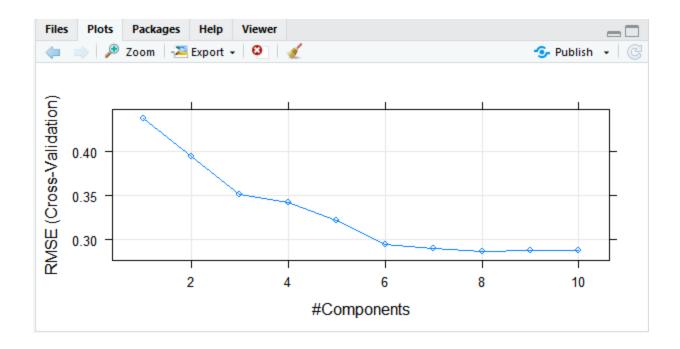


# > plot(varImp(pcr\_model)) > |



(f) (5 points) Fit a PLS model on the training set, with M chosen by cross validation. Report the test error obtained, along with the value of M selected by cross validation.

```
> pls_model <- train(x = x_train, y = y_train,</pre>
                      method = 'pls',
trControl = trainControl(method = 'cv', number = 10),
+
                      tuneGrid = expand.grid(ncomp = 1:10))
> (pls_info <- postResample(predict(pls_model, x_test), y_test))</pre>
     RMSE Rsquared
                           MAE
0.2838297 0.9185383 0.1589992
> |
> coef(pls_model$finalModel)
, , 8 comps
                .outcome
Private.No 0.071464730
Private.Yes -0.071464730
Accept
            1.034690648
Enroll
            -0.123546500
Top10perc
            0.213894280
Top25perc
           -0.058237828
F.Undergrad -0.062708027
P.Undergrad 0.032841252
Outstate
           -0.091066817
Room. Board 0.028320810
Books
            0.009007362
Personal
            0.006781888
PhD
            -0.038723144
Terminal
            0.005282905
S.F.Ratio -0.004984041
perc.alumni -0.005719117
Expend
            0.066720575
Grad.Rate 0.042981237
> plot(pls_model)
```

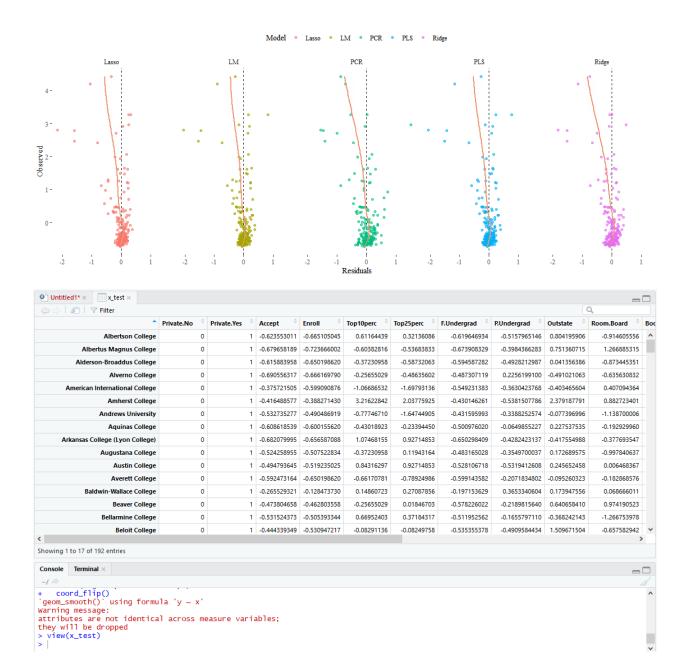


(g) (5 points) Comment on the results obtained. How accurately can we predict the number of college applications received? Is there much difference among the test errors resulting from these five approaches?

```
> as_data_frame(rbind(lin_info,
                      ridge_info,
                      lasso_info,
+
                      pcr_info,
+
                      pls_info)) %>%
+
    mutate(model = c('Linear', 'Ridge', 'Lasso', 'PCR', 'PLS')) %>%
    select(model, RMSE, Rsquared)
# A tibble: 5 x 3
  model
          RMSE Rsquared
  <chr>
         <db7>
                  <db1>
1 Linear 0.280
                  0.920
2 Ridge 0.285
                  0.921
3 Lasso 0.291
                  0.914
4 PCR
         0.323
                  0.892
                  0.919
5 PLS
         0.284
Warning message:
`as_data_frame()` is deprecated as of tibble 2.0.0.
Please use `as_tibble()` instead.
The signature and semantics have changed, see `?as_tibble`.
This warning is displayed once every 8 hours.
Call `lifecycle::last_warnings()` to see where this warning was generated.
> |
```

