Life_expectancy project code

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```
library(boot)
library(pls)
library(leaps)
library(gam)
library(glmnet)

life_exp=read.csv("Life Expectancy Data.csv")
life_exp=na.omit(life_exp)
life_exp=life_exp[2:22] # remove the "country" predictor
attach(life_exp)
```

```
set.seed(1)
trainid <- sample(1:nrow(life_exp), nrow(life_exp)/2)
train <- life_exp[trainid,]
test <- life_exp[-trainid,]
```

```
require(boot)
glm.fit = glm(Life.expectancy~., data=life_exp)
loocv.err.OLS=cv.glm(life_exp, glm.fit)$delta[1]
loocv.err.OLS
```

```
## [1] 12.84627
```

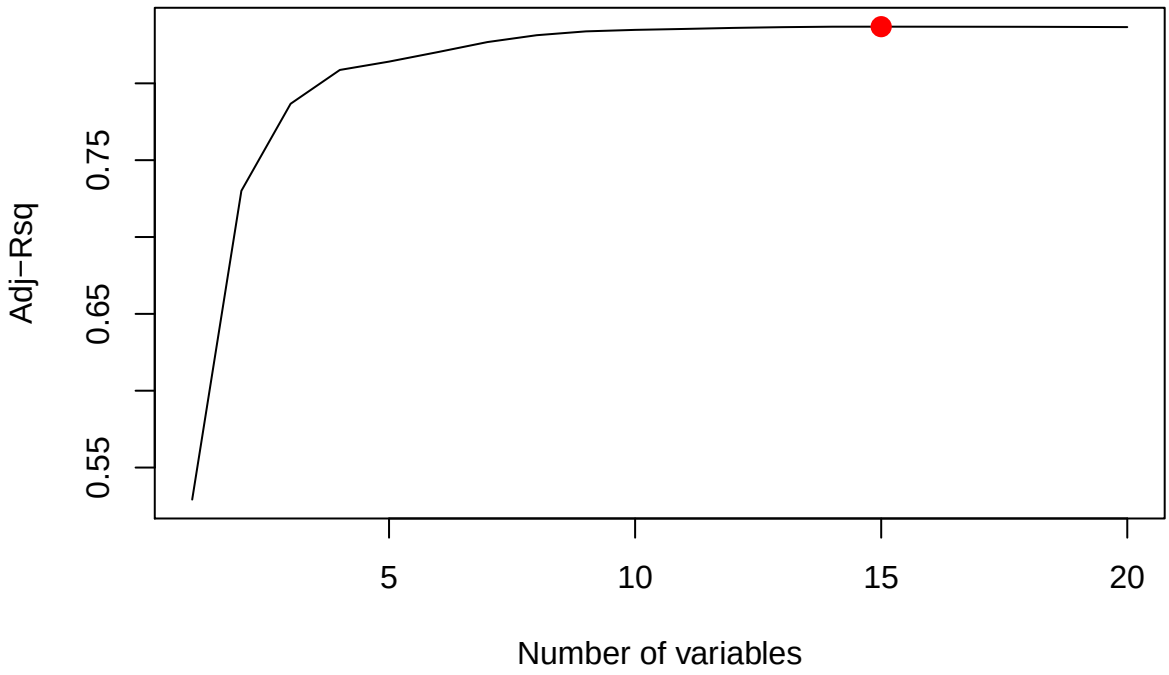
```
require(leaps)

set.seed(7)
regfit.full=regsubsets(Life.expectancy~., life_exp,nvmax=20)
reg.summary=summary(regfit.full)

plot(reg.summary$adjr2, xlab = "Number of variables", ylab = "Adj-Rsq",type ="l")
which.max(reg.summary$adjr2) # give 15
```

```
## [1] 15
```

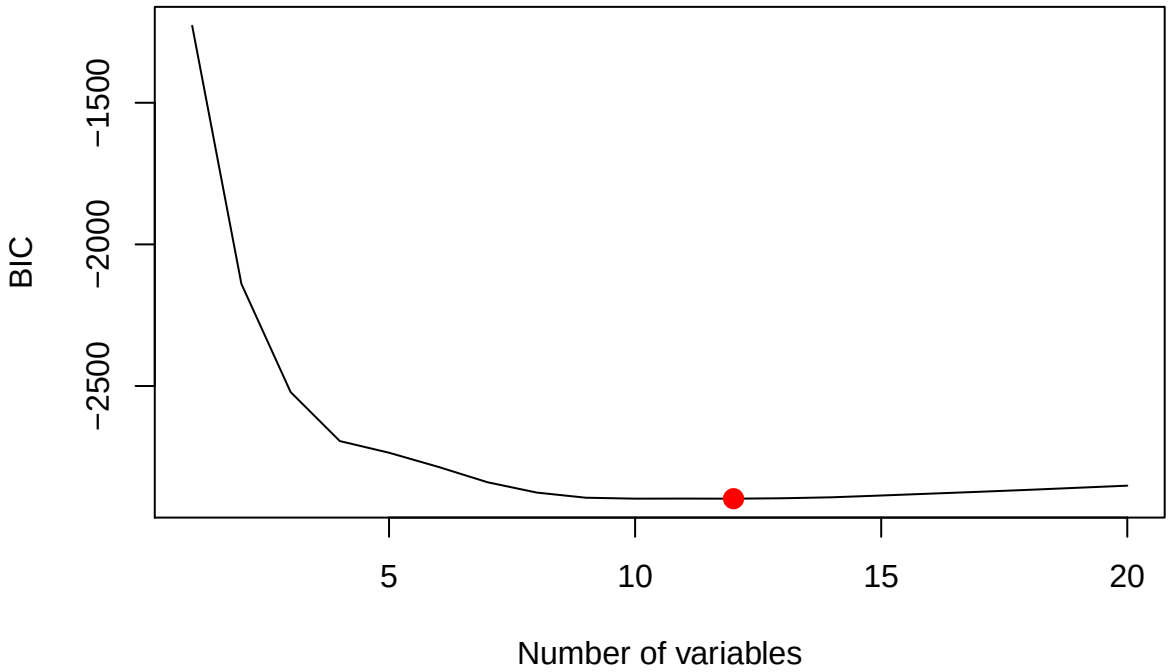
```
points(15,reg.summary$adjr2[15], col="red",cex=2,pch=20)
```




