

Data Mining Assignment 4

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8: Best subset selection & forward & backwards selection

(a)

```
> library(leaps)
> set.seed(2015)
> X = rnorm(100)
> es = rnorm(100)
```

(b)

```
> beta = c(2, 3, 4, 10)
> Y = beta[1] + beta[2] * X + beta[3] * X ^ 2 + beta[4] * X ^ 3 + es
> # plot(Y ~ X)
```

(c)

```
> df = data.frame(y = Y, x = X)
> fit.full = regsubsets(y ~ poly(x, 10, raw = T), df, nvmax = 10)
> fit.summary = summary(fit.full)
> fit.summary
```

Subset selection object

Call: regsubsets.formula(y ~ poly(x, 10, raw = T), df, nvmax = 10)
10 Variables (and intercept)

	Forced in	Forced out
poly(x, 10, raw = T)1	FALSE	FALSE
poly(x, 10, raw = T)2	FALSE	FALSE
poly(x, 10, raw = T)3	FALSE	FALSE
poly(x, 10, raw = T)4	FALSE	FALSE
poly(x, 10, raw = T)5	FALSE	FALSE
poly(x, 10, raw = T)6	FALSE	FALSE

```

poly(x, 10, raw = T)7      FALSE      FALSE
poly(x, 10, raw = T)8      FALSE      FALSE
poly(x, 10, raw = T)9      FALSE      FALSE
poly(x, 10, raw = T)10     FALSE      FALSE
1 subsets of each size up to 10
Selection Algorithm: exhaustive
      poly(x, 10, raw = T)1 poly(x, 10, raw = T)2 poly(x, 10, raw = T)3
1 ( 1 ) " " " " "*"
2 ( 1 ) " " "*" "*"
3 ( 1 ) "*" "*" "*"
4 ( 1 ) "*" "*" "*"
5 ( 1 ) "*" "*" "*"
6 ( 1 ) "*" "*" "*"
7 ( 1 ) "*" " " "*"
8 ( 1 ) "*" " " "*"
9 ( 1 ) "*" "*" "*"
10 ( 1 ) "*" "*" "*"
      poly(x, 10, raw = T)4 poly(x, 10, raw = T)5 poly(x, 10, raw = T)6
1 ( 1 ) " " " " " "
2 ( 1 ) " " " " " "
3 ( 1 ) " " " " " "
4 ( 1 ) " " " " " "
5 ( 1 ) " " " " "*"
6 ( 1 ) " " " " "*"
7 ( 1 ) "*" " " "*"
8 ( 1 ) "*" "*" "*"
9 ( 1 ) "*" "*" "*"
10 ( 1 ) "*" "*" "*"
      poly(x, 10, raw = T)7 poly(x, 10, raw = T)8 poly(x, 10, raw = T)9
1 ( 1 ) " " " " " "
2 ( 1 ) " " " " " "
3 ( 1 ) " " " " " "
4 ( 1 ) "*" " " " "
5 ( 1 ) " " "*" " "
6 ( 1 ) " " "*" " "
7 ( 1 ) " " "*" "*"
8 ( 1 ) " " "*" "*"
9 ( 1 ) "*" "*" " "
10 ( 1 ) "*" "*" "*"
      poly(x, 10, raw = T)10
1 ( 1 ) " "
2 ( 1 ) " "
3 ( 1 ) " "
4 ( 1 ) " "
5 ( 1 ) " "
6 ( 1 ) "*"
7 ( 1 ) "*"
8 ( 1 ) "*"
9 ( 1 ) "*"
10 ( 1 ) "*"

```

```
> which.max(fit.summary$adjr2)
```

```
[1] 9
```

```
> which.min(fit.summary$bic)
```

