Homework 3

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Link to the Github repository

❗ Due: Thu, Mar 2, 2023 @ 11:59pm

Please read the instructions carefully before submitting your assignment.

1. This assignment requires you to only upload a `PDF` file on Canvas
2. Don't collapse any code cells before submitting.
3. Remember to make sure all your code output is rendered properly before uploading your submission.

Please add your name to the author information in the frontmatter before submitting your assignment

For this assignment, we will be using the Wine Quality dataset from the UCI Machine Learning Repository. The dataset consists of red and white *vinho verde* wine samples, from the north of Portugal. The goal is to model wine quality based on physicochemical tests

We will be using the following libraries:

```r
library(readr)
library(tidyr)
library(dplyr)
```

```
Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

    filter, lag

The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union
```

```r
library(purrr)
library(car)
```

```
Loading required package: carData

Attaching package: 'car'

The following object is masked from 'package:purrr':

    some

The following object is masked from 'package:dplyr':

    recode
```

```r
library(glmnet)
```

```
Loading required package: Matrix

Attaching package: 'Matrix'

The following objects are masked from 'package:tidyr':

    expand, pack, unpack

Loaded glmnet 4.1-6
```

Question 1

50 points

Regression with categorical covariate and t-Test

1.1 (5 points)

Read the wine quality data-sets from the specified URLs and store them in data frames `df1` and `df2`.

```
url1 <- "https://archive.ics.uci.edu/ml/machine-learning-databases/wine-quality/winequalit

url2 <- "https://archive.ics.uci.edu/ml/machine-learning-databases/wine-quality/winequalit


df1 <- read.csv(url1, header = TRUE, sep = ";")
df2 <- read.csv(url2, header = TRUE, sep = ";")
```

1.2 (5 points)

Perform the following tasks to prepare the data frame `df` for analysis:

1. Combine the two data frames into a single data frame `df`, adding a new column called `type` to indicate whether each row corresponds to white or red wine.
2. Rename the columns of `df` to replace spaces with underscores
3. Remove the columns `fixed_acidity` and `free_sulfur_dioxide`
4. Convert the `type` column to a factor
5. Remove rows (if any) with missing values.

```
# add a new column "type" to each data frame
df1 <- df1 %>%
  mutate("type" = "White")
df2 <- df2 %>%
  mutate("type" = "Red")

# combine the two data frames into a single data frame
df <- rbind(df1, df2) %>%
  rename_with(~ gsub("\\.", "_", .x)) %>%
  select(!c(fixed_acidity, free_sulfur_dioxide))
```

```r
# Converting type to a factor
df$type <- as.factor(df$type)

#removing missing value rows
df <- na.omit(df)
```

```r
dim(df)
```

```
[1] 6497   11
```

Your output to `R dim(df)` should be

```
[1] 6497   11
```

1.3 (20 points)

Recall from STAT 200, the method to compute the t statistic for the the difference in means (with the equal variance assumption)

1. Using `df` compute the mean of `quality` for red and white wine separately, and then store the difference in means as a variable called `diff_mean`.
2. Compute the pooled sample variance and store the value as a variable called `sp_squared`.
3. Using `sp_squared` and `diff_mean`, compute the t Statistic, and store its value in a variable called `t1`.

```r
w_mean <- mean(df$quality[df$type == 'White'])
r_mean <- mean(df$quality[df$type == 'Red'])
diff_mean <- mean(w_mean - r_mean)

n1 <- length(df$quality[df$type == 'White'])
n2 <- length(df$quality[df$type == 'Red'])

v1 <- var(df$quality[df$type == 'White'])
v2 <- var(df$quality[df$type == 'Red'])

sp_squared <- ((n1-1)*v1 + (n2-1)*v2) / (n1+n2-2)
```

```r
s1 <- sd(df$quality[df$type == 'White'])
s2 <- sd(df$quality[df$type == 'Red'])

t1 <- diff_mean / sqrt((sp_squared*(1/n1 + 1/n2)))
t1
```

```
[1] 9.68565
```

1.4 (10 points)

Equivalently, R has a function called `t.test()` which enables you to perform a two-sample t-Test without having to compute the pooled variance and difference in means.

Perform a two-sample t-test to compare the quality of white and red wines using the `t.test()` function with the setting `var.equal=TRUE`. Store the t-statistic in `t2`.

```r
t_test <- t.test(df$quality[df$type == "White"], df$quality[df$type == "Red"], var.equal =
t2 <- t_test$statistic
t2
```

```
     t
9.68565
```

1.5 (5 points)

Fit a linear regression model to predict `quality` from `type` using the `lm()` function, and extract the t-statistic for the `type` coefficient from the model summary. Store this t-statistic in `t3`.

```r
fit <- lm(quality ~ type, data = df)
t3 <- summary(fit)$coefficients[2, "t value"]
t3
```

```
[1] 9.68565
```

1.6 (5 points)