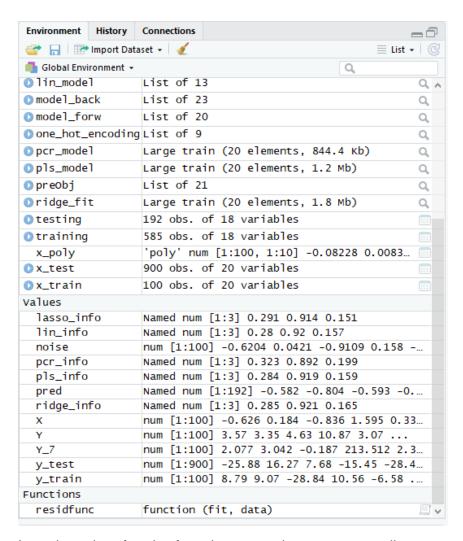
The models all perform similarly, with the exception of the PCR model.  $R_2 \ge 94R2 \ge 94$  for them all and RMSE $\le 20$ RMSE $\le 20$ . When we compare the RMSE scores with the mean and standard deviation of the response variable we see that the models all have phenomenal accuracy!

```
Terminal ×
Console
~/ @
> require(ggthemes)
> residfunc <- function(fit, data) {</pre>
    predict(fit, data) - testing$Apps
+
+
> data_frame(Observed = testing$Apps,
             LM = residfunc(lin_model, testing),
+
             Ridge = residfunc(ridge_fit, x_test),
             Lasso = residfunc(lasso_fit, x_test),
+
             PCR = residfunc(pcr_model, x_test),
+
             PLS = residfunc(pls_model, x_test)) %>%
+
    gather(Model, Residuals, -Observed) %>%
+
    ggplot(aes(Observed, Residuals, col = Model)) +
    geom_hline(yintercept = 0, lty = 2) +
    geom_point(alpha = 0.6) +
    geom_smooth(method = 'loess', alpha = 0.01, col = 'lightsalmon2') +
    facet_wrap(\sim Model, ncol = 5) +
    theme_tufte() +
    theme(legend.position = 'top') +
    coord_flip()
'geom_smooth()' using formula 'y \sim x'
Warning message:
attributes are not identical across measure variables;
they will be dropped
```



- 4. (35 points total) We have seen that as the number of features used in a model increases, the training error will necessarily decrease, but the test error may not. We will now explore this in a simulated data set.
- (a) (5 points) Generate a data set with p = 20 features, n = 1, 000 observations, and an associated quantitative response vector generated according to the model Y =  $X\beta$  +  $\epsilon$ , where  $\beta$  has some elements that are exactly equal to zero.

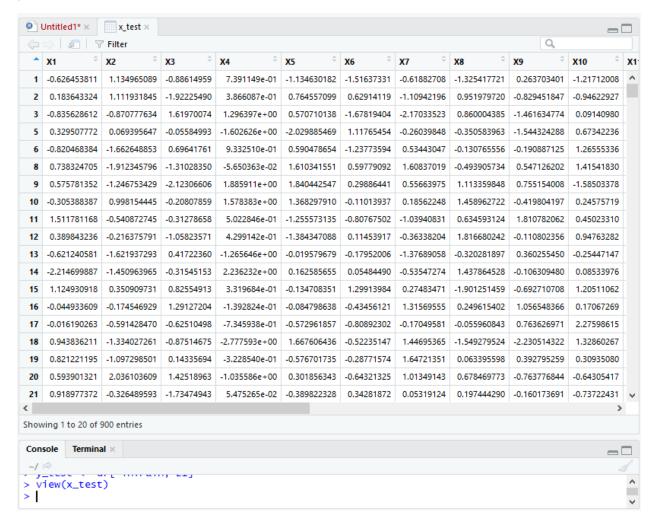
```
> require(tidyverse)
> set.seed(1)
> df <- data.frame(replicate(20, rnorm(n = 1000)))
>
> df %>%
+ reduce(function(y, x) y + ifelse(runif(1) < 0.5,
+ rnorm(1, mean = 5, sd = 1),
+ 0)*x + rnorm(1000)) -> df$Y
```