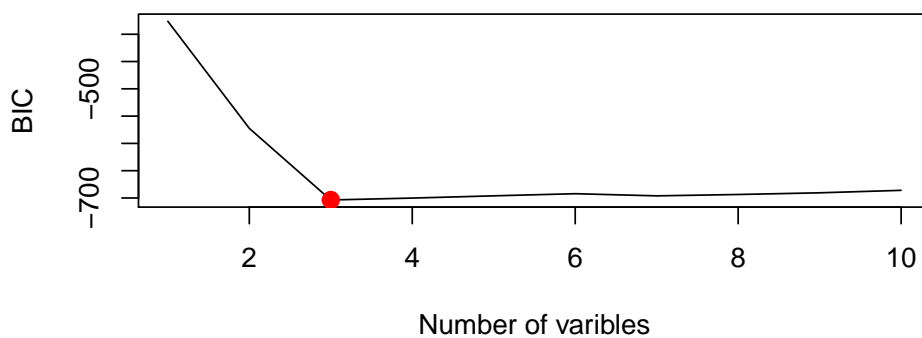
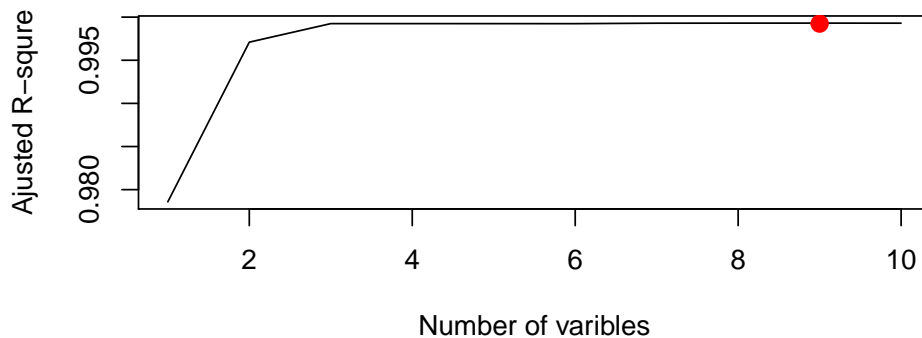
[1] 3

```
> par(mfrow = c(2, 1))
> plot(fit.summary$adjr2, xlab = 'Number of variables', ylab = 'Ajusted R-squre', type = 'l')
> points(9, fit.summary$adjr2[3], col = 'red', cex = 2, pch = 20)
> plot(fit.summary$bic, xlab = 'Number of variables', ylab = 'BIC', type = 'l')
> points(3, fit.summary$bic[3], col = 'red', cex = 2, pch = 20)
> coef(fit.full, 3)
```

```
      (Intercept) poly(x, 10, raw = T)1 poly(x, 10, raw = T)2
              1.965463              2.797556              3.962171
poly(x, 10, raw = T)3
              10.039204
```

```
> coef(fit.full, 9)
```

```
      (Intercept) poly(x, 10, raw = T)1 poly(x, 10, raw = T)2
              2.18111549              2.78095388              1.30454507
poly(x, 10, raw = T)3 poly(x, 10, raw = T)4 poly(x, 10, raw = T)5
              10.57519179              4.71751203              -0.40479624
poly(x, 10, raw = T)6 poly(x, 10, raw = T)7 poly(x, 10, raw = T)8
              -2.70359168              0.05942921              0.59029211
poly(x, 10, raw = T)10
              -0.04312750
```



1. Result of this problem is very UNSTABLE. Many facts will influence the final result of this problem:

- seed
- if we set raw = T in ploy function
- most importantly, how we choose beta.

Sometime, I get max adjr2 at index 7, sometimes at index 9 or 5.

But fortunately, BIC is relatively stable than adjr2, most of the time I get minimum BIC at index 3. Because BIC is more favorable to smaller number of variables.

2. As shown in the figure above, adjr2 reached its peak at index 3, and keep stable so on. BIC reached its global minimum value at index 3, and this is the only minimum value.

