

Honor statement:

"I have completed this work independently. The solutions given are entirely my own work"

1a.)

The following is the code used to perform Ridge Regression on the Piso2009 dataset:

```
View(Pisa2009)
library(glmnet)
```

```
# Get all rows and columns except for the 1st and 25th columns.
```

```
x <- data.matrix(Pisa2009[,2:24])
```

```
# Get the response variable and save it as a double data-type.
```

```
y <- as.double(Pisa2009[,25])
```

```
# Create the model w/ alpha = 0 for Ridge.
```

```
pisa_model <- glmnet(x, y, alpha = 0)
```

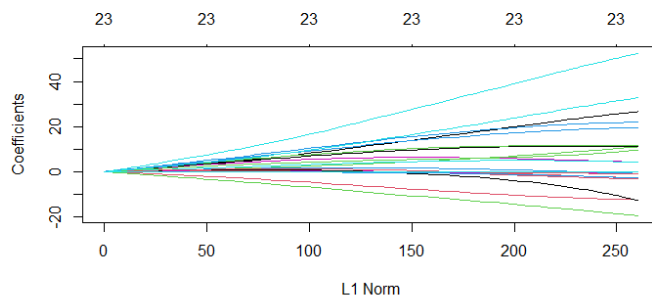
```
summary(pisa_model)
```

```
> summary(pisa_model)
```

	Length	Class	Mode
a0	100	-none-	numeric
beta	2300	dgCMatrix S4	
df	100	-none-	numeric
dim	2	-none-	numeric
lambda	100	-none-	numeric
dev.ratio	100	-none-	numeric
nulldev	1	-none-	numeric
npasses	1	-none-	numeric
jerr	1	-none-	numeric
offset	1	-none-	logical
call	5	-none-	call
nobs	1	-none-	numeric

```
# Displays Trace Plot
```

```
plot(pisa_model)
```



cv automatically does cross-validation to identify the lambda

```
pisa_ridge_cv <- cv.glmnet(x,y, family="gaussian", alpha=0)
pisa_ridge_cv
```

```
> pisa_ridge_cv
```

```
Call: cv.glmnet(x = x, y = y, family = "gaussian", alpha = 0)
```

```
Measure: Mean-Squared Error
```

	Lambda	Index	Measure	SE	Nonzero
min	3.36	99	5705	128.1	23
1se	41.41	72	5819	136.7	23

Get the lambda

```
pisa_lambda <- pisa_ridge_cv$lambda.min
pisa_lambda
```

```
> pisa_lambda <- pisa_ridge_cv$lambda.min
> pisa_lambda
[1] 3.359216
```

Find coefficients of the model

```
coef(pisa_ridge_cv, s=pisa_lambda)
```

```
> coef(pisa_ridge_cv, s=pisa_lambda)
24 x 1 sparse Matrix of class "dgCMatrix"
1
(Intercept)      178.907609883
grade            26.561537211
male             -12.406794130
raceeth          10.999647245
preschool        -0.740149794
expectBachelors  52.282541085
motherHS          4.342749265
motherBachelors  11.154201099
motherWork       -3.198076587
fatherHS          11.604885058
fatherBachelors  19.515312833
fatherWork        4.246623659
selfBornUS        0.134092464
motherBornUS     -12.584452833
fatherBornUS     -2.535264505
englishAtHome     9.588211699
computerForSchoolwork 21.916035046
read30MinsADay   32.661212423
minutesPerWeekEnglish 0.014312649
studentsInEnglish -0.027115779
schoolHasLibrary -1.045897572
publicSchool     -19.436026300
urban            -2.768863426
schoolSize        0.006535571
```

The following is the single-order model that was created with the coefficients of the Ridge Regression technique:

```
> pisa_model_1 <- lm(readingScore ~ grade + male + raceeth + preschool + expectBachelors + motherHS
+               + motherBachelors + motherWork + fatherHS + fatherBachelors + fatherWork + selfBornUS
+               + motherBornUS + fatherBornUS + englishAtHome + computerForSchoolwork + read30MinsADay
+               + minutesPerWeekEnglish + studentsInEnglish + schoolHasLibrary + publicSchool
+               + urban + schoolSize, data = Pisa2009)
> summary(pisa_model_1)
```

