# Data Mining Assignment 5

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## 8: Cross validation

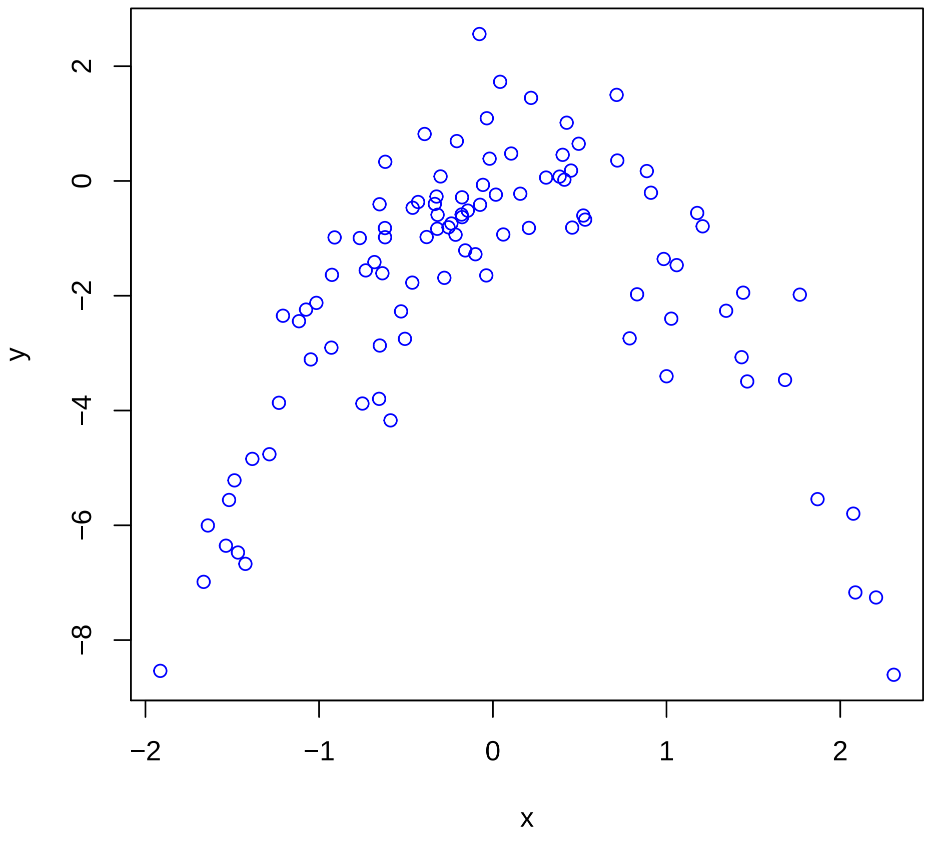
### (a)

```
> set.seed(1)
> y = rnorm(100)
> x = rnorm(100)
> y = x - 2 * x^2 + rnorm(100)
```

1. In this data set, n = 100, p = 2
2. $Y = X - 2X^2 + \epsilon$

### (b)

```
> plot(y ~ x, col = 'blue')
```



1. We can see that the data points are distributed along a parabola, just as we expected.
2. x goes from -2 to 2, y goes from -8 to 2.

**(c)**

```
> library(boot)
> set.seed(12)
> df = data.frame(X = x, Y = y)
> p = 4
> loocv.err = rep(NA, p)
> for(i in 1:p) {
+     glm.fit = glm(Y ~ poly(X, i), data = df)
+     loocv.err[i] = cv.glm(df, glm.fit)$delta[1]
+ }
> loocv.err

[1] 5.890979 1.086596 1.102585 1.114772
```

**(d)**

```
> set.seed(2015)
> loocv.err = rep(NA, p)
> for(i in 1:p) {
+     glm.fit = glm(Y ~ poly(X, i), data = df)
+     loocv.err[i] = cv.glm(df, glm.fit)$delta[1]
+ }
> loocv.err

[1] 5.890979 1.086596 1.102585 1.114772
```

1. The results obtained are exactly the same.
2. The reason is that for leave-one-out-CV, the results have nonthing to do with seed. It will evaluate 100 times no matter what the seed is. There is no randomness involved in the process of LOOCV.

**(e)**

1. The second model have the smallest LSSCV error. This is exactly what I expected.
2. Because the simulated data set is generated by power of 2 of X, if we use a lower order model such as power of 1 of X, it will have high bias; If we use a higher order model such as power of 3 or 4 of X, it will cause high variance. So, power of 2 have low bias and low variance.

