final test

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```
set.seed(1)
library("ISLR")
```

```
## Warning: package 'ISLR' was built under R version 4.0.5
```

```
data("swiss")
attach(swiss)
head(swiss)
```

```
##              Fertility Agriculture Examination Education Catholic
## Courtelary        80.2        17.0          15        12     9.96
## Delemont          83.1        45.1           6         9    84.84
## Franches-Mnt      92.5        39.7           5         5    93.40
## Moutier           85.8        36.5          12         7    33.77
## Neuveville        76.9        43.5          17        15     5.16
## Porrentruy        76.1        35.3           9         7    90.57
##              Infant.Mortality
## Courtelary               22.2
## Delemont                 22.2
## Franches-Mnt             20.2
## Moutier                  20.3
## Neuveville               20.6
## Porrentruy               26.6
```

a)

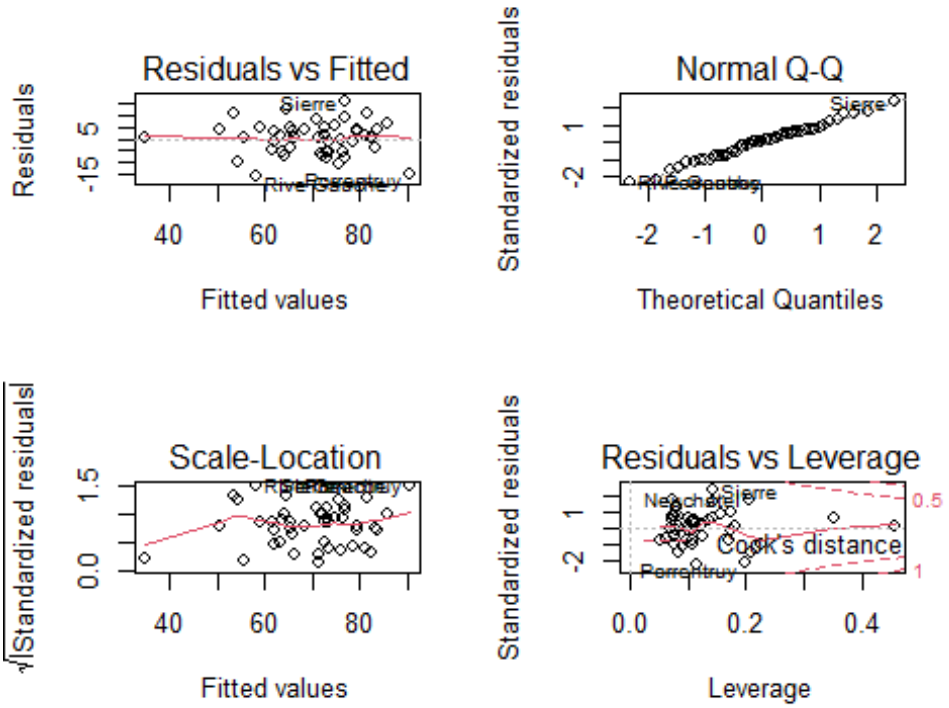
for make Full model and plot we have:

```
fit<-lm(Fertility~. , data=swiss)
summary(fit)
```

```
##
## Call:
## lm(formula = Fertility ~ ., data = swiss)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -15.2743  -5.2617   0.5032   4.1198  15.3213
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)      66.91518   10.70604   6.250 1.91e-07 ***
```