Print a vector containing the values of `t1`, `t2`, and `t3`. What can you conclude from this? Why?

```
c(t1, t2, t3)
```

```
             t
9.68565 9.68565 9.68565
```

> Based on the values of `t1`, `t2`, and `t3`, we can conclude that all three values are the same. We can also conclude that there is a substantial difference between the qualities of red and white wines. This is because linear regression determines the linear correlation between the predictor and response variables whereas the t-test determines the linear relationship. Hence, they are the same

---

Question 2

25 points

Collinearity

2.1 (5 points)

Fit a linear regression model with all predictors against the response variable `quality`. Use the `broom::tidy()` function to print a summary of the fitted model. What can we conclude from the model summary?

```
#fitting the linear regresion model
model_all <- lm(quality ~ ., data = df)

#printing the summary of the fitted model
library(broom)
summary_all <- broom::tidy(model_all)
summary_all
```

```
# A tibble: 11 x 5
   term                  estimate std.error statistic  p.value
   <chr>                    <dbl>     <dbl>     <dbl>    <dbl>
 1 (Intercept)           57.5       9.33         6.17  7.44e-10
 2 volatile_acidity      -1.61      0.0806     -20.0   4.07e-86
 3 citric_acid            0.0272    0.0783       0.347 7.28e- 1
 4 residual_sugar         0.0451    0.00416     10.8   3.64e-27
 5 chlorides             -0.964     0.333       -2.90  3.78e- 3
 6 total_sulfur_dioxide  -0.000329  0.000262    -1.25  2.10e- 1
 7 density              -55.2       9.32        -5.92  3.34e- 9
 8 pH                     0.188     0.0661       2.85  4.38e- 3
 9 sulphates              0.662     0.0758       8.73  3.21e-18
10 alcohol                0.277     0.0142      19.5   1.87e-82
11 typeWhite              -0.386     0.0549      -7.02  2.39e-12
```

From the model summary, we can see that several of the predictor variables have a statistically significant effect on the quality of wine, as indicated by their p-value. On the other hand, the `fixed_acidity` and `free_sulfur_dioxide` predictors have been removed due to their p-value.

2.2 (10 points)

Fit two **simple** linear regression models using `lm()`: one with only `citric_acid` as the predictor, and another with only `total_sulfur_dioxide` as the predictor. In both models, use `quality` as the response variable. How does your model summary compare to the summary from the previous question?

```r
model_citric <- lm(quality ~ citric_acid, data = df)
summary_citric <- broom::tidy(model_citric)
summary_citric
```

```
# A tibble: 2 x 5
  term        estimate std.error statistic  p.value
  <chr>          <dbl>     <dbl>     <dbl>    <dbl>
1 (Intercept)    5.65     0.0260    217.   0
2 citric_acid    0.514    0.0743      6.92 5.00e-12
```

```r
model_sulfur <- lm(quality ~ total_sulfur_dioxide, data = df)
summary_sulfur <- broom::tidy(model_sulfur)
```

```
summary_sulfur
```

```
# A tibble: 2 x 5
  term                  estimate std.error statistic  p.value
  <chr>                    <dbl>     <dbl>     <dbl>    <dbl>
1 (Intercept)           5.89      0.0247      239.   0
2 total_sulfur_dioxide -0.000639  0.000192     -3.34 0.000848
```

Comparing these models with the model from the previous question, we can see that the coefficients and t-Statistics for these predictors in the multiple regression model and simple regression model are consistent. However, in the multiple regression model, several other predictors also have an effect on the `quality`.

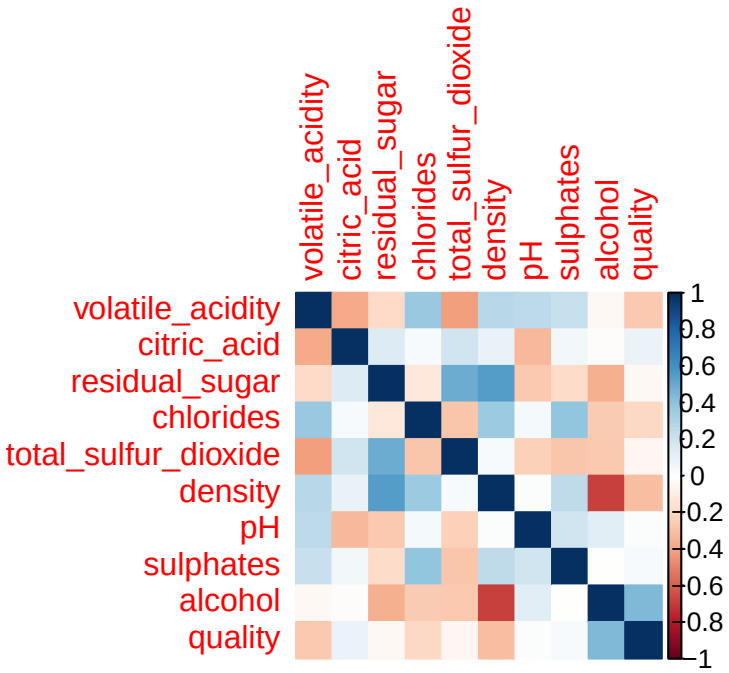
2.3 (5 points)