Call:

```
lm(formula = readingScore ~ grade + male + raceeth + preschool +
    expectBachelors + motherHS + motherBachelors + motherWork +
    fatherHS + fatherBachelors + fatherWork + selfBornUS + motherBornUS +
    fatherBornUS + englishAtHome + computerForSchoolwork + read30MinsADay +
    minutesPerWeekEnglish + studentsInEnglish + schoolHasLibrary +
    publicSchool + urban + schoolSize, data = Pisa2009)
```

Residuals:

```
    Min      1Q  Median      3Q      Max
-252.698 -48.479   0.481  49.936  247.243
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	299.488737	55.703871	5.376	8.11e-08 ***
grade9	40.285804	52.722943	0.764	0.444859
grade10	90.414303	52.582799	1.719	0.085621 .
grade11	104.977136	52.650018	1.994	0.046247 *
grade12	153.124134	64.477284	2.375	0.017612 *
male1	-12.629264	2.644476	-4.776	1.87e-06 ***
raceethAsian	59.289097	15.422137	3.844	0.000123 ***
raceethBlack	-3.245780	14.086553	-0.230	0.817782
raceethHispanic	28.478156	13.967874	2.039	0.041545 *
raceethMore than one race	42.834427	15.091587	2.838	0.004563 **
raceethNative Hawaiian/Other Pacific Islander	52.643342	20.069600	2.623	0.008754 **
raceethWhite	62.865269	13.555355	4.638	3.66e-06 ***
preschool1	-2.008505	2.956941	-0.679	0.497026
expectBachelors1	53.227613	3.576399	14.883	< 2e-16 ***