I use the reduce function from the purr package to more easily compute the y variable.

(b) (5 points) Split your data set into a training set containing 100 observations and a test set containing 900 observations.

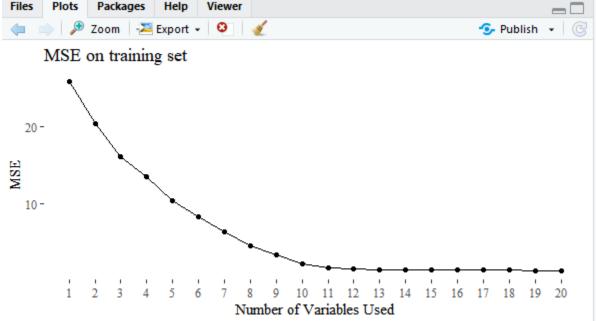
```
> require(caret)
>
> inTrain <- createDataPartition(df$Y, p = 0.1, list = F)
>
> x_train <- df[inTrain, -21]
> y_train <- df[inTrain, 21]
> x_test <- df[-inTrain, -21]
> y_test <- df[-inTrain, 21]
> |
```



The *createDataPartition* function from the *caret* creates train/test splits. In case of unbalanced classes it also makes sure one gets an even split of the response variable.

(c) (5 points) Perform best subset selection on the training set, and plot the training set MSE associated with the best model of each size.

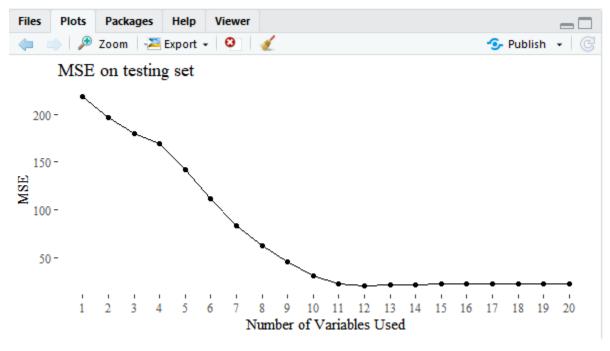
```
Console
        Terminal ×
~/ @
> require(leaps); require(ggplot2); require(dplyr); require(ggthemes)
> best_set <- regsubsets(x = x_train, y = y_train, nvmax = 20)</pre>
> best_set_summary <- summary(best_set)</pre>
> data_frame(MSE = best_set_summary$rss/900) %>%
    mutate(id = row_number()) %>%
    ggplot(aes(id, MSE)) +
    geom_line() + geom_point(type = 9) +
    xlab('Number of Variables Used') +
    ggtitle('MSE on training set') +
    theme_tufte() +
    scale_x_continuous(breaks = 1:20)
Warning message:
Ignoring unknown parameters: type
     Plots
           Packages
                    Help
                          Viewer
```



From above ss one would expect, the training MSE reduces with the addition of any new variable. Even after we've reached 10 predictors.