Visualize the correlation matrix of all numeric columns in `df` using `corrplot()`

```
library(corrplot)
```

```
corrplot 0.92 loaded
```

```
numeric_cols <- df %>%
  select_if(is.numeric)

corr <- cor(numeric_cols)

corrplot(corr, method = "color")
```



2.4 (5 points)

Compute the variance inflation factor (VIF) for each predictor in the full model using `vif()` function. What can we conclude from this?

```
library(car)

model <- lm(quality ~ ., data = df)
vif(model)
```

```
  volatile_acidity          citric_acid       residual_sugar
          2.103853             1.549248             4.680035
        chlorides total_sulfur_dioxide              density
          1.625065             2.628534             9.339357
               pH            sulphates              alcohol
          1.352005             1.522809             3.419849
             type
          6.694679
```

From the output, we can conclude that there is some degree of multicollinearity between some of the predictors in the model. Predictors with VIF values greater than 5, are highly correlated with other predictors, suggesting that their coefficients may be difficult to interpret.

Question 3

40 points

Variable selection

3.1 (5 points)

Run a backward stepwise regression using a `full_model` object as the starting model. Store the final formula in an object called `backward_formula` using the built-in `formula()` function in R

```
full_model <- lm(quality ~ ., data = df)
backward_formula <- step(full_model, direction = "backward", scope = formula(full_model))
```

```
Start:  AIC=-3953.43
quality ~ volatile_acidity + citric_acid + residual_sugar + chlorides +
    total_sulfur_dioxide + density + pH + sulphates + alcohol +
    type

                      Df Sum of Sq    RSS     AIC
- citric_acid          1     0.066 3523.6 -3955.3
- total_sulfur_dioxide 1     0.854 3524.4 -3953.9
<none>                             3523.5 -3953.4
- pH                   1     4.413 3527.9 -3947.3
- chlorides            1     4.559 3528.1 -3947.0
- density              1    19.054 3542.6 -3920.4
- type                 1    26.794 3550.3 -3906.2
- sulphates            1    41.399 3564.9 -3879.5
- residual_sugar       1    63.881 3587.4 -3838.7
- alcohol              1   206.860 3730.4 -3584.8
- volatile_acidity     1   216.549 3740.0 -3567.9
```

```
Step:  AIC=-3955.3
quality ~ volatile_acidity + residual_sugar + chlorides + total_sulfur_dioxide +
    density + pH + sulphates + alcohol + type

                       Df Sum of Sq    RSS     AIC
- total_sulfur_dioxide  1     0.818 3524.4 -3955.8
<none>                              3523.6 -3955.3
- chlorides             1     4.495 3528.1 -3949.0
- pH                    1     4.536 3528.1 -3948.9
- density               1    20.794 3544.4 -3919.1
- type                  1    26.943 3550.5 -3907.8
- sulphates             1    41.491 3565.1 -3881.2
- residual_sugar        1    67.371 3590.9 -3834.3
- alcohol               1   235.151 3758.7 -3537.6
- volatile_acidity      1   252.565 3776.1 -3507.5

Step:  AIC=-3955.8
quality ~ volatile_acidity + residual_sugar + chlorides + density +
    pH + sulphates + alcohol + type

                   Df Sum of Sq    RSS     AIC
<none>                          3524.4 -3955.8
- pH                1     4.295 3528.7 -3949.9
- chlorides         1     4.523 3528.9 -3949.5
- density           1    21.540 3545.9 -3918.2
- sulphates         1    40.711 3565.1 -3883.2
- type              1    43.664 3568.0 -3877.8
- residual_sugar    1    66.572 3591.0 -3836.2
- alcohol           1   244.545 3768.9 -3521.9
- volatile_acidity  1   256.695 3781.1 -3501.0
```

3.2 (5 points)

