HW4

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Question 1

```
if(!require("pacman")) install.packages("pacman")
## Loading required package: pacman
p_load(MASS, pls, mctest, glmnet, knitr, kableExtra)
fit <- lm(medv ~ crim + zn + indus + nox + rm + age + tax, Boston)</pre>
sumsq <- anova(fit)$"Sum Sq"</pre>
VIF <- (1 - sumsq[-length(sumsq)] / sum(sumsq))^(-1)</pre>
VIF
## [1] 1.177552 1.090760 1.063519 1.000671 1.381436 1.001737 1.009707
mean(VIF)
## [1] 1.103626
omcdiag(Boston[, -14], Boston[, 14])
##
## Call:
## omcdiag(x = Boston[, -14], y = Boston[, 14])
##
##
## Overall Multicollinearity Diagnostics
##
                           MC Results detection
##
## Determinant |X'X|:
                               0.0001
                                              1
## Farrar Chi-Square:
                            4486.4729
                                              1
## Red Indicator:
                               0.4432
                                               0
## Sum of Lambda Inverse:
                              45.1229
                                               0
## Theil's Method:
                                               0
                              -1.2643
## Condition Number:
                              87.3183
                                               1
##
## 1 --> COLLINEARITY is detected by the test
## 0 --> COLLINEARITY is not detected by the test
```

Since VIF < 10, there is no multicollinearity. But we have VIF bar is larger than 1, so there is little multicollinearity.

From the diagnostics, we could see that condition number method showing there is collinearity while some other methods do not. So we can conclude that there exists little but not serious multicollinearity.

Remedial measures: we could use ridge regression or we can use PCR to avoid multicollinearity.

Question 2

```
variables <- c("crim", "zn", "indus", "nox", "rm", "age", "tax")
varmatrix <- as.matrix(Boston[variables])
depmatrix <- as.matrix(Boston["medv"])
summary(fit)</pre>
```

```
##
## Call:
## lm(formula = medv ~ crim + zn + indus + nox + rm + age + tax,
##
      data = Boston)
##
## Residuals:
##
     Min
             1Q Median
                           3Q
                                 Max
## -16.625 -3.161 -0.833
                        2.089 41.042
##
## Coefficients:
              Estimate Std. Error t value Pr(>|t|)
##
## (Intercept) -19.615259 3.221482 -6.089 2.27e-09 ***
             ## crim
## zn
              -0.014980 0.072282 -0.207 0.835909
## indus
              0.010643
## nox
                       4.230468 0.003 0.997994
              7.606508   0.418424   18.179   < 2e-16 ***
## rm
             ## age
## tax
             -0.009006
                       0.002662 -3.384 0.000772 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 5.989 on 498 degrees of freedom
## Multiple R-squared: 0.5818, Adjusted R-squared: 0.576
## F-statistic: 98.99 on 7 and 498 DF, p-value: < 2.2e-16
```

```
pred_linear <- predict(fit, newx=varmatrix)
mse_linear <- mean((depmatrix - pred_linear) ^ 2)
mse_linear</pre>
```

```
## [1] 35.30022
```

```
fit_pcr <- pcr(medv ~ crim + zn + indus + nox + rm + age + tax, data = Boston)
summary(fit_pcr)</pre>
```

```
## Data:
                    X dimension: 506 7
## Y dimension: 506 1
## Fit method: svdpc
## Number of components considered: 7
## TRAINING: % variance explained
##
                1 \hspace{0.1cm} \text{comps} \hspace{0.1cm} 2 \hspace{0.1cm} \text{comps} \hspace{0.1cm} 3 \hspace{0.1cm} \text{comps} \hspace{0.1cm} 4 \hspace{0.1cm} \text{comps} \hspace{0.1cm} 5 \hspace{0.1cm} \text{comps} \hspace{0.1cm} 6 \hspace{0.1cm} \text{comps} \hspace{0.1cm} 7 \hspace{0.1cm} \text{comps}
## X
                   96.17
                                   98.89
                                                   99.78
                                                                   99.95
                                                                               100.00
                                                                                                 100.00
                                                                                                                  100.00
## medv
                   22.29
                                   26.77
                                                   27.40
                                                                   29.06
                                                                                   30.52
                                                                                                   58.18
                                                                                                                   58.18
```