```
## Agriculture      -0.17211    0.07030  -2.448  0.01873 *
## Examination      -0.25801    0.25388  -1.016  0.31546
## Education        -0.87094    0.18303  -4.758 2.43e-05 ***
## Catholic          0.10412    0.03526   2.953  0.00519 **
## Infant.Mortality  1.07705    0.38172   2.822  0.00734 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.165 on 41 degrees of freedom
## Multiple R-squared:  0.7067, Adjusted R-squared:  0.671
## F-statistic: 19.76 on 5 and 41 DF,  p-value: 5.594e-10
```

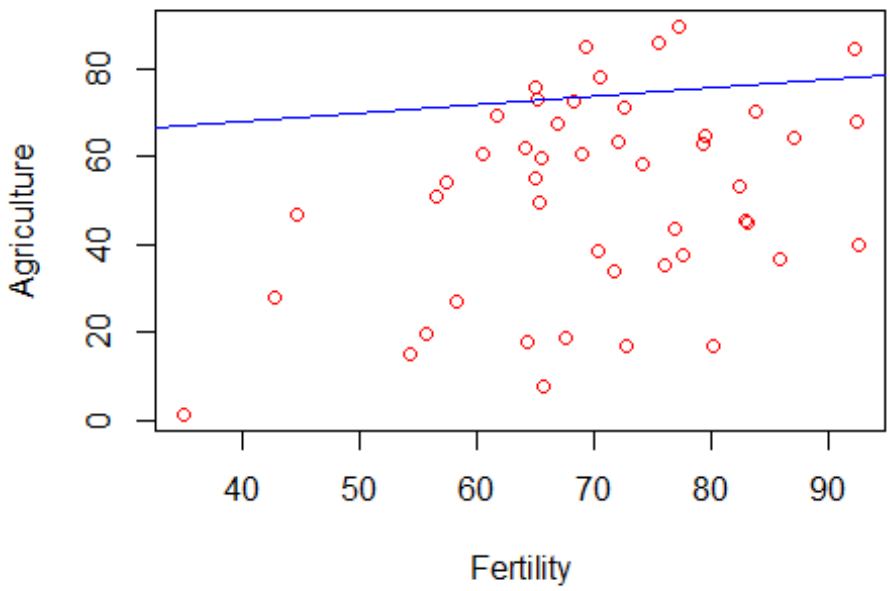
```
par(mfrow=c(2,2))
plot(fit)
```



we can see that just Examination and Agriculture variables (predictors) are not signifact and anothers are becuse they have a p-values less than 0.05(alpha). the adjust R sqrue is 0.67 and R squre is 0.7 and our standard error is 7.165 and Agriculture , Examination , Education predictors have negative relationships with our response.

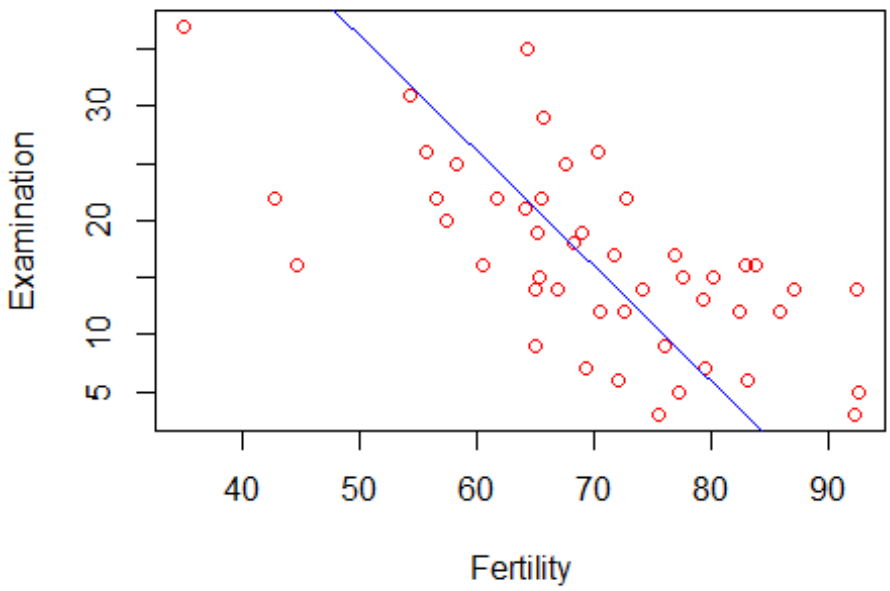
for make plot of each varibale with response we have:

```
par(mfrow=c(1,1))
plot(Fertility,Agriculture , col="red")
abline(lm(Fertility~Agriculture), col="Blue")
```



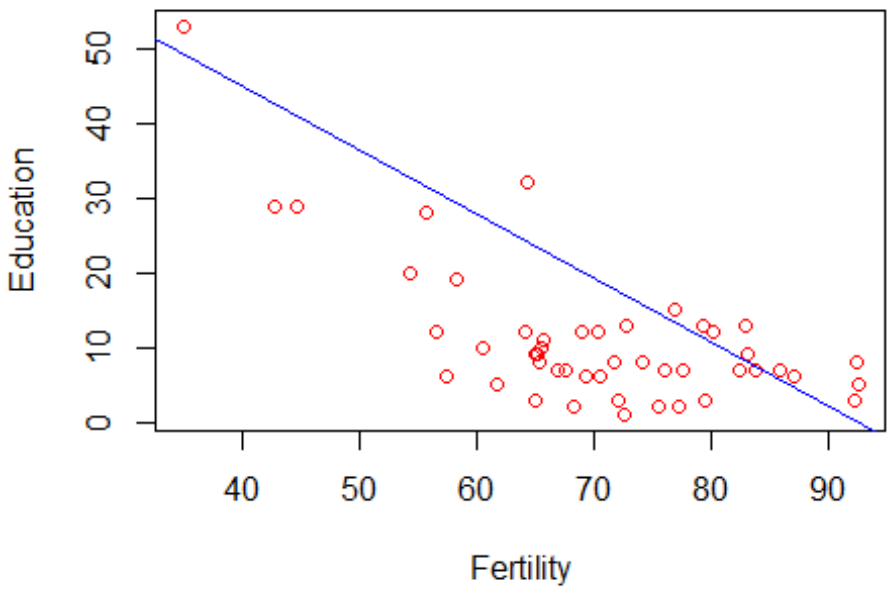
According to this plot we see the approxmiatly posetive realationships and we have 1 High leverage point (the left and down side of plot).