Run a forward stepwise regression using a `null_model` object as the starting model. Store the final formula in an object called `forward_formula` using the built-in `formula()` function in R

```r
null_model <- lm(quality ~ 1, df)
forward_formula <- step(null_model, direction = "forward", scope = formula(full_model))
```

```
Start:  AIC=-1760.04
quality ~ 1

                      Df Sum of Sq    RSS     AIC
+ alcohol              1    977.95 3975.7 -3186.9
+ density              1    463.41 4490.3 -2396.2
+ volatile_acidity     1    349.71 4604.0 -2233.7
+ chlorides            1    199.47 4754.2 -2025.1
+ type                 1     70.53 4883.2 -1851.2
+ citric_acid          1     36.24 4917.4 -1805.7
+ total_sulfur_dioxide 1      8.48 4945.2 -1769.2
+ sulphates            1      7.34 4946.3 -1767.7
+ residual_sugar       1      6.77 4946.9 -1766.9
+ pH                   1      1.88 4951.8 -1760.5
<none>                             4953.7 -1760.0

Step:  AIC=-3186.88
quality ~ alcohol

                      Df Sum of Sq    RSS     AIC
+ volatile_acidity     1   307.508 3668.2 -3707.9
+ residual_sugar       1    85.662 3890.1 -3326.4
+ type                 1    54.335 3921.4 -3274.3
+ citric_acid          1    40.303 3935.4 -3251.1
+ chlorides            1    39.696 3936.0 -3250.1
+ total_sulfur_dioxide 1    31.346 3944.4 -3236.3
+ sulphates            1     7.859 3967.9 -3197.7
+ pH                   1     5.938 3969.8 -3194.6
<none>                             3975.7 -3186.9
+ density              1     0.005 3975.7 -3184.9

Step:  AIC=-3707.89
quality ~ alcohol + volatile_acidity

                      Df Sum of Sq    RSS     AIC
+ sulphates            1    48.259 3620.0 -3791.9
+ density              1    38.704 3629.5 -3774.8
+ residual_sugar       1    29.751 3638.5 -3758.8
+ type                 1    28.895 3639.3 -3757.3
+ total_sulfur_dioxide 1     5.619 3662.6 -3715.9
+ pH                   1     5.533 3662.7 -3715.7
<none>                             3668.2 -3707.9
+ chlorides            1     0.162 3668.1 -3706.2
```

```
+ citric_acid           1     0.099 3668.1 -3706.1

Step:  AIC=-3791.94
quality ~ alcohol + volatile_acidity + sulphates

                      Df Sum of Sq    RSS     AIC
+ residual_sugar       1    43.989 3576.0 -3869.4
+ density              1    18.661 3601.3 -3823.5
+ type                 1     6.012 3614.0 -3800.7
+ chlorides            1     4.988 3615.0 -3798.9
+ citric_acid          1     2.031 3617.9 -3793.6
+ pH                   1     1.903 3618.1 -3793.4
<none>                             3620.0 -3791.9
+ total_sulfur_dioxide 1     0.817 3619.2 -3791.4

Step:  AIC=-3869.37
quality ~ alcohol + volatile_acidity + sulphates + residual_sugar

                      Df Sum of Sq    RSS     AIC
+ type                 1   20.7581 3555.2 -3905.2
+ total_sulfur_dioxide 1   13.3542 3562.6 -3891.7
+ pH                   1    6.6430 3569.3 -3879.5
+ citric_acid          1    4.3384 3571.6 -3875.3
+ chlorides            1    1.8907 3574.1 -3870.8
<none>                             3576.0 -3869.4
+ density              1    0.0071 3576.0 -3867.4

Step:  AIC=-3905.19
quality ~ alcohol + volatile_acidity + sulphates + residual_sugar +
    type

                      Df Sum of Sq    RSS     AIC
+ density              1   20.4623 3534.8 -3940.7
+ chlorides            1    6.6602 3548.6 -3915.4
+ citric_acid          1    5.2242 3550.0 -3912.7
+ pH                   1    3.9477 3551.3 -3910.4
+ total_sulfur_dioxide 1    1.2539 3554.0 -3905.5
<none>                             3555.2 -3905.2

Step:  AIC=-3940.7
quality ~ alcohol + volatile_acidity + sulphates + residual_sugar +
    type + density
```

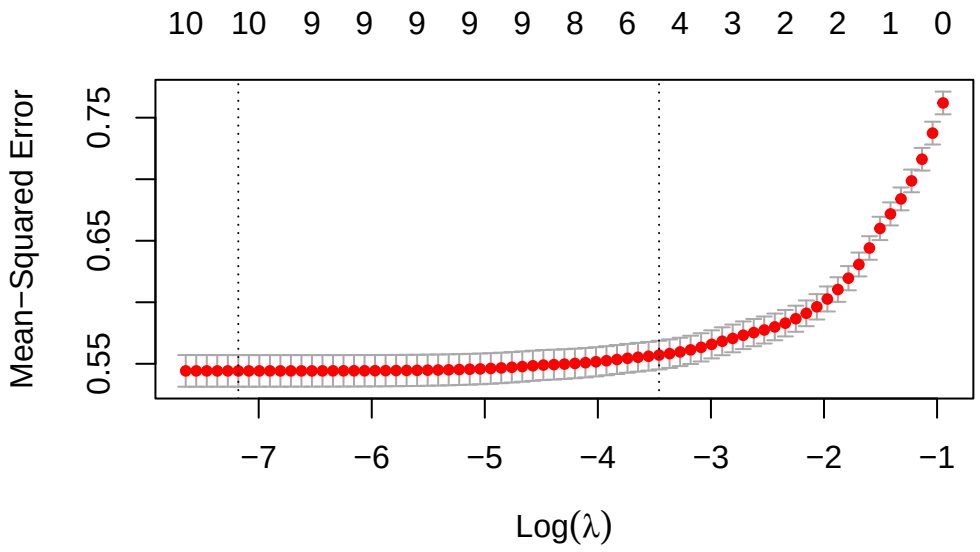
```
                       Df Sum of Sq    RSS     AIC
+ chlorides             1    6.0826 3528.7 -3949.9
+ pH                    1    5.8541 3528.9 -3949.5
<none>                              3534.8 -3940.7
+ citric_acid           1    0.8471 3533.9 -3940.3
+ total_sulfur_dioxide  1    0.5646 3534.2 -3939.7

Step:  AIC=-3949.89
quality ~ alcohol + volatile_acidity + sulphates + residual_sugar +
    type + density + chlorides

                       Df Sum of Sq    RSS     AIC
+ pH                    1    4.2945 3524.4 -3955.8
<none>                              3528.7 -3949.9
+ total_sulfur_dioxide  1    0.5765 3528.1 -3948.9
+ citric_acid           1    0.2338 3528.4 -3948.3

Step:  AIC=-3955.8
quality ~ alcohol + volatile_acidity + sulphates + residual_sugar +
    type + density + chlorides + pH

                       Df Sum of Sq    RSS     AIC
<none>                              3524.4 -3955.8
+ total_sulfur_dioxide  1   0.81762 3523.6 -3955.3
+ citric_acid           1   0.02919 3524.4 -3953.9
```