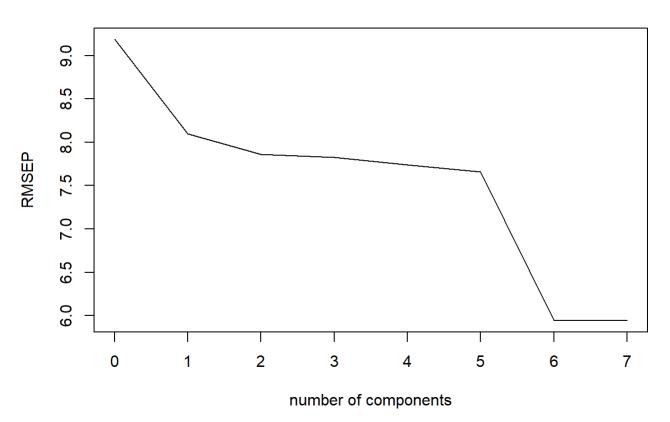
fit_pcr\$coefficients

```
## , , 1 comps
##
##
                 medv
## crim -7.602935e-04
## zn
         1.150884e-03
## indus -7.542334e-04
## nox
       -1.184132e-05
## rm
         3.133808e-05
## age
       -2.213204e-03
        -2.547918e-02
## tax
##
## , , 2 comps
##
##
                 medv
## crim -0.0016853343
## zn
         0.0446402402
## indus -0.0068021172
## nox
       -0.0001366212
         0.0003397777
## rm
        -0.0540646790
## age
## tax
        -0.0188037200
##
## , , 3 comps
##
##
                 medv
## crim -0.0004213788
         0.0788779816
## zn
## indus -0.0073933769
## nox
       -0.0001059403
## rm
         0.0006096457
## age
        -0.0254242782
## tax
        -0.0197649097
##
## , , 4 comps
##
##
                 medv
## crim -1.700791e-01
## zn
         8.153525e-02
## indus 2.692739e-03
## nox
        -8.996815e-05
## rm
         1.489102e-03
        -2.076327e-02
## age
        -1.528469e-02
## tax
##
## , , 5 comps
##
##
                 medv
## crim -0.186159901
## zn
         0.062658498
## indus -0.274628965
## nox
        -0.001638117
## rm
         0.011031329
## age
        -0.003089130
```

```
## tax
         -0.008971014
##
##
   , , 6 comps
##
##
                 medv
        -0.132536071
## crim
## zn
          0.022100922
## indus -0.014931710
          0.002233208
## nox
## rm
          7.606510824
         -0.023185138
## age
         -0.009004800
## tax
##
##
   , , 7 comps
##
##
                 medv
## crim -0.132538486
## zn
          0.022103317
## indus -0.014979611
## nox
          0.010642684
## rm
          7.606508171
         -0.023197907
## age
         -0.009006005
## tax
```

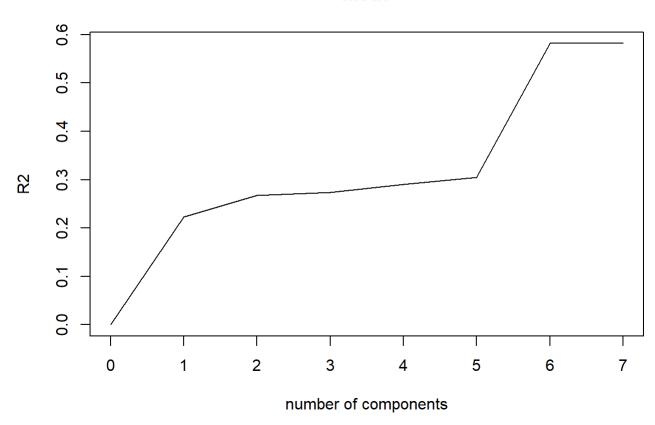
validationplot(fit_pcr)

medv



validationplot(fit_pcr, "R2")





```
pred_pcr5 <- predict(fit_pcr, ncomp=5, newx=varmatrix)
mse_pcr5 <- mean((depmatrix - as.numeric(pred_pcr5)) ^ 2)
mse_pcr5</pre>
```

```
## [1] 58.65863
```

```
pred_pcr6 <- predict(fit_pcr, ncomp=6, newx=varmatrix)
mse_pcr6 <- mean((depmatrix - as.numeric(pred_pcr6)) ^ 2)
mse_pcr6</pre>
```

```
## [1] 35.30022
```