motherHS1	4.375418	5.063943	0.864	0.387631
motherBachelors1	11.151077	3.281944	3.398	0.000687 ***
motherWork1	-2.268512	2.953436	-0.768	0.442486
fatherHS1	6.891077	4.667189	1.476	0.139905
fatherBachelors1	17.604801	3.384319	5.202	2.09e-07 ***
fatherWork1	3.033776	3.695971	0.821	0.411799
selfBornUS1	0.796308	5.976750	0.133	0.894016
motherBornUS1	-8.337533	5.669328	-1.471	0.141482
fatherBornUS1	2.556788	5.369816	0.476	0.634005
englishAtHome1	10.905428	5.835964	1.869	0.061757 .
computerForSchoolwork1	19.807206	4.856144	4.079	4.63e-05 ***
read30MinsADay1	32.736380	2.862328	11.437	< 2e-16 ***
minutesPerWeekEnglish	0.011938	0.009016	1.324	0.185567
studentsInEnglish	-0.182103	0.192915	-0.944	0.345260
schoolHasLibrary1	-1.019002	7.570382	-0.135	0.892933
publicSchool1	-18.794210	5.590012	-3.362	0.000782 ***
urban1	-1.563926	3.320545	-0.471	0.637682
schoolSize	0.007573	0.001813	4.177	3.03e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 74.07 on 3372 degrees of freedom

Multiple R-squared: 0.3161, Adjusted R-squared: 0.3099

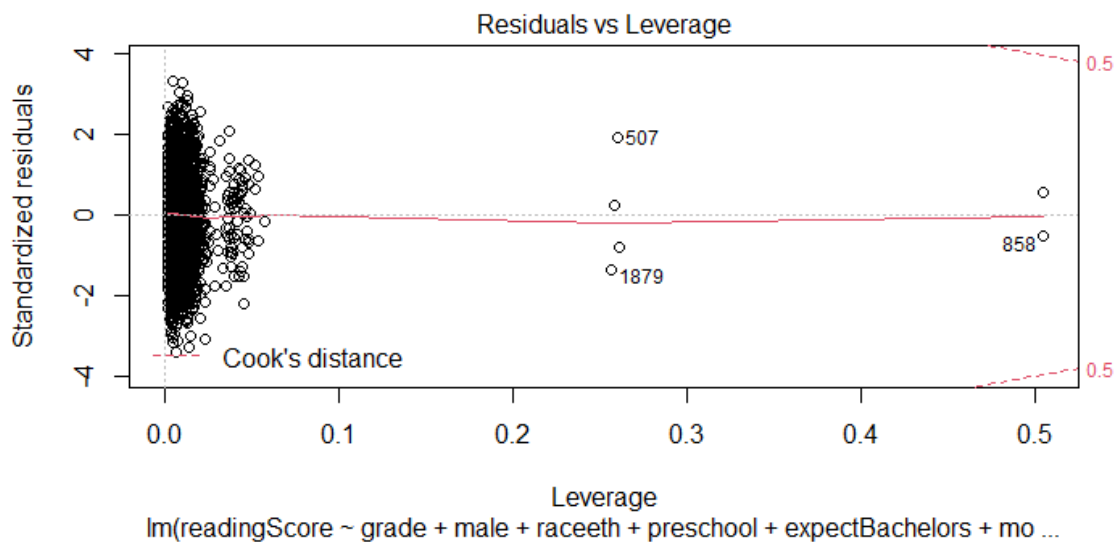
F-statistic: 50.29 on 31 and 3372 DF, p-value: < 2.2e-16

The following were continued to check the Residual Standard Error and the Adjusted R-Square value that was calculated in the above model:

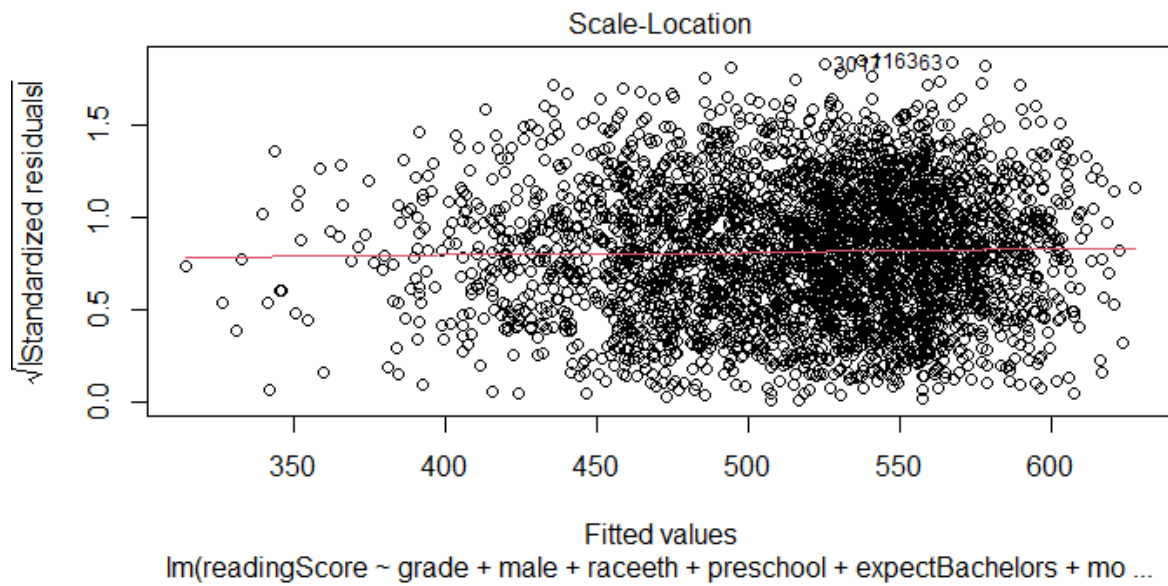
```
> y_predicted <- predict(pisa_ridge_cv, s = pisa_lambda, newx = x)
> sst <- sum((y - mean(y))^2)
> sse <- sum((y_predicted - y)^2)
> rsq <- 1 - sse/sst
> rsq
[1] 0.2925447
> RMSE = sqrt(sse/nrow(Pisa2009))
> RMSE
[1] 74.98547
```

The Ridge Trace Plot listed earlier demonstrates how Ridge Regression adds a degree of bias to the estimates and reduces the standard errors. The idea is for this technique to provide more reliable estimates.

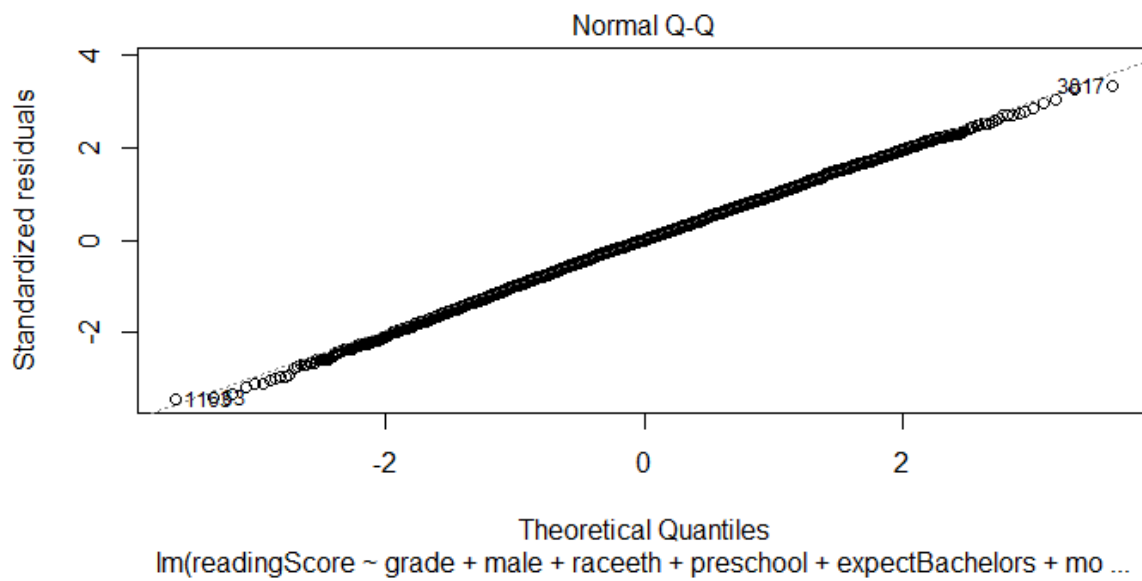
The residual plots are as follows:



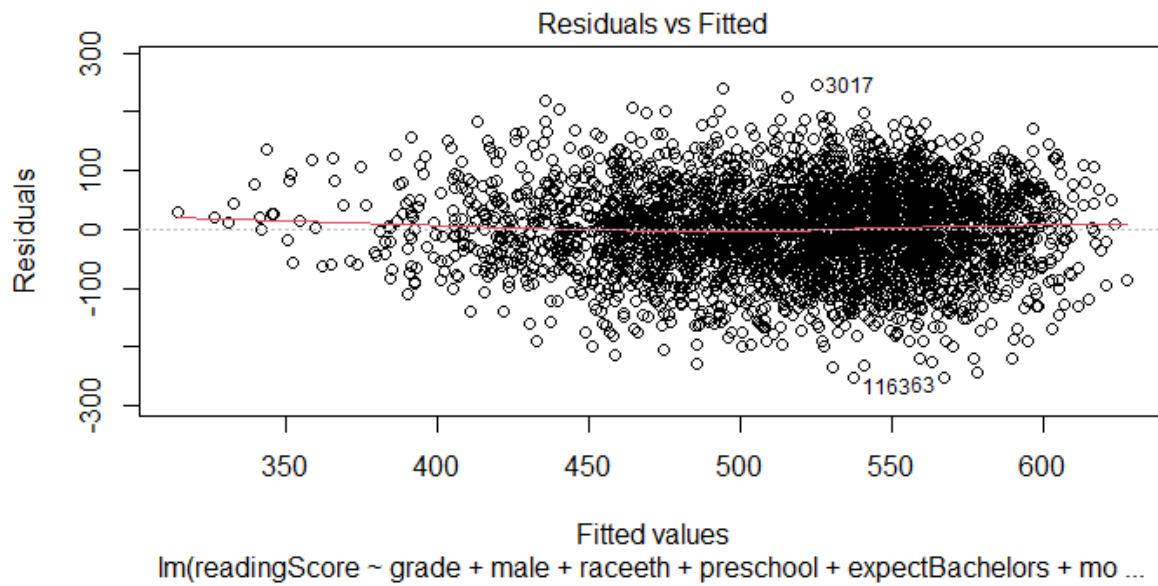
The “Residuals vs Leverage” plot will assist us with identifying outliers which may have influence on the change in the slope of the line.



The Scale-Location Plot above verifies the homoskedasticity assumption.



The above QQ Plot displays that a majority of the data are on the line, which indicates that the residuals are normal.



The above "Residuals vs Fitted" Plot displays heteroscedacity as there is different variance between that data points at the left-end and right-end of the plot. I suppose that there could be some argument for homoscedacity as well. This is something that I'll need to investigate further.

1.b)

The following commands were used to generate the LASSO coefficients:

```
set.seed(123) # random numbers
pisa_lasso <- cv.glmnet(x,y, family="gaussian", alpha=1)
coef(pisa_lasso, s=pisa_lambda)
```

The coefficients are as follows:

```
> set.seed(123) # random numbers
> pisa_lasso <- cv.glmnet(x,y, family="gaussian", alpha=1)
> coef(pisa_lasso, s=pisa_lambda)
24 x 1 sparse Matrix of class "dgCMatrix"
              1
(Intercept)  196.693536580
grade        23.868517417
male         -6.181739917
raceeth      8.823500814
preschool    .
expectBachelors 51.560027629
motherHS     .
motherBachelors 7.896835697
motherWork   .
fatherHS     5.882282620
fatherBachelors 20.590565216
fatherWork   .
selfBornUS   .
motherBornUS  .
fatherBornUS  .
englishAtHome .
computerForSchoolwork 17.527065546
read30MinsADay 28.089591247
minutesPerWeekEnglish .
studentsInEnglish .
schoolHasLibrary .
publicSchool  -4.643123913
urban         .
schoolSize    0.001126722
```

The following is the model created that uses the features generated via LASSO:

Call:

```
lm(formula = readingScore ~ grade + male + raceeth + expectBachelors +
    motherBachelors + fatherHS + fatherBachelors + computerForSchoolwork +
    read30MinsADay + publicSchool + schoolSize, data = Pisa2009)
```

Residuals:

Min	1Q	Median	3Q	Max
-256.107	-48.660	1.594	49.687	244.674

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	304.822253	54.450077	5.598	2.34e-08 ***
grade9	38.727433	52.641785	0.736	0.461977
grade10	88.635051	52.493357	1.689	0.091407 .
grade11	103.518161	52.557953	1.970	0.048966 *
grade12	155.501148	64.278458	2.419	0.015608 *
male1	-12.442632	2.634792	-4.722	2.43e-06 ***
raceethAsian	58.293463	14.887589	3.916	9.20e-05 ***
raceethBlack	-3.686041	14.056466	-0.262	0.793159
raceethHispanic	26.763415	13.724340	1.950	0.051250 .
raceethMore than one race	43.606069	15.051915	2.897	0.003791 **
raceethNative Hawaiian/Other Pacific Islander	54.683162	19.837983	2.756	0.005874 **
raceethWhite	62.922968	13.517890	4.655	3.37e-06 ***
expectBachelors1	53.096680	3.559075	14.919	< 2e-16 ***
motherBachelors1	11.212567	3.233992	3.467	0.000533 ***
fatherHS1	9.574209	4.179756	2.291	0.022047 *
fatherBachelors1	18.147346	3.355885	5.408	6.83e-08 ***
computerForSchoolwork1	20.322678	4.797978	4.236	2.34e-05 ***
read30MinsADay1	32.886562	2.851702	11.532	< 2e-16 ***
publicSchool1	-17.583400	4.962743	-3.543	0.000401 ***
schoolSize	0.006759	0.001623	4.165	3.19e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 74.05 on 3384 degrees of freedom

Multiple R-squared: 0.3141, Adjusted R-squared: 0.3102

F-statistic: 81.55 on 19 and 3384 DF, p-value: < 2.2e-16

1c.)

In this particular case, the models are not identical, but they are very close as the Adj. R-Squared value of the model based on Ridge is 30.99% and the Adj. R-Squared value for the model based on LASSO is 31%. Another difference is how the model variables are created. Ridge creates all of the variables and they are then added to model. For LASSO, the variables that are not initially needed are zeroed out. This demonstrates how useful LASSO regression is with feature selection.