```
plot(reg.summary$bic, xlab = "Number of variables", ylab = "BIC",type ="l")
which.min(reg.summary$bic) # give 12
```

```
## [1] 12
```

```
points(12,reg.summary$bic[12], col="red",cex=2,pch=20)
```




```
coef(regfit.full,12)
```

```
##                  (Intercept)                         Year
##                3.048802e+02                -1.251579e-01
##           StatusDeveloping              Adult.Mortality
```

```
##                   -9.240120e-01                   -1.646155e-02
##                   infant.deaths                         Alcohol
##                    8.361896e-02                   -1.172219e-01
##          percentage.expenditure                             BMI
##                    4.638867e-04                    3.697864e-02
##                under.five.deaths                       Diphtheria
##                   -6.395703e-02                    1.541662e-02
##                        HIV.AIDS Income.composition.of.resources
##                   -4.457164e-01                    1.056436e+01
##                       Schooling
##                    9.154314e-01
```

```
regfit.fwd=regsubsets(Life.expectancy~., life_exp, nvmax=20, method = "forward")
coef(regfit.fwd,12)
```

```
##                      (Intercept)                             Year
##                     3.048802e+02                   -1.251579e-01
##                  StatusDeveloping                  Adult.Mortality
##                     -9.240120e-01                   -1.646155e-02
##                     infant.deaths                         Alcohol
##                     8.361896e-02                   -1.172219e-01
##           percentage.expenditure                             BMI
##                     4.638867e-04                    3.697864e-02
##                 under.five.deaths                       Diphtheria
##                     -6.395703e-02                    1.541662e-02
##                          HIV.AIDS Income.composition.of.resources
##                     -4.457164e-01                    1.056436e+01
##                         Schooling
##                     9.154314e-01
```

```
regfit.bwd=regsubsets(Life.expectancy~., life_exp, nvmax=20, method = "backward")
coef(regfit.bwd,12)
```

```
##                      (Intercept)                             Year
##                     3.048802e+02                   -1.251579e-01
##                  StatusDeveloping                  Adult.Mortality
##                     -9.240120e-01                   -1.646155e-02
##                     infant.deaths                         Alcohol
##                     8.361896e-02                   -1.172219e-01
##           percentage.expenditure                             BMI
##                     4.638867e-04                    3.697864e-02
##                 under.five.deaths                       Diphtheria
##                     -6.395703e-02                    1.541662e-02
##                          HIV.AIDS Income.composition.of.resources
##                     -4.457164e-01                    1.056436e+01
##                         Schooling
##                     9.154314e-01
```

```
# Using 12 predictors, BSS, forward selection and backward selection all give the identical model
```

```
require(leaps)