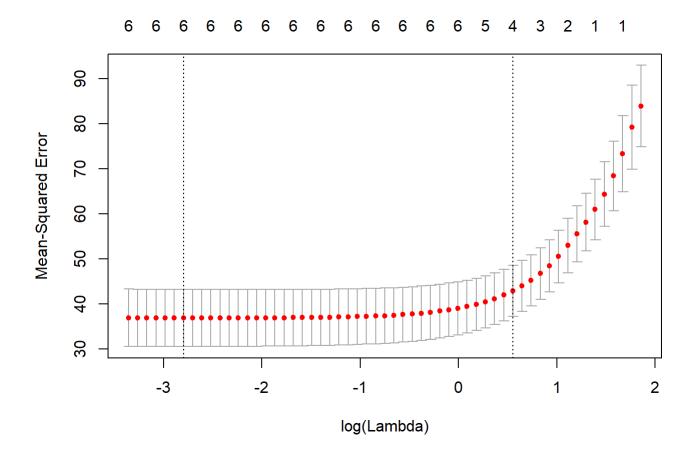
```
pred_pcr7 <- predict(fit_pcr, ncomp=7, newx=varmatrix)
mse_pcr7 <- mean((depmatrix - as.numeric(pred_pcr7)) ^ 2)
mse_pcr7</pre>
```

```
## [1] 35.30022
```

From these two methods, we could see that when PCR has 6 or more comp, it will have the same M SE as the linear regression.

Question 3

fit_lasso <- cv.glmnet(varmatrix, depmatrix)
plot(fit_lasso)</pre>



lambda <- fit_lasso\$lambda.min
lambda</pre>

[1] 0.06098586

coef <- coef(fit_lasso, "lambda.min")
coef</pre>

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```
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## 8 x 1 sparse Matrix of class "dgCMatrix"
##
## (Intercept) -19.346619579
## crim
                -0.128613180
## zn
                 0.020751561
## indus
                -0.016321199
## nox
## rm
                 7.552663663
## age
                 -0.022484475
                 -0.008901037
## tax
pred_lasso <- predict(fit_lasso, newx=varmatrix, s="lambda.min")</pre>
mse lasso <- mean((depmatrix - pred lasso) ^ 2)</pre>
mse lasso
## [1] 35.3082
fit_forward <- lm(medv ~ 1, data=Boston)</pre>
fit backward <- lm(medv ~ crim + zn + indus + nox + rm +age + tax, data=Boston)
forward <- stepAIC(fit_forward, direction="forward", scope=list(upper=fit_backward, lower=fit_fo
rward), trace=F)
forward
##
## lm(formula = medv ~ rm + tax + crim + age + zn, data = Boston)
##
## Coefficients:
```

```
## (Intercept)
                          rm
                                      tax
                                                   crim
                                                                  age
                                              -0.131852
##
   -19.713176
                    7.625253
                                -0.009323
                                                            -0.024121
##
##
      0.022947
```

```
backward <- stepAIC(fit backward, direction="backward", scope=list(upper=fit backward, lower=fit
_forward), trace=F)
backward
```

```
##
## lm(formula = medv ~ crim + zn + rm + age + tax, data = Boston)
##
## Coefficients:
## (Intercept)
                       crim
                                       zn
                                                                age
##
   -19.713176
                  -0.131852
                                0.022947
                                              7.625253
                                                          -0.024121
##
           tax
##
     -0.009323
```

```
pred_forward <- predict(forward, newx=varmatrix)
mse_forward <- mean((depmatrix - pred_forward) ^ 2)
mse_forward</pre>
```

```
## [1] 35.30361
```

```
pred_backward <- predict(backward, newx=varmatrix)
mse_backward <- mean((depmatrix - pred_backward) ^ 2)
mse_backward</pre>
```

```
## [1] 35.30361
```

From these two methods, we could see that their MSE are very close, so their performance of pr edicting are pretty much the same. But since stepwise procedure used less variables, it is bette r since Lasso used more variables and might lead to overfitting.

Table

Table

	OLS	Ridge	Lasso	Elastic Net
Performance n>>p	3	2	2	1
Performance Multicollinearity	3	2	2	1
Unbiased Estimators	1	3	3	3
Model Selection	2	3	1	2
Simplicity	1	2	1	3

Performance n>>p

Performance Multicollinearity

Unibased Estimators

Model Selection

Simplicity