3.3 (10 points)

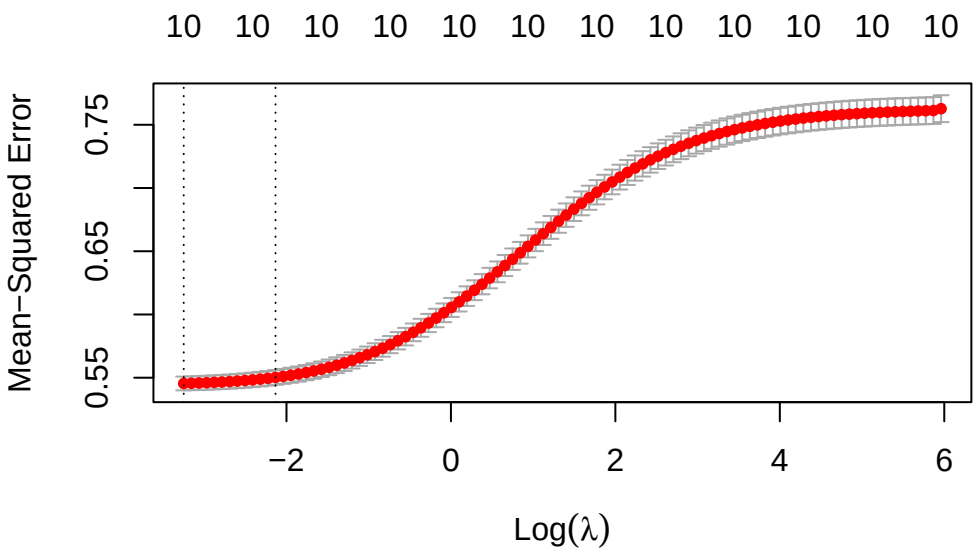
1. Create a `y` vector that contains the response variable (`quality`) from the `df` dataframe.
2. Create a design matrix `X` for the `full_model` object using the `make_model_matrix()` function provided in the Appendix.
3. Then, use the `cv.glmnet()` function to perform LASSO and Ridge regression with `X` and `y`.

```
#making y vector
y <- df$quality

#creating a design matrix
make_model_matrix <- function(formula){
```

```
  X <- model.matrix(full_model, df)[, -1]
  cnames <- colnames(X)
  for(i in 1:ncol(X)){
    if(!cnames[i] == "typeWhite"){
      X[, i] <- scale(X[, i])
    } else {
      colnames(X)[i] <- "type"
    }
  }
  return(X)
}

#lasso regression and plot
lasso <- cv.glmnet(x = make_model_matrix(forward_formula), y, alpha = 1)
plot(lasso)
```

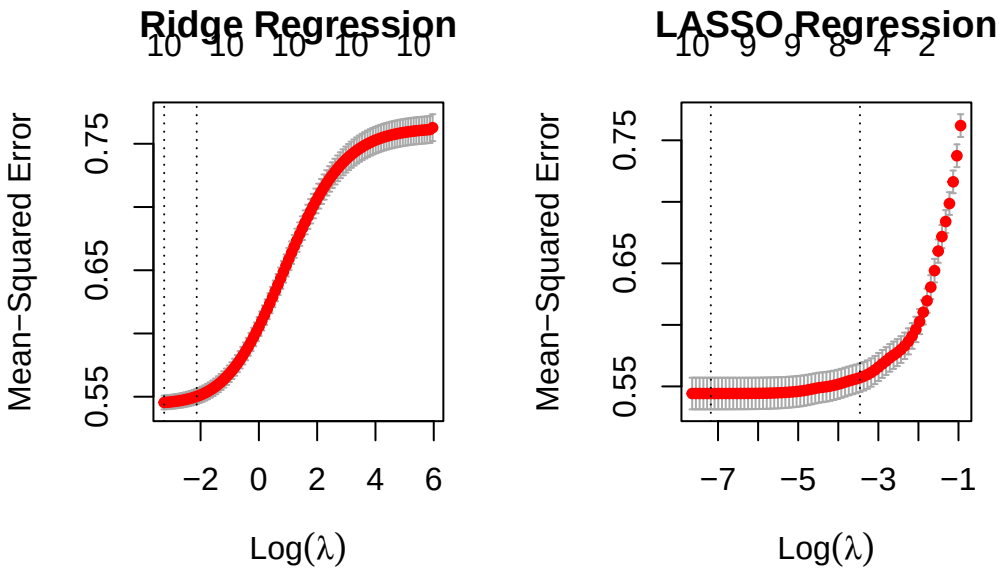



```
#ridge regression and plot
ridge <- cv.glmnet(x = make_model_matrix(forward_formula), y, alpha = 0, nfolds = 5)
plot(ridge)
```