3. The best predicted coef by BIC are close to its true value, as shown above.

4. However, the best predicted coef by adjr2 is not so, as shown above.

(d)

```
> fit.fwd = regsubsets(y ~ poly(x, 10, raw = T), df, nvmax = 10, method = 'forward')
> fit.fwd.summary = summary(fit.fwd)
> # fit.fwd.summary
> which.max(fit.fwd.summary$adjr2)

[1] 10

> which.min(fit.fwd.summary$bic)

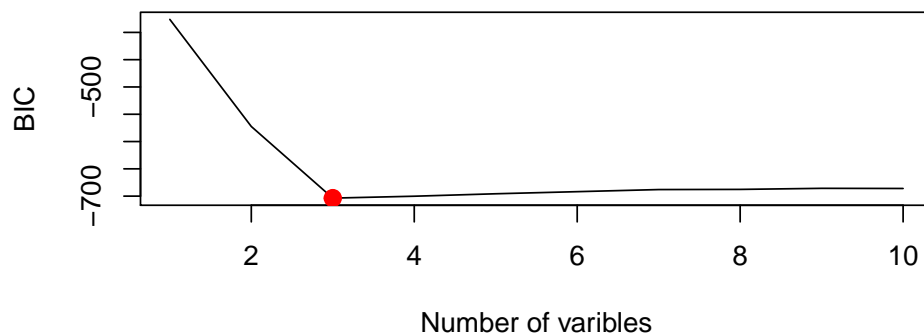
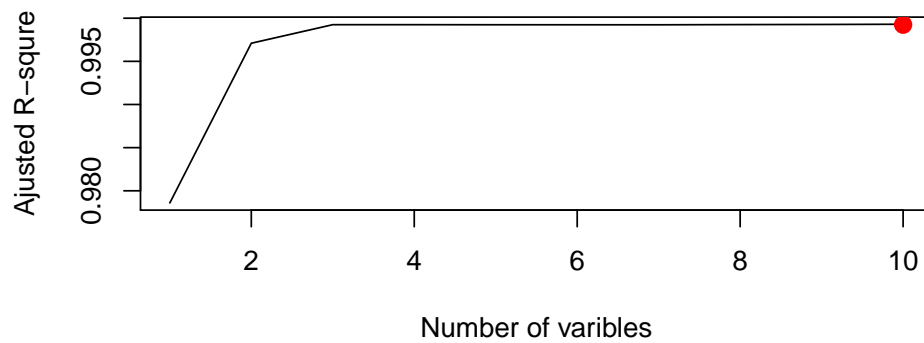
[1] 3

> par(mfrow = c(2, 1))
> plot(fit.fwd.summary$adjr2, xlab = 'Number of variables', ylab = 'Ajusted R-squre', type = 'l')
> points(10, fit.fwd.summary$adjr2[3], col = 'red', cex = 2, pch = 20)
> plot(fit.fwd.summary$bic, xlab = 'Number of variables', ylab = 'BIC', type = 'l')
> points(3, fit.fwd.summary$bic[3], col = 'red', cex = 2, pch = 20)
> coef(fit.fwd, 3)

      (Intercept) poly(x, 10, raw = T)1 poly(x, 10, raw = T)2
              1.965463              2.797556              3.962171
poly(x, 10, raw = T)3
              10.039204

> coef(fit.fwd, 10)

      (Intercept) poly(x, 10, raw = T)1 poly(x, 10, raw = T)2
              2.169580713              2.659987801              1.451684521
poly(x, 10, raw = T)3 poly(x, 10, raw = T)4 poly(x, 10, raw = T)5
              10.967635428              4.435167654              -0.730805121
poly(x, 10, raw = T)6 poly(x, 10, raw = T)7 poly(x, 10, raw = T)8
              -2.516525214              0.154188775              0.541918393
poly(x, 10, raw = T)9 poly(x, 10, raw = T)10
              -0.008679161              -0.038986881
```