**(f)**

```
> glm.fit = glm(Y ~ poly(X, 1), data = df)
> summary(glm.fit)$coeff

             Estimate Std. Error    t value     Pr(>|t|)
(Intercept) -1.827707  0.2362206 -7.7372898 9.181461e-12
poly(X, 1)   2.316401  2.3622062  0.9806091 3.292002e-01

> glm.fit = glm(Y ~ poly(X, 2), data = df)
> summary(glm.fit)$coeff

              Estimate Std. Error   t value     Pr(>|t|)
(Intercept)  -1.827707  0.1032351 -17.70431 3.804657e-32
poly(X, 2)1   2.316401  1.0323515   2.24381 2.711854e-02
poly(X, 2)2 -21.058587  1.0323515 -20.39866 7.333860e-37
```

```
> glm.fit = glm(Y ~ poly(X, 3), data = df)
> summary(glm.fit)$coeff

                Estimate Std. Error     t value     Pr(>|t|)
(Intercept)   -1.8277074  0.1037248 -17.6207390 7.610579e-32
poly(X, 3)1    2.3164010  1.0372479   2.2332183 2.785714e-02
poly(X, 3)2  -21.0585869  1.0372479 -20.3023667 1.636959e-36
poly(X, 3)3   -0.3048398  1.0372479  -0.2938929 7.694742e-01

> glm.fit = glm(Y ~ poly(X, 4), data = df)
> summary(glm.fit)$coeff

                Estimate Std. Error     t value     Pr(>|t|)
(Intercept)   -1.8277074  0.1041467 -17.5493533 1.444977e-31
poly(X, 4)1    2.3164010  1.0414671   2.2241711 2.850549e-02
poly(X, 4)2  -21.0585869  1.0414671 -20.2201171 3.457023e-36
poly(X, 4)3   -0.3048398  1.0414671  -0.2927023 7.703881e-01
poly(X, 4)4   -0.4926249  1.0414671  -0.4730105 6.372907e-01

>
```

1. From the coefficient estimates we can see that liner and quradradic term of X have vary low p-value while cubic and higher order have high p-value. This results agree with the conclusion dran based on the CV results.

## 9: Surgical

### (a)

```
> X <- read.table('surgical.txt')
> dimnames(X)[[2]] <- c('blood', 'prog', 'enz', 'liver','age',
+                       'female', 'modAlc', 'heavyAlc', 'surv', 'lsurv')
> X = X[, -9]
> N = dim(X)[1]
> d = dim(X)[2]
> mu.hat = mean(X$lsurv)
> mu.hat

[1] 6.430481
```

### (b)

```
> se = sd(X$lsurv) / sqrt(N)
> se

[1] 0.06689616
```

1. This result suggests that the expected deviation of sample mean of lsurv is 0.875

### (c)

```
> boot.fn = function(data, index) return (mean(data[index]))
> boot(X$lsurv, boot.fn, R = 1000)

ORDINARY NONPARAMETRIC BOOTSTRAP


Call:
boot(data = X$lsurv, statistic = boot.fn, R = 1000)


Bootstrap Statistics :
    original        bias    std. error
t1* 6.430481 -0.003804222   0.06627289
```

1. We can see that the results are very close. Before se is 0.066896, now it is 0.066885

### (d)

```
> confd.low = mu.hat - 2 * se
> confd.high = mu.hat + 2 * se
> c(confd.low, confd.high)

[1] 6.296689 6.564274

> t.test(X$lsurv)

        One Sample t-test

data:  X$lsurv
t = 96.126, df = 53, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0
```

```
95 percent confidence interval:
 6.296305 6.564658
sample estimates:
mean of x
 6.430481
```

1. It is clear that the results are very close.

### (e)

```
> md.hat = median(X$lsurv)
> md.hat

[1] 6.406
```

### (f)

```
> boot.fn = function(data, index) return(median(data[index]))
> boot(X$lsurv, boot.fn, R = 1000)

ORDINARY NONPARAMETRIC BOOTSTRAP


Call:
boot(data = X$lsurv, statistic = boot.fn, R = 1000)


Bootstrap Statistics :
    original    bias    std. error
t1*    6.406 0.009343  0.05701799
```

1. Median estimated by bootstrap is 6.046 which is exactly the same above.
2. The std.error estimated by bootstrap is 0.0576, which is small std error.