# predict function from chapter 6 labs
predict.regsubsets <- function(object, newdata, id, ...){
  form <- as.formula(object$call[[2]])
  mat <- model.matrix(form, newdata)
```

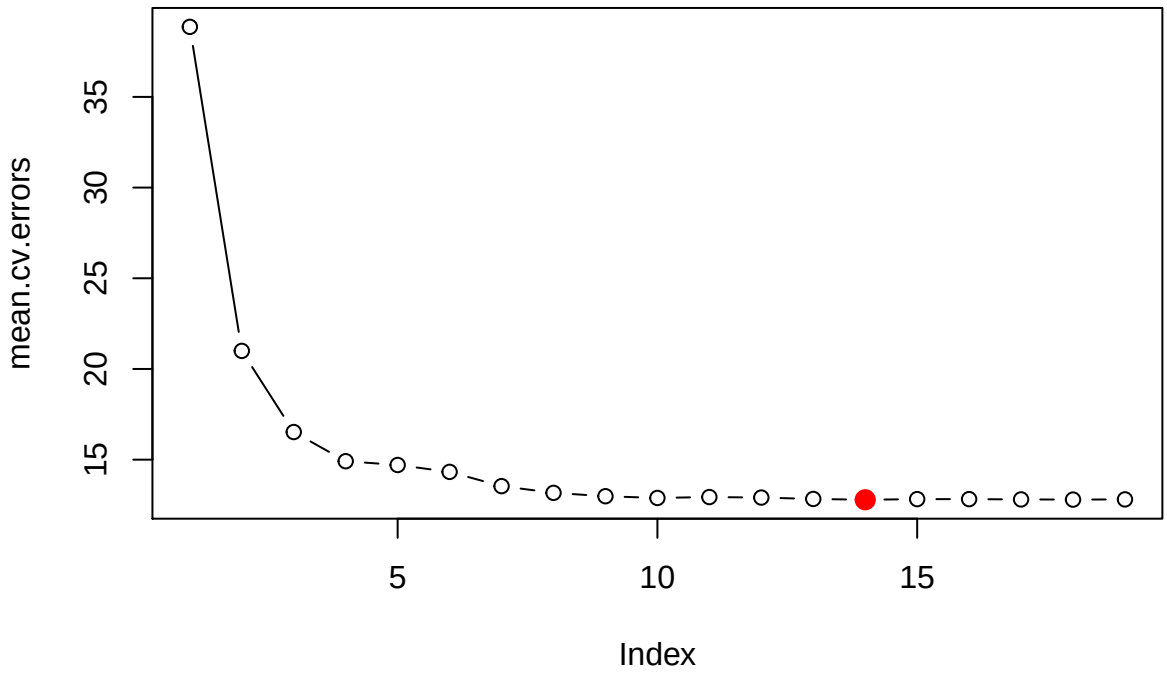
```
  coefi <- coef(object, id=id)
  xvars <- names(coefi)
  mat[,xvars]%*%coefi
}

k=10
set.seed(5)
folds=sample(1:k, nrow(life_exp),replace = TRUE)
cv.errors=matrix(NA,k,19,dimnames=list(NULL,paste(1:19)))

for(j in 1:k){
  best.fit=regsubsets(Life.expectancy~., data=life_exp[folds!=j,], nvmax = 20)
  for(i in 1:19){
    pred=predict(best.fit, life_exp[folds==j,],id=i)
    cv.errors[j,i]=mean((life_exp$Life.expectancy[folds==j]-pred)^2)
  }
}
mean.cv.errors=apply(cv.errors,2,mean)
plot(mean.cv.errors,type="b")
which.min(mean.cv.errors) # give 14, depend on the random seed
```

```
## 14
## 14
```

```
points(14,mean.cv.errors[14], col="red",cex=2,pch=20)
```




```
mean.cv.errors[14]
```

```
##       14
## 12.78913
```

```
#use 14 predictors to fit the model
regfit.cv.select=regsubsets(Life.expectancy~.,data=life_exp, nvmax = 14)
coef(regfit.cv.select, 14)
```

```
##                     (Intercept)                            Year
##                   310.086873211                  -0.127717305
##                StatusDeveloping                 Adult.Mortality
##                    -0.897508949                  -0.016262157
##                   infant.deaths                         Alcohol
##                     0.086080629                  -0.129897924
##          percentage.expenditure                             BMI
##                     0.000452335                   0.031993887
##               under.five.deaths               Total.expenditure
##                    -0.065159011                   0.092009080
##                      Diphtheria                      HIV.AIDS
##                     0.015089120                  -0.447801053
##             thinness.5.9.years Income.composition.of.resources
##                    -0.052118455                  10.523194825
##                       Schooling
##                     0.904719271
```

```
fit.lm <- lm(Life.expectancy~., data=train)
pred.lm <- predict(fit.lm, test)
(err.lm <- mean((test$Life.expectancy - pred.lm)^2))
```

```
## [1] 13.77854
```

```
#err.lm may inflate the error since it uses validation set approach, which does not use whole data to b
```

```
require(glmnet)
xmat.train <- model.matrix(Life.expectancy~., data=train)[,-1]
xmat.test <- model.matrix(Life.expectancy~., data=test)[,-1]
fit.ridge <- cv.glmnet(xmat.train, train$Life.expectancy, alpha=0)
(lambda <- fit.ridge$lambda.min)  # optimal lambda
```

```
## [1] 0.7133576
```

```
pred.ridge <- predict(fit.ridge, s=lambda, newx=xmat.test)
(err.ridge <- mean((test$Life.expectancy - pred.ridge)^2))  # test error
```

```
## [1] 14.39299
```

```
lifetest.avg <- mean(life_exp$Life.expectancy)
#ridge.r2 <- 1 - mean((pred.ridge - xmat.test$Life.expectancy)^2) / mean((lifetest.avg - xmat.test$Life
```

```
xmat.train <- model.matrix(Life.expectancy~., data=train)[,-1]
xmat.test <- model.matrix(Life.expectancy~., data=test)[,-1]
fit.lasso <- cv.glmnet(xmat.train, train$Life.expectancy, alpha=1)
(lambda <- fit.lasso$lambda.min)  # optimal lambda
```

```
## [1] 0.002879837
```

```
pred.lasso <- predict(fit.lasso, s=lambda, newx=xmat.test)
(err.lasso <- mean((test$Life.expectancy - pred.lasso)^2))  # test error
```