```
plot(Fertility,Examination , col="red")
abline(lm(Fertility~Examination), col="Blue")
```



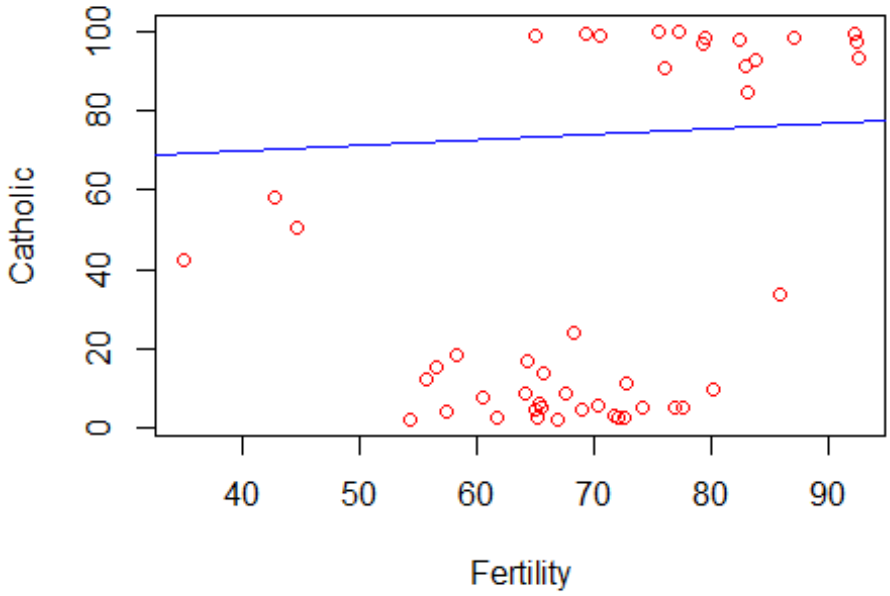
now we can see the negative realationships between response and this predictor and we have 3 High leverage points (the left side).

```
plot(Fertility,Education , col="red")
abline(lm(Fertility~Education), col="Blue")
```



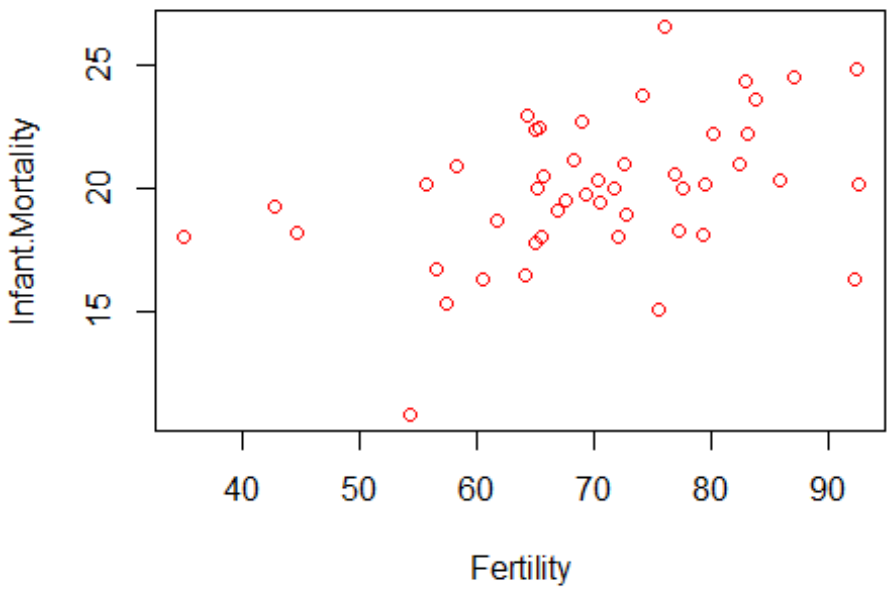
now we can see the negative realationships between response and this predictor and we have 3 High leverage points (the left side).