1. Forward selection, basically, does not change too much from full selection.
2. This time adjr2 choose model at index 10. And BIC still choose model at index 3.
3. The coef of model at index 3 is still close to the true value.

```
> fit.bwd = regsubsets(y ~ poly(x, 10, raw = T), df, nvmax = 10, method = 'backward')
> fit.bwd.summary = summary(fit.bwd)
> # fit.bwd.summary
> which.max(fit.bwd.summary$adjr2)
```

```
[1] 9
```

```
> which.min(fit.bwd.summary$bic)
```

```
[1] 3
```

```
> par(mfrow = c(2, 1))
> plot(fit.bwd.summary$adjr2, xlab = 'Number of variables', ylab = 'Adjusted R-squre', type = 'l')
> points(9, fit.bwd.summary$adjr2[3], col = 'red', cex = 2, pch = 20)
> plot(fit.bwd.summary$bic, xlab = 'Number of variables', ylab = 'BIC', type = 'l')
> points(3, fit.bwd.summary$bic[3], col = 'red', cex = 2, pch = 20)
> coef(fit.bwd, 3)
```

```

      (Intercept) poly(x, 10, raw = T)1 poly(x, 10, raw = T)2
      1.965463      2.797556      3.962171
poly(x, 10, raw = T)3
      10.039204

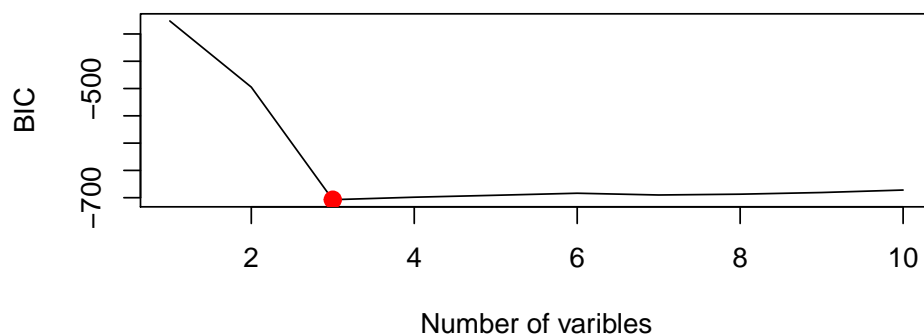
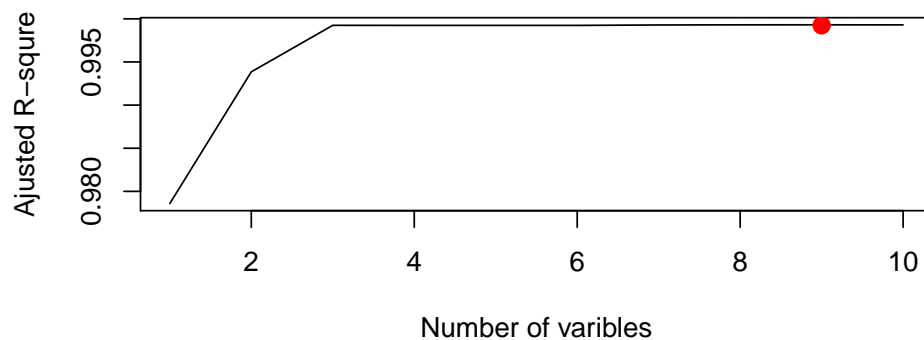
```

```
> coef(fit.fwd, 9)
```

```

      (Intercept) poly(x, 10, raw = T)1 poly(x, 10, raw = T)2
      2.00486068      2.18385089      3.35711858
poly(x, 10, raw = T)3 poly(x, 10, raw = T)4 poly(x, 10, raw = T)5
      12.56088616      1.03637630      -2.15396284
poly(x, 10, raw = T)6 poly(x, 10, raw = T)7 poly(x, 10, raw = T)8
      -0.45527056      0.60137906      0.05275883
poly(x, 10, raw = T)9
      -0.05228977

```



1. Backward selection, also, does not change too much from full selection.
2. This time adjr2 choose model at index 9. And BIC still choose model at index 3.
3. The coef of model at index 3 is still close to the true value.

11 - 1: Predict per capita crime rate in Boston

1. Since Boston dataset only has 506 data points, we should use 10-folds cross validation to justify performance of model.
2. We use best selection to select candidate models, since there are only 13 predictors.

(a & b) best selection & cross-validation

```
> library(MASS)
> bos = Boston
> attach(bos)
> predict.regsubsets = function(object, newdata, id, ...) {
+   form = as.formula(object$call[[2]])
+   mat = model.matrix(form, newdata)
+   coefi = coef(object, id = id)
+   xvars = names(coefi)
+   mat[, xvars] %*% coefi
+ }
> set.seed(0)
> k = 10
> pred.count = ncol(bos) - 1
> folds = sample(1:k, nrow(bos), replace = T)
> err.matrix = matrix(NA, k, pred.count)
> for (i in 1:k) {
+   fit.best = regsubsets(crim ~ ., bos[folds != i, ], nvmax = 13)
+   for (j in 1:pred.count) {
+     if (j == 9) {
+       print(coef(fit.best, j))
+     }
+     pred = predict(fit.best, bos[folds == i, ], id = j)
+     err.matrix[i, j] = mean((bos$crim[folds == i] - pred) ^ 2)
+   }
+ }
> mean.err = apply(err.matrix, 2, mean)
> which.min(mean.err)
```