```
## [1] 13.78092
```

```
coef.lasso <- predict(fit.lasso, type="coefficients", s=lambda)[1:ncol(life_exp),]
coef.lasso[coef.lasso != 0]
```

```
##                     (Intercept)                            Year
##                    3.744972e+02                   -1.592786e-01
##                StatusDeveloping                 Adult.Mortality
```

```
##                  -1.382550e+00                  -1.667109e-02
##                  infant.deaths                        Alcohol
##                   7.489124e-02                  -1.564712e-01
##          percentage.expenditure                    Hepatitis.B
##                   3.947122e-04                  -4.639169e-03
##                       Measles                            BMI
##                  -9.974977e-06                   3.011031e-02
##                under.five.deaths                          Polio
##                  -5.695558e-02                   8.483315e-04
##               Total.expenditure                     Diphtheria
##                  -1.158607e-02                   1.553190e-02
##                       HIV.AIDS                             GDP
##                  -4.171617e-01                   7.686975e-06
##                     Population             thinness..1.19.years
##                  -9.191059e-10                  -2.193032e-02
##              thinness.5.9.years Income.composition.of.resources
##                  -2.439081e-02                   1.055896e+01
##                      Schooling
##                   9.344881e-01
```

```
length(coef.lasso[coef.lasso != 0])
```

```
## [1] 21
```

```
require(pls)

set.seed(1)
fit.pcr <- pcr(Life.expectancy~., data=train, scale=TRUE, validation="CV")
validationplot(fit.pcr, val.type="MSEP") # I choose M = 7
```

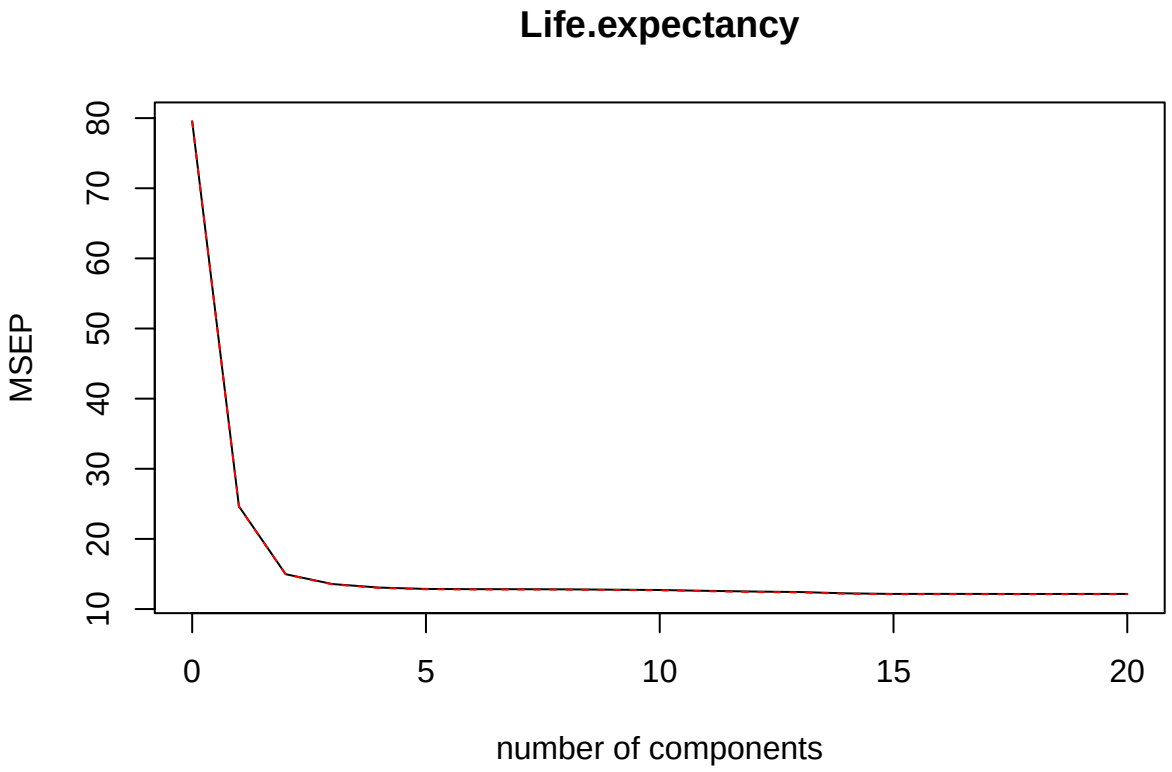
```r
summary(fit.pcr)
```