2a. & 2b.)

The following code was used to create the Logistic model:

```
# Convert to factor because the current variable contains two-levels
```

```
remission$remiss <- as.factor(remission$remiss)
```

```
summary(remission)
```

```
# Using "family = binomial" to tell us that we're using Logistic Regression
```

```
rem_model <- glm(remiss ~., family = "binomial", data=remission)
```

```
summary(rem_model)
```

Call:

```
glm(formula = remiss ~ ., family = "binomial", data = remission)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.95165	-0.66491	-0.04372	0.74304	1.67069

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	58.0385	71.2364	0.815	0.4152
cell	24.6615	47.8377	0.516	0.6062
smear	19.2936	57.9500	0.333	0.7392
infil	-19.6013	61.6815	-0.318	0.7507
li	3.8960	2.3371	1.667	0.0955
blast	0.1511	2.2786	0.066	0.9471
temp	-87.4339	67.5735	-1.294	0.1957

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 34.372 on 26 degrees of freedom
Residual deviance: 21.751 on 20 degrees of freedom
AIC: 35.751

Number of Fisher Scoring iterations: 8

2c.)

The glm() function means “General Linear Model”. The lm() function fits models in the form of $Y = Xb + e$, where glm() fits models in the form of $f(Y) = Xb + e$ and the “e” or distribution of the error term can be specified.

2d.)

Using the glm() function doesn't appear to create a model that fits the dataset “remission”. The p-values for each of the variables aren't good.

The following will display the confidence interval and coefficients of the model, however, since this model appears to be a bad fit, I'm unsure if we should proceed with these steps:

Confidence interval of the model at 95%

```
confint(rem_model)
```

Coefficients of the model

```
coef(rem_model)
```

This "delogs" the coefficient

```
exp(coef(rem_model)) -1
```

```
> confint(rem_model) # Confidence interval of the model.. at 95%
              2.5 %      97.5 %
(Intercept) -70.9683777 222.202990
cell         -27.7332544 138.404531
smear        -60.4544868 152.174139
infil        -159.7565104 67.536927
li           0.1944541   9.526820
blast        -4.5238625  4.715064
temp         -244.7720744 24.913187
There were 26 warnings (use warnings() to see them)

> coef(rem_model) # Coefficients of the model
(Intercept)    cell      smear      infil      li      blast      temp
58.0384871  24.6615439 19.2935746 -19.6012612  3.8959633  0.1510923 -87.4339024
>
>
> exp(coef(rem_model)) -1 # This "delogs" the coefficient..
(Intercept)      cell      smear      infil      li      blast
1.606182e+25 5.133014e+10 2.393828e+08 -1.000000e+00 4.820343e+01 1.631040e-01
temp
-1.000000e+00
```