Create side-by-side plots of the ridge and LASSO regression results. Interpret your main findings.

```
#combining plots for both regressions
par(mfrow=c(1, 2))
plot(ridge, pch = 20, main = "Ridge Regression")
plot(lasso, pch = 20, main = "LASSO Regression")
```



We can see from the graphs that the x-axis represents the λ values and the y -axis displays the $mean - squarederror$ for the predictor variables. We can see that as the value of λ increases the model becomes more regularized giving simpler coefficients and simpler models.

3.4 (5 points)

Print the coefficient values for LASSO regression at the `lambda.1se` value? What are the variables selected by LASSO?

```
lasso_coef <- coef(lasso, s = "lambda.1se")
lasso_coef
```

```
11 x 1 sparse Matrix of class "dgCMatrix"
                              s1
(Intercept)           5.81837771
volatile_acidity     -0.19128674
citric_acid           .
residual_sugar        0.03943232
chlorides             .
```

```
total_sulfur_dioxide  .
density               .
pH                    .
sulphates             0.05379620
alcohol               0.36366674
type                  .
```

> The variables selected by the LASSO regression are `volatile_acidity`, `residual_sugar`, `chlorides`, `total_sulfur_dioxide`, `pH`, `sulphates`, `alcohol` and `type`

Store the variable names with non-zero coefficients in `lasso_vars`, and create a formula object called `lasso_formula` using the `make_formula()` function provided in the Appendix.

```
lasso_vars <- rownames(lasso_coef)[which(abs(lasso_coef) > 0)][-1]

make_formula <- function(x){
  as.formula(
    paste("quality ~ ", paste(x, collapse = " + "))
  )
}

lasso_formula <- make_formula(lasso_vars)
lasso_formula
```

```
quality ~ volatile_acidity + residual_sugar + sulphates + alcohol
<environment: 0x7fbaee845cf0>
```

3.5 (5 points)

Print the coefficient values for ridge regression at the `lambda.1se` value? What are the variables selected here?

```
ridge_coef <- coef(ridge, s = "lambda.1se")
ridge_coef
```

```
11 x 1 sparse Matrix of class "dgCMatrix"
                              s1
(Intercept)           5.91356141
```

```
volatile_acidity     -0.20112449
citric_acid           0.01438054
residual_sugar        0.12458389
chlorides            -0.04300238
total_sulfur_dioxide -0.03952269
density              -0.09301822
pH                    0.02651557
sulphates             0.08894679
alcohol               0.29829971
type                 -0.12625734
```

Store the variable names with non-zero coefficients in `ridge_vars`, and create a formula object called `ridge_formula` using the `make_formula()` function provided in the Appendix.

```
ridge_vars <- rownames(ridge_coef)[which(abs(ridge_coef) > 0)][-1]
ridge_formula <- make_formula(ridge_vars)

ridge_formula
```

```
quality ~ volatile_acidity + citric_acid + residual_sugar + chlorides +
    total_sulfur_dioxide + density + pH + sulphates + alcohol +
    type
<environment: 0x7fbb0b1d5fe0>
```

3.6 (10 points)

What is the difference between stepwise selection, LASSO and ridge based on you analyses above?

> Based on the analyses above, we can see that stepwise selection resulted in a model with eight predictors, while LASSO and ridge regression selected different sets of predictors. The LASSO model had a four non-zero coefficients, while the ridge model had non-zero coefficients for ten predictors, but they were smaller in magnitude than the coefficients in the full model.

—

Question 4

70 points

Variable selection

4.1 (5 points)

Excluding `quality` from `df` we have 10 possible predictors as the covariates. How many different models can we create using any subset of these 10 covariates as possible predictors? Justify your answer.

> There are $2^{10} = 1024$ different possible models that can be created using any subset of the 10 covariates as possible predictors. This is because for each of the models, we can either include or exclude them from the model.