```
## Data:    X dimension: 824 20
##  Y dimension: 824 1
## Fit method: svdpc
## Number of components considered: 20
##
## VALIDATION: RMSEP
## Cross-validated using 10 random segments.
##        (Intercept)  1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV           8.919    5.928    5.432    5.376    4.594    4.352    4.075
## adjCV        8.919    5.925    5.429    5.381    4.586    4.345    4.070
##        7 comps  8 comps  9 comps  10 comps  11 comps  12 comps  13 comps
## CV       3.934    3.882    3.883     3.776     3.770     3.726     3.721
## adjCV    3.892    3.874    3.878     3.761     3.764     3.693     3.714
##        14 comps  15 comps  16 comps  17 comps  18 comps  19 comps
## CV        3.718     3.664     3.593     3.583     3.588     3.589
## adjCV     3.712     3.661     3.587     3.577     3.582     3.582
##        20 comps
## CV        3.487
## adjCV     3.481
##
## TRAINING: % variance explained
##                   1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## X                   29.45    43.08    51.87    59.66    66.19    71.25
## Life.expectancy     56.59    63.56    64.48    74.17    76.93    79.94
##                   7 comps  8 comps  9 comps  10 comps  11 comps  12 comps
## X                   75.65    79.78    83.46     86.40     89.13     91.29
## Life.expectancy     81.91    81.91    81.96     83.01     83.01     83.61
##                   13 comps  14 comps  15 comps  16 comps  17 comps
## X                    93.43     95.37     96.99     98.49     99.43
## Life.expectancy      83.62     83.74     84.14     84.68     84.79
##                   18 comps  19 comps  20 comps
## X                    99.79     99.98    100.00
## Life.expectancy      84.80     84.81     85.52
```

```r
pred.pcr <- predict(fit.pcr, test, ncomp=10)
(err.pcr <- mean((test$Life.expectancy - pred.pcr)^2))  # test error
```

```
## [1] 15.37257
```

```r
set.seed(1)
fit.pls <- plsr(Life.expectancy~., data=train, scale=TRUE, validation="CV")
validationplot(fit.pls, val.type="MSEP")
```




```
summary(fit.pls)
```

```
## Data:    X dimension: 824 20
##  Y dimension: 824 1
## Fit method: kernelpls
## Number of components considered: 20
##
## VALIDATION: RMSEP
## Cross-validated using 10 random segments.
##        (Intercept)  1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## CV           8.919    4.965    3.869    3.683    3.614    3.587    3.582
## adjCV        8.919    4.960    3.866    3.677    3.607    3.581    3.576
##        7 comps  8 comps  9 comps  10 comps  11 comps  12 comps  13 comps
## CV       3.582    3.579    3.572     3.566     3.549     3.535     3.525
## adjCV    3.576    3.573    3.566     3.560     3.542     3.526     3.517
##        14 comps  15 comps  16 comps  17 comps  18 comps  19 comps
## CV        3.498     3.487     3.488     3.487     3.486     3.487
## adjCV     3.490     3.480     3.482     3.481     3.480     3.481
##        20 comps
## CV        3.487
## adjCV     3.481
##
## TRAINING: % variance explained
##                  1 comps  2 comps  3 comps  4 comps  5 comps  6 comps
## X                  28.66    39.26    49.10    54.46    58.75    64.63
## Life.expectancy    69.91    81.89    83.91    84.58    84.77    84.81
##                  7 comps  8 comps  9 comps  10 comps  11 comps  12 comps
## X                  69.49    74.42    77.38     80.49     82.20     83.61
## Life.expectancy    84.83    84.85    84.90     84.97     85.15     85.31
##                  13 comps  14 comps  15 comps  16 comps  17 comps
```

```
## X                    86.71     87.60     89.26     92.80     94.02
## Life.expectancy      85.35     85.47     85.51     85.51     85.52
##                   18 comps  19 comps  20 comps
## X                    95.14     97.84    100.00
## Life.expectancy      85.52     85.52     85.52
```

```
pred.pls <- predict(fit.pls, test, ncomp=5)  # min Cv at M=5
(err.pls <- mean((test$Life.expectancy - pred.pls)^2))  # test error
```

```
## [1] 14.24667
```

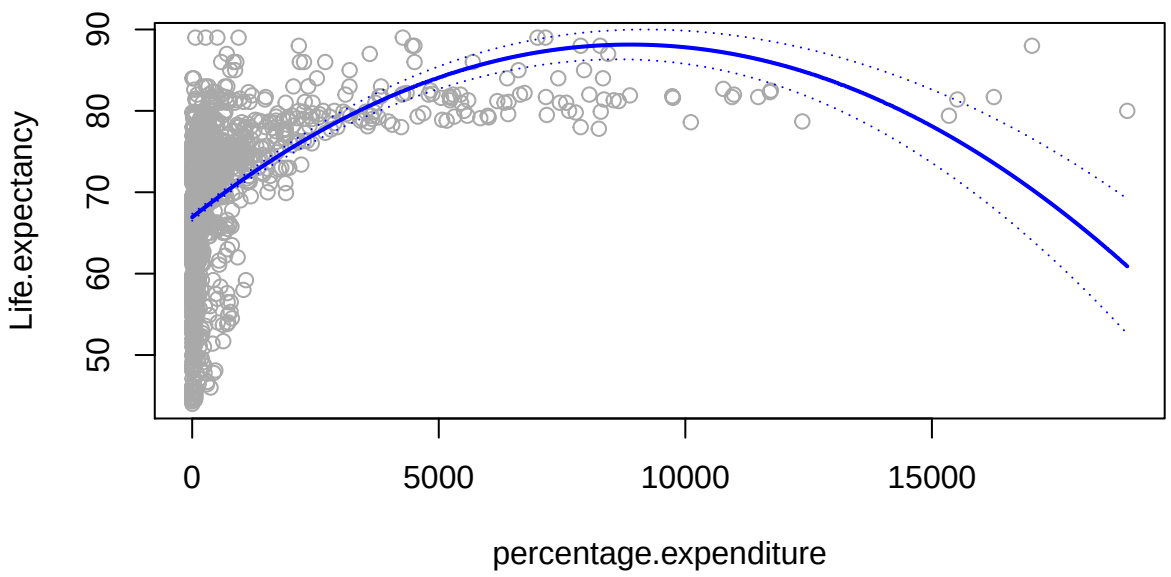
fit the CV_chosen model into poly, regression spline and GAM:

```
poly.fit=lm(Life.expectancy~poly(percentage.expenditure,2))
summary(poly.fit)
```

```
##
## Call:
## lm(formula = Life.expectancy ~ poly(percentage.expenditure, 2))
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -22.946  -4.079   1.315   5.288  21.765
##
## Coefficients:
##                                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)                       69.3023     0.1889  366.83   <2e-16 ***
## poly(percentage.expenditure, 2)1 146.2843     7.6718   19.07   <2e-16 ***
## poly(percentage.expenditure, 2)2 -96.1937     7.6718  -12.54   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.672 on 1646 degrees of freedom
## Multiple R-squared:  0.2404, Adjusted R-squared:  0.2394
## F-statistic: 260.4 on 2 and 1646 DF,  p-value: < 2.2e-16
```

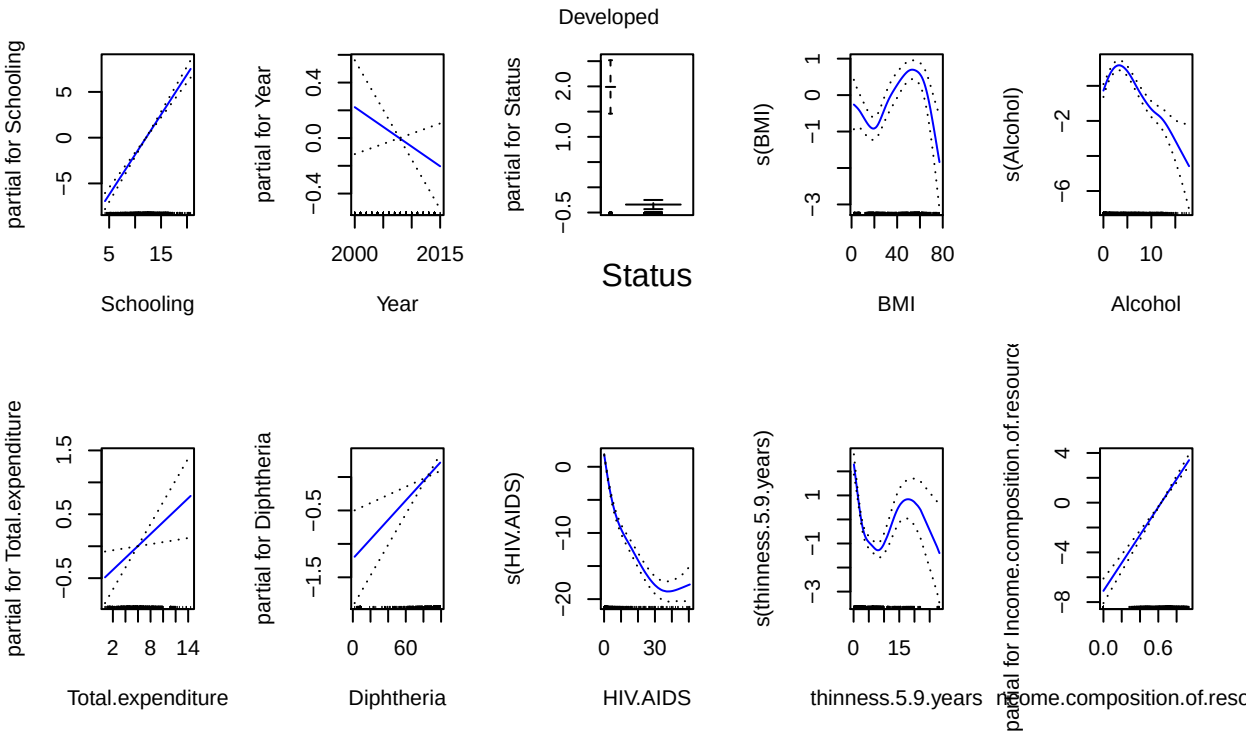
```
percentage.expenditurelims = range(percentage.expenditure)
percentage.expenditure.grid=seq(from=percentage.expenditurelims[1], to=percentage.expenditurelims[2])
preds=predict(poly.fit,newdata = list(percentage.expenditure=percentage.expenditure.grid), se=TRUE)
se.bands=cbind(preds$fit+2*preds$se.fit, preds$fit-2*preds$se.fit)

par(oma=c(0,0,3,0))
plot(percentage.expenditure,Life.expectancy, xlim=percentage.expenditurelims, col="darkgrey")
title("Degree-2 Polynomial",outer=T)
lines(percentage.expenditure.grid, preds$fit, lwd="2",col="blue")
matlines(percentage.expenditure.grid, se.bands, lwd=1, col="blue",lty=3)
```



The graph shows that as people increase there expenditure on health, the life expenctancy first increase, then decrease (or unchange).