```
plot(Fertility,Catholic , col="red")
abline(lm(Fertility~Catholic), col="Blue")
```



we can see the posetive realationships and 3High leverage points (the left side).

```
plot(Fertility,Infant.Mortality , col="red")
abline(lm(Fertility~Infant.Mortality), col="Blue")
```



here we can see the posetive realationships with one outlires and high leverage point.

for make covariance matrix of variables we have:

```
cov(swiss)
```

```
##                  Fertility Agriculture Examination   Education   Catholic
## Fertility        156.04250  100.169149  -64.366929  -79.729510  241.56320
## Agriculture      100.16915  515.799417 -124.392831 -139.657401  379.90438
## Examination      -64.36693 -124.392831   63.646623   53.575856 -190.56061
## Education        -79.72951 -139.657401   53.575856   92.456059  -61.69883
## Catholic         241.56320  379.904376 -190.560611  -61.698830 1739.29454
## Infant.Mortality  15.15619   -4.025851   -2.649537   -2.781684   21.31812
##                  Infant.Mortality
## Fertility               15.156193
## Agriculture             -4.025851
## Examination             -2.649537
## Education               -2.781684
## Catholic                21.318116
## Infant.Mortality         8.483802
```

according to this out put we see all of the covariance between each variables.

b)

best subset selection:

at the first we need to library this package:

```
library(leaps)

## Warning: package 'leaps' was built under R version 4.0.5
```

Now we make our model from swiss data:

```
best.subset.fit1<-regsubsets(Fertility~. , data = swiss , nvmax = 19)
summary(best.subset.fit1)

## Subset selection object
## Call: regsubsets.formula(Fertility ~ ., data = swiss, nvmax = 19)
## 5 Variables  (and intercept)
##                  Forced in Forced out
## Agriculture          FALSE      FALSE
## Examination          FALSE      FALSE
## Education            FALSE      FALSE
## Catholic             FALSE      FALSE
## Infant.Mortality     FALSE      FALSE
## 1 subsets of each size up to 5
## Selection Algorithm: exhaustive
##          Agriculture Examination Education Catholic Infant.Mortality
## 1  ( 1 ) " "         " "         "*"       " "      " "
## 2  ( 1 ) " "         " "         "*"       "*"      " "
## 3  ( 1 ) " "         " "         "*"       "*"      "*"
## 4  ( 1 ) "*"         " "         "*"       "*"      "*"
## 5  ( 1 ) "*"         "*"         "*"       "*"      "*"
```

now here we can see that in the first step we have select M1 model or a model with one predictors from all of the models with one predictors and we can see that this method choose the Education predictors from these models. like this for the model with 2 predictors we choose model with M1 + Catholic=M2 predictors from all of them. like this for the model with 3 predictors we choose model with M2+Infant.Mortality =M3 predictors from all of them. like this for the model with 4 preditos we choose model with M3+Agriculture =M4 and at the last for model with all of predictors we have just 1 model or full model with all of the predictors M4 +Examinarion=M5

backward subset selection:

```
backward.fit1<-regsubsets(Fertility~.,data=swiss ,nvmax= 19 , method =
"backward")
summary(backward.fit1)