### (g)

```
> quantile(X$lsurv, 0.1)

   10%
5.8711
```

### (h)

```
> boot.fn = function(data, index) return(quantile(data[index], 0.1))
> boot(X$lsurv, boot.fn, R = 1000)

ORDINARY NONPARAMETRIC BOOTSTRAP


Call:
boot(data = X$lsurv, statistic = boot.fn, R = 1000)


Bootstrap Statistics :
    original    bias    std. error
t1*   5.8711 0.011588    0.113706
```

1. The tenth quantile is the same with above.
2. Here we get a small std error for the tenth quantile, which is 0.11

## 9: Ridge and Lasso

### (a)

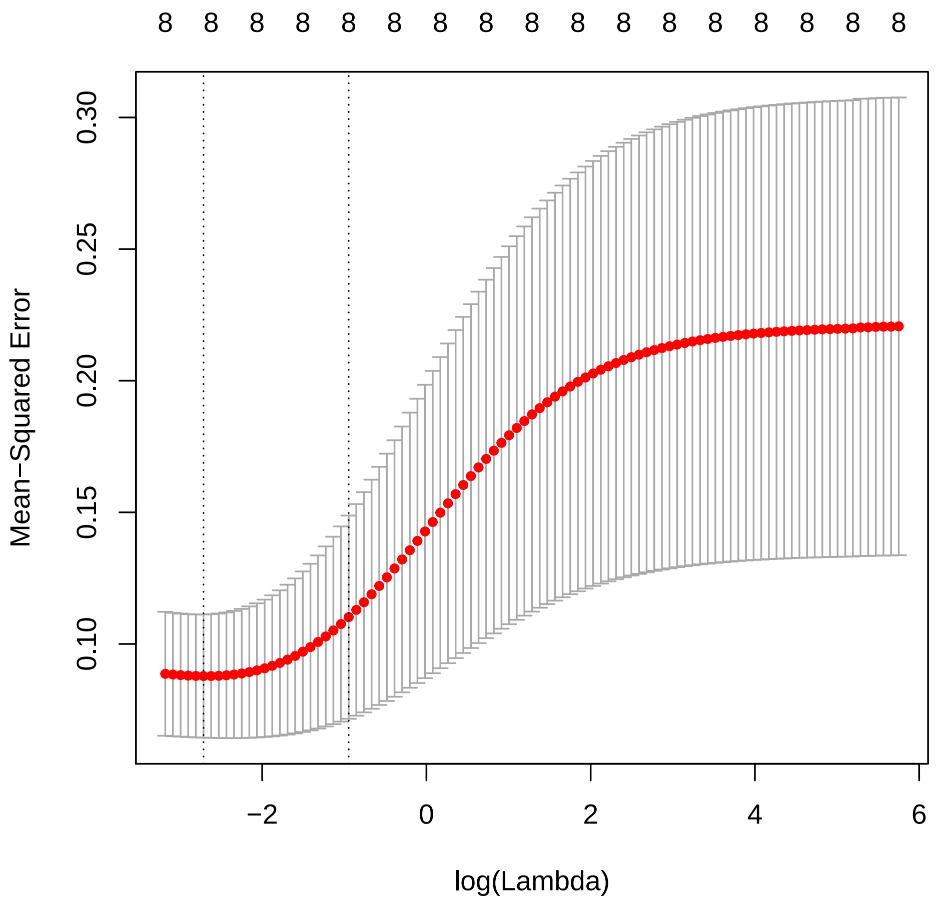
```
> set.seed(1)
> test = sample(1:N, N / 2)
> train = -test
> X.train = X[train,]
> X.test = X[test, ]
```

### (b)

```
> lm.fit = lm(lsurv ~ ., data = X.train)
> mrs = mean((predict.lm(lm.fit, X.test) - X.test$lsurv) ^ 2)
> mrs

[1] 0.05299499
```