4.2 (20 points)

Store the names of the predictor variables (all columns except `quality`) in an object called `x_vars`.

```
x_vars <- colnames(df %>% select(-quality))
```

Use:

- the `combn()` function (built-in R function) and
- the `make_formula()` (provided in the Appendix)

to **generate all possible linear regression formulas** using the variables in `x_vars`. This is most optimally achieved using the `map()` function from the `purrr` package.

```
formulas <- map(
  1:length(x_vars),
  function(x){
    vars <- combn(x_vars, x, simplify = FALSE)
    map(vars, make_formula)
  }
) %>% unlist()
```

If your code is right the following command should return something along the lines of:

```
sample(formulas, 4) %>% as.character()
```

```
[1] "quality ~ volatile_acidity + citric_acid + residual_sugar + pH + sulphates"
[2] "quality ~ citric_acid + residual_sugar + total_sulfur_dioxide + pH + alcohol + type"
[3] "quality ~ chlorides + sulphates + alcohol"
[4] "quality ~ citric_acid + density + pH + sulphates"
```

```
# Output:
# [1] "quality ~ volatile_acidity + residual_sugar + density + pH + alcohol"
# [2] "quality ~ citric_acid"
# [3] "quality ~ volatile_acidity + citric_acid + residual_sugar + total_sulfur_dioxide +
# [4] "quality ~ citric_acid + chlorides + total_sulfur_dioxide + pH + alcohol + type"
```

4.3 (10 points)

Use `map()` and `lm()` to fit a linear regression model to each formula in `formulas`, using `df` as the data source. Use `broom::glance()` to extract the model summary statistics, and bind them together into a single tibble of summaries using the `bind_rows()` function from `dplyr`.

```
models <- map(formulas, ~lm(.x, data = df))
summaries <- map(models, broom::glance) %>%
  bind_rows()
summaries
```

```
# A tibble: 1,023 x 12
   r.squared adj.r.~1 sigma stati~2   p.value    df logLik    AIC    BIC devia~3
       <dbl>    <dbl> <dbl>   <dbl>     <dbl> <dbl>  <dbl>  <dbl>  <dbl>   <dbl>
 1  0.0706   0.0705   0.842  493.   2.06e-105     1 -8100. 16206. 16226.   4604.
 2  0.00732  0.00716  0.870   47.9  5.00e- 12     1 -8314. 16634. 16654.   4917.
 3  0.00137  0.00121  0.873    8.89 2.87e-  3     1 -8333. 16673. 16693.   4947.
 4  0.0403   0.0401   0.856  273.   5.32e- 60     1 -8204. 16415. 16435.   4754.
 5  0.00171  0.00156  0.873   11.1  8.48e-  4     1 -8332. 16671. 16691.   4945.
 6  0.0935   0.0934   0.831  670.   9.66e-141     1 -8019. 16044. 16064.   4490.
 7  0.000380 0.000227 0.873    2.47 1.16e-  1     1 -8337. 16679. 16700.   4952.
 8  0.00148  0.00133  0.873    9.63 1.92e-  3     1 -8333. 16672. 16692.   4946.
 9  0.197    0.197    0.782 1598.   1.50e-312     1 -7623. 15253. 15273.   3976.
10  0.0142   0.0141   0.867   93.8  4.89e- 22     1 -8291. 16588. 16609.   4883.
# ... with 1,013 more rows, 2 more variables: df.residual <int>, nobs <int>,
#   and abbreviated variable names 1: adj.r.squared, 2: statistic, 3: deviance
```

4.4 (5 points)

Extract the `adj.r.squared` values from `summaries` and use them to identify the formula with the ***highest*** adjusted R-squared value.

```
#Extracting the adj.r.squared values
adj_r_squared <- summaries$adj.r.squared

#Formula to identify the highest adjusted R-squared value
max_rsq_index <- which.max(adj_r_squared)
```

Store resulting formula as a variable called `rsq_formula`.

```
rsq_formula <- formulas[which.max(adj_r_squared)]
rsq_formula
```

```
[[1]]
quality ~ volatile_acidity + residual_sugar + chlorides + total_sulfur_dioxide +
    density + pH + sulphates + alcohol + type
<environment: 0x7fbaf1420440>
```

4.5 (5 points)

Extract the `AIC` values from `summaries` and use them to identify the formula with the ***lowest*** AIC value.

```
#Extracting the AIC values from summaries
aic_values <- summaries$AIC

#Finding the index of the formula with lowest AIC
min_aic_index <- which.min(aic_values)
```

Store resulting formula as a variable called `aic_formula`.

```
aic_formula <- formulas[min_aic_index]
aic_formula
```

```
[[1]]
quality ~ volatile_acidity + residual_sugar + chlorides + density +
    pH + sulphates + alcohol + type
<environment: 0x7fbaf14624e8>
```

4.6 (15 points)

Combine all formulas shortlisted into a single vector called `final_formulas`.

```
null_formula <- formula(null_model)
full_formula <- formula(full_model)

final_formulas <- c(
  null_formula,
  full_formula,
  backward_formula,
  forward_formula,
  lasso_formula,
  ridge_formula,
  rsq_formula,
  aic_formula
)
```

- Are `aic_formula` and `rsq_formula` the same? How do they differ from the formulas shortlisted in question 3?