```
require(gam)
# Choose from best subset model of 14 predictors. Then remove "Adult.Mortality","infant.deaths" , "unde
gam10.fit=gam(Life.expectancy~Schooling+Year+Status+s(BMI)+ s(Alcohol)+Total.expenditure+Diphtheria+s(H
par(mfrow=c(2,5))
par(oma=c(0,0,3,0))
plot.Gam(gam10.fit, se=TRUE, col="blue")
title("GAM: linear + smoothing spline fit", outer=TRUE)
```




```
gam1.fit=gam(Life.expectancy~Schooling)
gam2.fit=gam(Life.expectancy~Schooling+Year)
gam3.fit=gam(Life.expectancy~Schooling+Year+Status)
gam4.fit=gam(Life.expectancy~Schooling+Year+Status+s(BMI))
gam5.fit=gam(Life.expectancy~Schooling+Year+Status+s(BMI)+s(Alcohol))
gam6.fit=gam(Life.expectancy~Schooling+Year+Status+s(BMI)+s(Alcohol)+Total.expenditure)
gam7.fit=gam(Life.expectancy~Schooling+Year+Status+s(BMI)+s(Alcohol)+Total.expenditure+Diphtheria)
gam8.fit=gam(Life.expectancy~Schooling+Year+Status+s(BMI)+s(Alcohol)+Total.expenditure+Diphtheria+s(HIV
gam9.fit=gam(Life.expectancy~Schooling+Year+Status+s(BMI)+s(Alcohol)+Total.expenditure+Diphtheria+s(HIV

anova(gam1.fit, gam2.fit, gam3.fit, gam4.fit, gam5.fit, gam6.fit,gam7.fit,gam8.fit,gam9.fit,gam10.fit)
```

```
## Analysis of Deviance Table
##
## Model  1: Life.expectancy ~ Schooling
## Model  2: Life.expectancy ~ Schooling + Year
## Model  3: Life.expectancy ~ Schooling + Year + Status
## Model  4: Life.expectancy ~ Schooling + Year + Status + s(BMI)
## Model  5: Life.expectancy ~ Schooling + Year + Status + s(BMI) + s(Alcohol)
## Model  6: Life.expectancy ~ Schooling + Year + Status + s(BMI) + s(Alcohol) +
##     Total.expenditure
## Model  7: Life.expectancy ~ Schooling + Year + Status + s(BMI) + s(Alcohol) +
##     Total.expenditure + Diphtheria
## Model  8: Life.expectancy ~ Schooling + Year + Status + s(BMI) + s(Alcohol) +
##     Total.expenditure + Diphtheria + s(HIV.AIDS)
## Model  9: Life.expectancy ~ Schooling + Year + Status + s(BMI) + s(Alcohol) +
##     Total.expenditure + Diphtheria + s(HIV.AIDS) + s(thinness.5.9.years)
```

```
## Model 10: Life.expectancy ~ Schooling + Year + Status + s(BMI) + s(Alcohol) +
##     Total.expenditure + Diphtheria + s(HIV.AIDS) + s(thinness.5.9.years) +
##     Income.composition.of.resources
##    Resid. Df Resid. Dev     Df Deviance  Pr(>Chi)
## 1       1647      60009
## 2       1646      59985 1.0000     24.5  0.149053
## 3       1645      59160 1.0000    824.7 < 2.2e-16 ***
## 4       1641      51395 4.0001   7765.8 < 2.2e-16 ***
## 5       1637      48722 4.0001   2672.9 < 2.2e-16 ***
## 6       1636      48597 1.0000    125.1  0.001098 **
## 7       1635      47673 1.0000    923.1 < 2.2e-16 ***
## 8       1631      22994 4.0002  24679.9 < 2.2e-16 ***
## 9       1627      21220 3.9998   1773.8 < 2.2e-16 ***
## 10      1626      19099 1.0000   2120.8 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
set.seed(1)
trainid <- sample(1:nrow(life_exp), nrow(life_exp)/2)
train <- life_exp[trainid,]
test <- life_exp[-trainid,]

#according to the ANOVA test, we find the gam6 has a low p-value, to keep the model easier to grasp, we

# get the test error by VS approach
gam.fit.train=gam(Life.expectancy~Schooling+Year+Status+s(BMI)+ s(Alcohol)+Diphtheria+s(HIV.AIDS)+ s(thi
gam.final.pred = predict(gam.fit.train, test)
(gam.error = mean((test$Life.expectancy - gam.final.pred)^2))
```