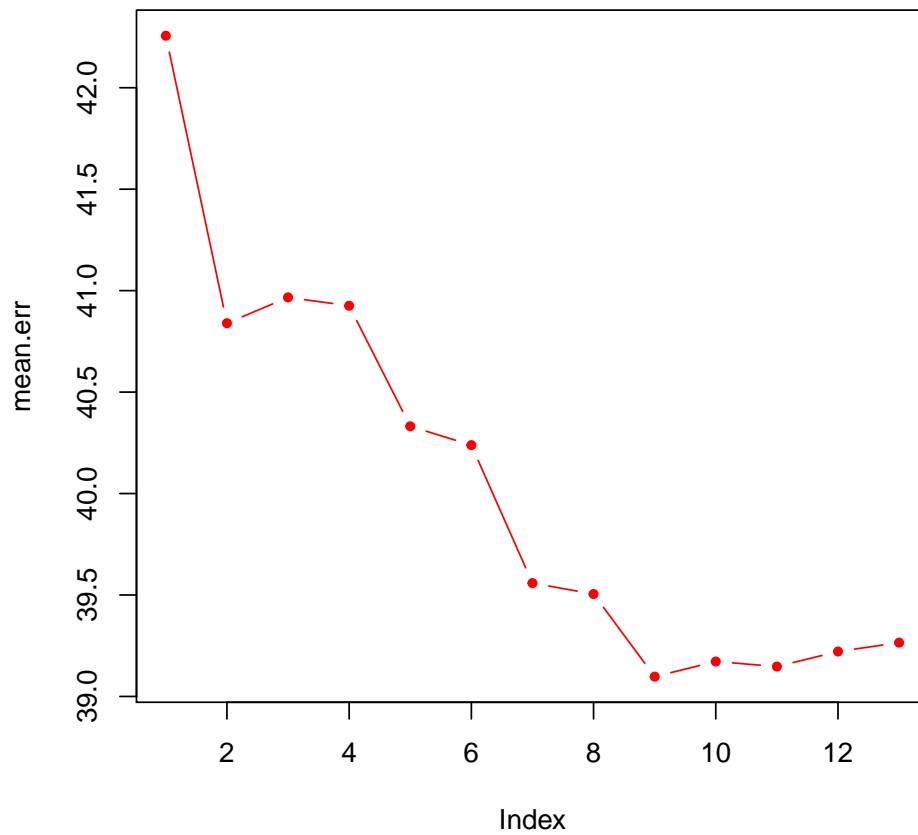
```
[1] 9
```

```
> mean.err[which.min(mean.err)]
```

```
[1] 39.09773
```

```
> plot(mean.err, pch = 20, type = "b", col = 'red')
> fit.best = regsubsets(crim ~ ., bos, nvmax = 13)
> coef(fit.best, which.min(mean.err))
```

(Intercept)	zn	indus	nox	dis
19.124636156	0.042788127	-0.099385948	-10.466490364	-1.002597606
rad	ptratio	black	lstat	medv
0.539503547	-0.270835584	-0.008003761	0.117805932	-0.180593877



1. Finally, it's easy to see that with 9 predictors we get the best performance on CV.
2. The best predictors and its coefficients are shown above.

(c) analysis

1. The finally choosen model does not contain all of the features in the data sets.
2. Because as shown in the experiment above, model with 9 predictors has the lowest MSE on cross-validation sets.

11 - 2: Predict lsurv in Surgical

1. Since Surgical dataset only has 54 data points, I choose to use 5-folds cross validation to justify performance of model.
2. We use best selection to select candidate models, since there are only 8 predictors.
3. We only use log-survival time as reponse.