#### (d) (5 points) Plot the test set MSE associated with the best model of each size.

```
> test_errors = rep(NA,19)
> test.mat <- model.matrix(Y ~ ., data = df[-inTrain,])</pre>
> for (i in 1:20){
    coefs = coef(best_set, id=i)
    pred = test.mat[,names(coefs)]%*%coefs
    test_errors[i] = mean((y_test-pred)^2)
+ }
>
>
> data_frame(MSE = test_errors) %>%
    mutate(id = row_number()) %>%
    ggplot(aes(id, MSE)) +
    geom_line() + geom_point(type = 9) +
    xlab('Number of Variables Used') +
    ggtitle('MSE on testing set') +
    theme_tufte() +
    scale_x_continuous(breaks = 1:20)
Warning message:
Ignoring unknown parameters: type
```



> which.min(test\_errors)
[1] 12

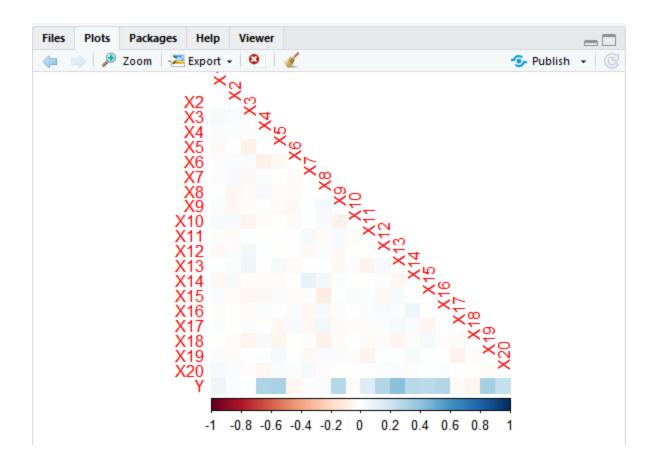
The test error settles at a minimum test error at 11 predictors and then stops decreasing.

(e) (5 points) For which model size does the test set MSE take on its minimum value? Comment on your results. If it takes on its minimum value for a model containing only an intercept or a model containing all of the features, then play around with the way that you are generating the data in (a) until you come up with a scenario in which the test set MSE is minimized for an intermediate model size.

```
> which.min(test_errors)
[1] 12
> |
```

The reported MSE minimum on the test set is achieved with 11 coefficients. This makes sense when we look at the corrplot below.

```
> require(corrplot)
Loading required package: corrplot
corrplot 0.84 loaded
Warning message:
package 'corrplot' was built under R version 3.6.3
> corrplot(cor(df), method = 'color', type = 'lower',diag = F)
> |
```

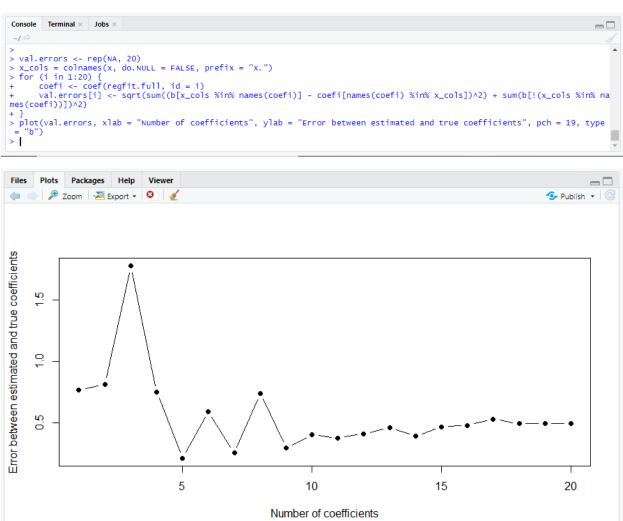


We can see on the corrplot that there are about 10 variables that correlate well with the response variable.

(f) (5 points) How does the model at which the test set MSE is minimized compare to the true model used to generate the data? Comment on the coefficient values.

Thinking back to the calculation of Y: If runif(1) > 0.5 the coefficient would be 0. That means in about 50% of cases the coefficient will be 0.50% of 20 is 10.

(g) (5 points) Create a plot displaying  $V\sum p j=1(\beta j-\beta^r j)$  2 for a range of values of r, where  $\beta^r j$  is the jth coefficient estimate for the best model containing r coefficients. Comment on what you observe. How does this compare to the test MSE plot from (d)?



We may see that the model with 3 variables minimizes the error between the estimated and true coefficients. However test error is minimized by the model with 14 variables. So, a better fit of true coefficients doesn't necessarily mean a lower test MSE.