  > The **`aic_formula`** and **`rsq_formula`** are not the same, as they are based on different criteria for model selection. **`rsq_formula`** was selected based on the highest adjusted R-squared value, while **`aic_formula`** was selected based on the lowest AIC value. The formulas shortlisted in question 3 were obtained by exhaustively searching through all possible subsets of the predictor variables, while the other methods (null, full, backward, forward, LASSO, and Ridge regression) used different algorithms to select a subset of variables based on certain criteria.

- Which of these is more reliable? Why?

  > In terms of which method is more reliable `rsq_formula`. With a large dataset `rsq` is going to have a higher predictive power than the AIC model.

- If we had a dataset with $10,000$ columns, which of these methods would you consider for your analyses? Why?

If we had a dataset with 10,000 columns, exhaustive search through all possible models would be computationally indefeasible. In this case, LASSO option would be better because it can handle high-dimensional datasets and automatically shrink the coefficients of irrelevant predictors towards zero. Also, LASSO is preferred over Ridge, because it has feature selection.

4.7 (10 points)

Use `map()` and `glance()` to extract the `sigma, adj.r.squared, AIC, df`, and `p.value` statistics for each model obtained from `final_formulas`. Bind them together into a single data frame `summary_table`. Summarize your main findings.

```
summary_table <- map(
  final_formulas, ~ lm(.x, data = df) %>%
    broom::glance() %>%
    select(sigma, adj.r.squared, AIC, df, p.value)
) %>% bind_rows()

summary_table %>% knitr::kable()
```

We can see that all the models have extremely significant p-values. The p-values were so small that they were nearing zero. We can also see that a couple of the methods came up with the same model. Backward, forward, and AIC methods all came up with the same model, while the ridge method was the same as the full model. We can also see that besides the null model, all the sigma values, adjusted r-squared values, and AIC values were extremely close for all the models.

Appendix

Convenience function for creating a formula object

The following function which takes as input a vector of column names `x` and outputs a `formula` object with `quality` as the response variable and the columns of `x` as the covariates.

```
make_formula <- function(x){
  as.formula(
    paste("quality ~ ", paste(x, collapse = " + "))
  )
}

# For example the following code will
# result in a formula object
# "quality ~ a + b + c"
make_formula(c("a", "b", "c"))
```

```
quality ~ a + b + c
<environment: 0x7fbb0d8cdaf8>
```

Convenience function for `glmnet`

The `make_model_matrix` function below takes a `formula` as input and outputs a rescaled model matrix `X` in a format amenable for `glmnet()`

```
make_model_matrix <- function(formula){
  X <- model.matrix(formula, df)[, -1]
  cnames <- colnames(X)
  for(i in 1:ncol(X)){
    if(!cnames[i] == "typewhite"){
      X[, i] <- scale(X[, i])
    } else {
      colnames(X)[i] <- "type"
    }
  }
  return(X)
}
```

Session Information

Print your R session information using the following command

```
sessionInfo()
```

```
R version 4.2.2 (2022-10-31)
Platform: x86_64-apple-darwin17.0 (64-bit)
Running under: macOS Big Sur ... 10.16

Matrix products: default
BLAS:   /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRlapack.dylib

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

attached base packages:
[1] stats     graphics  grDevices datasets  utils     methods   base

other attached packages:
 [1] corrplot_0.92 broom_1.0.3   glmnet_4.1-6  Matrix_1.5-1  car_3.1-1
 [6] carData_3.0-5 purrr_1.0.1   dplyr_1.1.0   tidyr_1.3.0   readr_2.1.4

loaded via a namespace (and not attached):
 [1] Rcpp_1.0.10      pillar_1.8.1     compiler_4.2.2   iterators_1.0.14
 [5] tools_4.2.2      digest_0.6.31    jsonlite_1.8.4   evaluate_0.20
 [9] lifecycle_1.0.3  tibble_3.1.8     lattice_0.20-45  pkgconfig_2.0.3
[13] rlang_1.0.6      foreach_1.5.2    cli_3.6.0        rstudioapi_0.14
[17] yaml_2.3.7       xfun_0.37        fastmap_1.1.0    withr_2.5.0
[21] knitr_1.42       generics_0.1.3   vctrs_0.5.2      hms_1.1.2
[25] grid_4.2.2       tidyselect_1.2.0 glue_1.6.2       R6_2.5.1
[29] fansi_1.0.4      survival_3.4-0   rmarkdown_2.20   tzdb_0.3.0
[33] magrittr_2.0.3   backports_1.4.1  splines_4.2.2    codetools_0.2-18
[37] ellipsis_0.3.2   htmltools_0.5.4  abind_1.4-5      shape_1.4.6
[41] renv_0.16.0-53   utf8_1.2.3
```