```
## [1] 12.7334
```

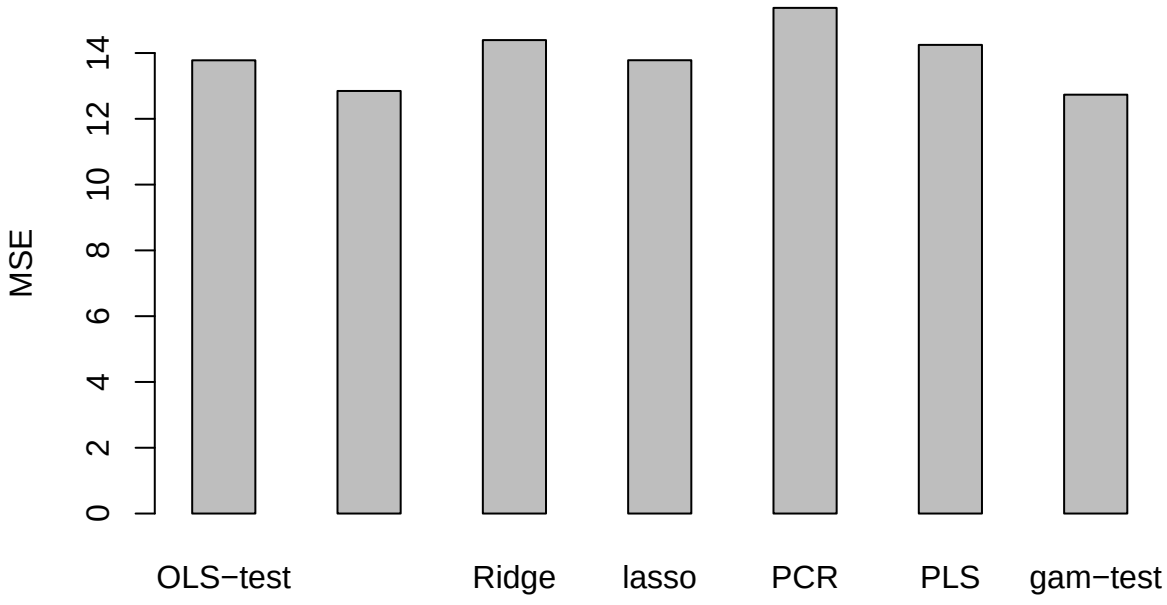
```r
# fit the model with 9 predictors:
gam.final.fit=gam(Life.expectancy~Schooling+Year+Status+s(BMI)+ s(Alcohol)+Diphtheria+s(HIV.AIDS)+ s(thi
summary(gam.final.fit)
```

```
##
## Call: gam(formula = Life.expectancy ~ Schooling + Year + Status + s(BMI) +
##     s(Alcohol) + Diphtheria + s(HIV.AIDS) + s(thinness.5.9.years) +
##     Income.composition.of.resources)
## Deviance Residuals:
##     Min      1Q  Median      3Q     Max
## -14.707  -1.973   0.102   1.948  12.569
##
## (Dispersion Parameter for gaussian family taken to be 11.7727)
##
##     Null Deviance: 127529.3 on 1648 degrees of freedom
## Residual Deviance: 19154.26 on 1627 degrees of freedom
## AIC: 8769.594
##
## Number of Local Scoring Iterations: 2
##
## Anova for Parametric Effects
##                                 Df Sum Sq Mean Sq  F value    Pr(>F)
## Schooling                        1  50254   50254 4268.698 < 2.2e-16 ***
## Year                             1    259     259   22.028 2.912e-06 ***
```

```
## Status                              1   1186    1186  100.731 < 2.2e-16 ***
## s(BMI)                              1   2424    2424  205.879 < 2.2e-16 ***
## s(Alcohol)                          1    903     903   76.690 < 2.2e-16 ***
## Diphtheria                          1    715     715   60.697 1.178e-14 ***
## s(HIV.AIDS)                         1  23362   23362 1984.455 < 2.2e-16 ***
## s(thinness.5.9.years)               1    364     364   30.961 3.073e-08 ***
## Income.composition.of.resources     1   2399    2399  203.785 < 2.2e-16 ***
## Residuals                        1627  19154      12
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Anova for Nonparametric Effects
##                                 Npar Df  Npar F     Pr(F)
## (Intercept)
## Schooling
## Year
## Status
## s(BMI)                                3  15.117 1.048e-09 ***
## s(Alcohol)                            3  26.929 < 2.2e-16 ***
## Diphtheria
## s(HIV.AIDS)                           3 107.825 < 2.2e-16 ***
## s(thinness.5.9.years)                 3  55.714 < 2.2e-16 ***
## Income.composition.of.resources
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The MSE of those methods are pretty close,while GAM has the best performace.

```
err.all <- c(err.lm, loocv.err.OLS, err.ridge, err.lasso, err.pcr, err.pls, gam.error)
names(err.all) <- c("OLS-test", "OLS-LOOCV", "Ridge", "lasso", "PCR", "PLS","gam-test")
barplot(err.all, space=1.3, ylab = "MSE")
```




```
err.all
```

```
##  OLS-test OLS-LOOCV     Ridge     lasso       PCR       PLS  gam-test
##  13.77854  12.84627  14.39299  13.78092  15.37257  14.24667  12.73340
```