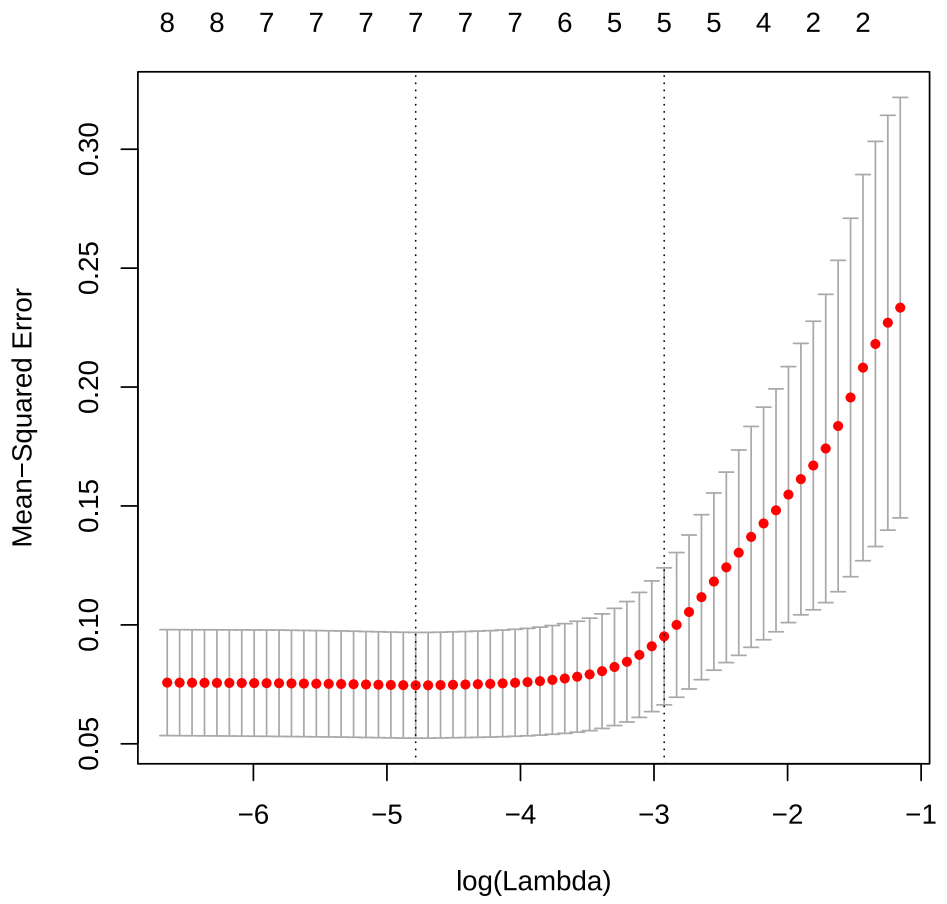
### (c)

```
> library(glmnet)
> x.train = model.matrix(lsurv ~ ., X.train)[, -1]
> y.train = X.train$lsurv
> grid = 10 ^ seq(10, -2, length = 100)
> ridge.mod = glmnet(x.train, y.train, alpha = 0, lambda = grid, thresh = 1e-12)
> cv.out = cv.glmnet(x.train, y.train, alpha = 0, nfolds = 10)
> plot(cv.out)
> bestlam = cv.out$lambda.min
> bestlam

[1] 0.06623395

> x.test = model.matrix(lsurv ~ ., X.test)[, -1]
> y.test = X.test$lsurv
> ridge.pred = predict(ridge.mod, s = bestlam, newx = x.test)
> ridge.mrs = mean((ridge.pred - y.test)^2)
> ridge.mrs

[1] 0.06356988
```



**(d)**

```
> ridge.mod = glmnet(x.train, y.train, alpha = 1, lambda = grid, thresh = 1e-12)
> cv.out = cv.glmnet(x.train, y.train, alpha = 1)
> plot(cv.out)
> bestlam = cv.out$lambda.min
> bestlam

[1] 0.008357777

> ridge.pred = predict(ridge.mod, s = bestlam, newx = x.test)
> lasso.mrs = mean((ridge.pred - y.test) ^ 2)
> lasso.mrs

[1] 0.05464687

> lasso.coef = predict(cv.out, type = 'coeff', s = bestlam)
> lasso.coef

9 x 1 sparse Matrix of class "dgCMatrix"
                       1
(Intercept)  4.370137313
blood        0.050607955
prog         0.009716315
enz          0.011266202
liver        0.116956233
age         -0.002251710
female       0.024308981
modAlc       .
heavyAlc     0.391001280
```



**(g)**

1. We get a test error of 0.053 for linear model; 0.064 for ridge; 0.054 for lasso
2. The test error get from ridge and lasso are higher than test error directly from a linear mode.
3. From lass we see that coeff of predictor modAlc is set zero.

```
> y.test.mu = mean(y.test)
> lm.r2 = 1 - mrs / mean((y.test - y.test.mu) ^ 2)
> ridge.r2 = 1 - ridge.mrs /mean((y.test - y.test.mu) ^ 2)
> lasso.r2 = 1 - lasso.mrs / mean((y.test - y.test.mu) ^ 2)
> lm.r2

[1] 0.7983984

> ridge.r2

[1] 0.7581698

> lasso.r2

[1] 0.7921144
```

1. From the $R^2$ statistic we can see that these three model only explained 79% of the variance of the data, so the accuracy of our model is moderate.