(a & b) best selection & cross-validation

```
> rawdata = read.table('surgical.txt')
> surgical = rawdata[, -9]
> dimnames(surgical)[[2]] <- c('blood', 'prog', 'enz', 'liver',
+                               'age', 'female', 'modAlc', 'heavyAlc', 'lsurv')
> set.seed(0)
> k = 5
> pred.count = ncol(surgical) - 1
> folds = sample(1:k, nrow(surgical), replace = T)
> err.matrix = matrix(NA, k, pred.count)
> for (i in 1:k) {
+   fit.best = regsubsets(lsurv ~ ., surgical[folds != i, ], nvmax = 8)
+
+   for (j in 1:pred.count) {
+     if (j == 4) {
+       print(coef(fit.best, j))
+     }
+     pred = predict(fit.best, surgical[folds == i, ], id = j)
+     err.matrix[i, j] = mean((surgical$lsurv[folds == i] - pred) ^ 2)
+   }
+ }
> mean.err = apply(err.matrix, 2, mean)
> which.min(mean.err)
```

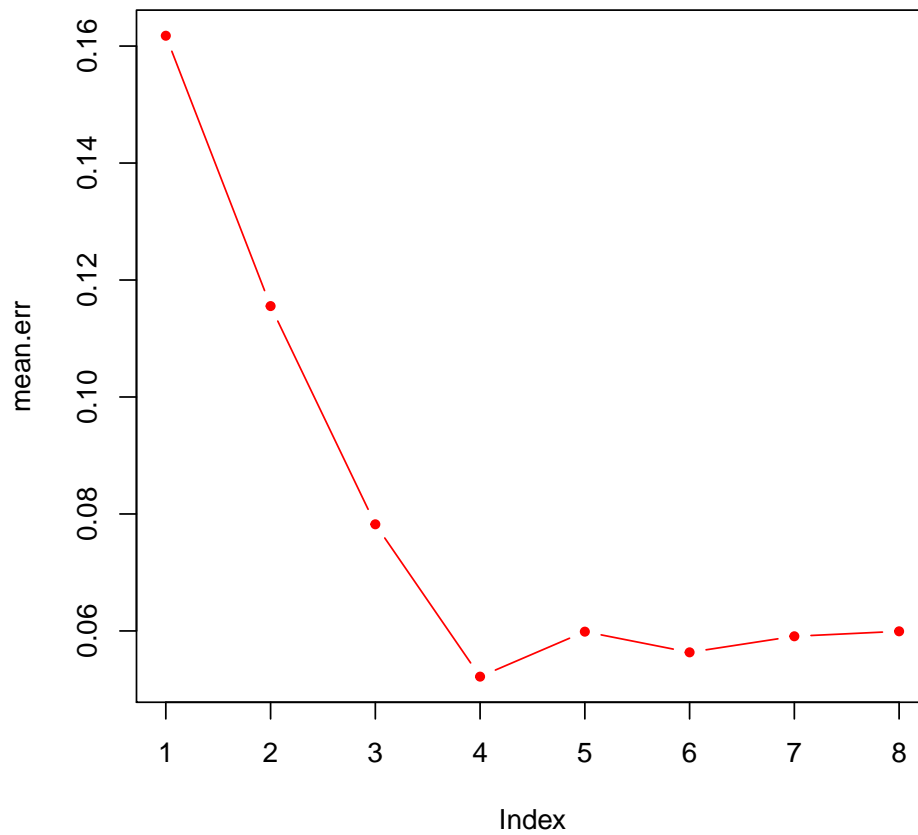
```
[1] 4
```

```
> mean.err[which.min(mean.err)]
```

```
[1] 0.05218958
```

```
> plot(mean.err, pch = 20, type = "b", col = 'red')
> fit.best = regsubsets(lsurv ~ ., surgical, nvmax = 8)
> coef(fit.best, which.min(mean.err))
```

```
(Intercept)      blood      prog      enz      heavyAlc
 3.85241856  0.07332263  0.01418507  0.01545270  0.35296762
```



1. Finally, it's easy to see that with 4 predictors we get the best performance on CV.
2. The best predictors and its coefficients are shown above.

(c)

1. Obviously my best model does not contain all the predictors. Since with 4 predictors my model get lowest MSE on CV.