## Subset selection object
## Call: regsubsets.formula(Fertility ~ ., data = swiss, nvmax = 19, method =
```

```
"backward")
## 5 Variables  (and intercept)
##                  Forced in Forced out
## Agriculture          FALSE      FALSE
## Examination          FALSE      FALSE
## Education            FALSE      FALSE
## Catholic             FALSE      FALSE
## Infant.Mortality     FALSE      FALSE
## 1 subsets of each size up to 5
## Selection Algorithm: backward
##          Agriculture Examination Education Catholic Infant.Mortality
## 1  ( 1 ) " "         " "         "*"       " "      " "
## 2  ( 1 ) " "         " "         "*"       "*"      " "
## 3  ( 1 ) " "         " "         "*"       "*"      "*"
## 4  ( 1 ) "*"         " "         "*"       "*"      "*"
## 5  ( 1 ) "*"         "*"         "*"       "*"      "*"
```

here at the first we have compelte model(M0) with all of the predictors in the M1 we just delete the Education preditor from our M0 it means that M1=M0-Education in the next step we have: M2= M1-Catholic the next step we have: M3= M2-Infant.mortality the next step we have: M4 = M3 - Agriculture the M5 is the model with 0 predictor. M5= M4-Examination

c)

Now we want to make a training and test data with probabilty (0.7 , 0.3) and again chek models with bic:

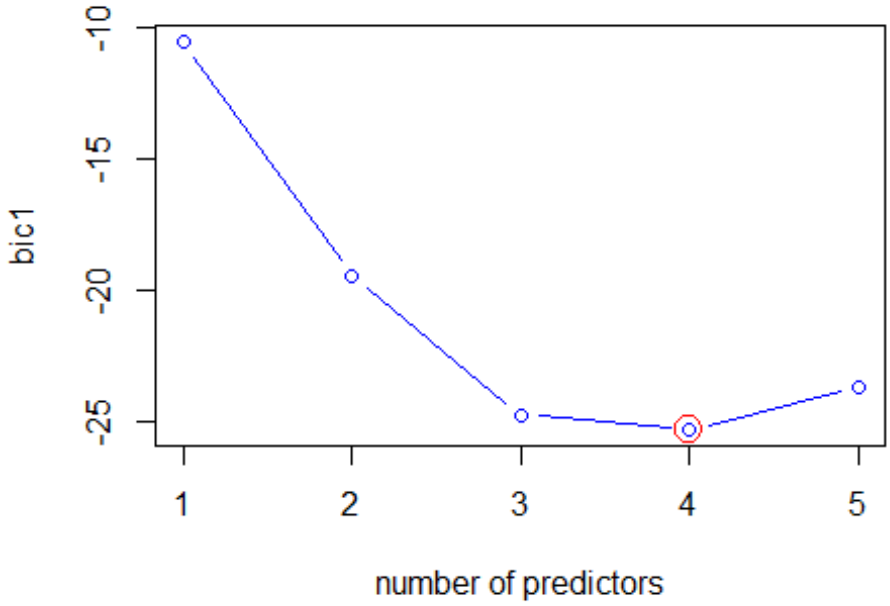
```
sample<-sample(c(TRUE , FALSE ) , nrow(swiss) , replace = T ,
prob=c(0.7,0.3))
train<-swiss[sample,]
test<-swiss[!sample,]
```

Now again we make model with best subset selection and backward method here:

```
best.subset.fit2<-regsubsets(Fertility~. , data = train , nvmax = 19)
backward.fit2<-regsubsets(Fertility~.,data= train ,nvmax= 19 , method =
"backward")
```

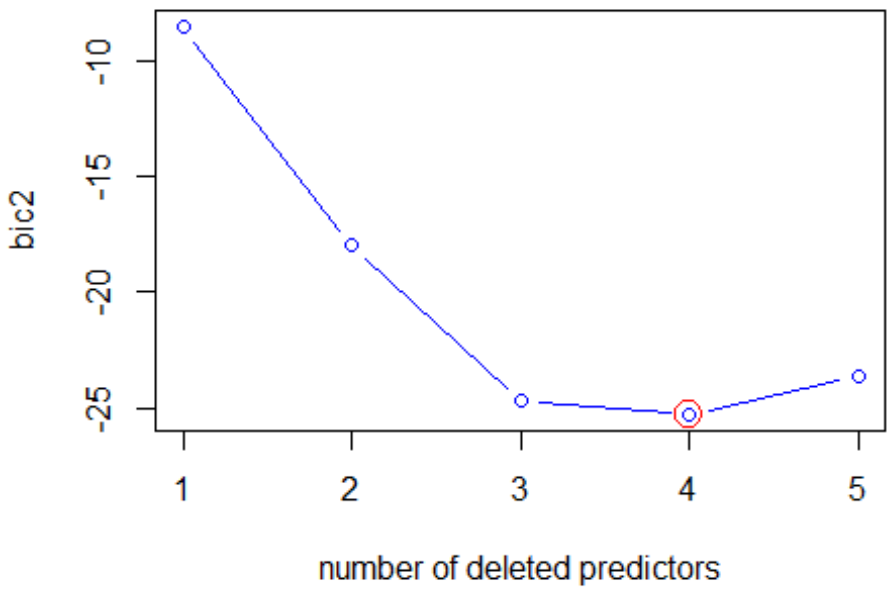
now we want to calculate and see the bic of each method here:

```
bic1<-summary(best.subset.fit2)$bic
plot(bic1 , type="b" , col="Blue" , xlab="number of predictors")
points(4,bic1[which.min(bic1)] ,cex=2 , col="red")
```



according to this plot we choose the model with 4 predictors that have the minimum of the BIC.

```
bic2<-summary(backward.fit2)$bic
plot(bic2 , type="b" , col="Blue",xlab="number of deleted predictors")
points(4,bic2[which.min(bic1)] ,cex=2 , col="red")
```



according to this plot we choose the model with 1 predictor that have the minimum of the BIC.attention:backward method.

End. by: Mehrab Atighi