MATH-650 Assignment 9

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Chapter 12: 14

```
require(leaps)
```

```
## Loading required package: leaps
```

```
data <- read.csv('case1102.csv')
data$logY = log(data$Brain/data$Liver)
Y <- data$logY
X <- data[,c('Days', 'Sex', 'Weight', 'Loss', 'Tumor')]
```

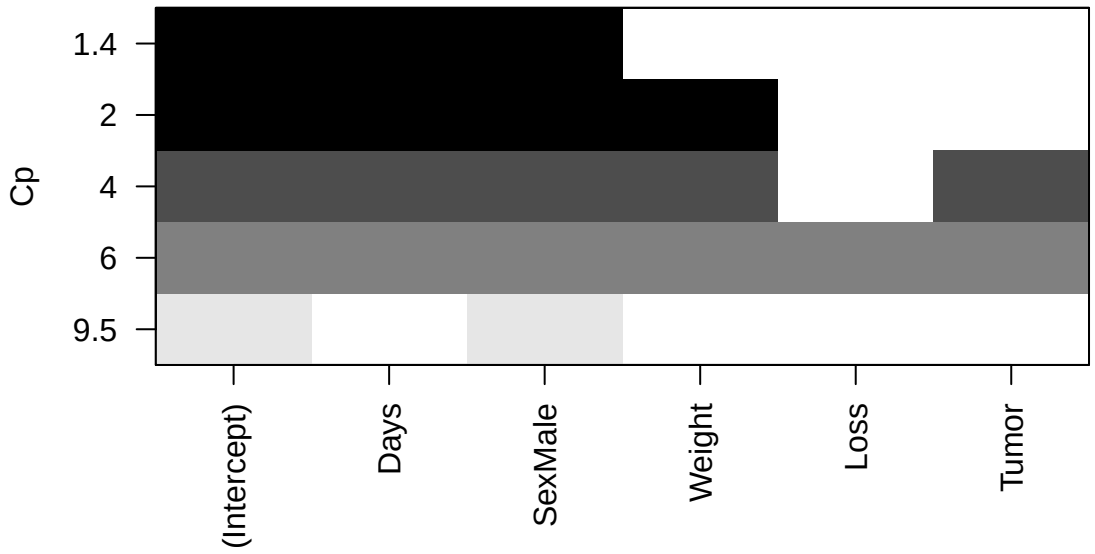
We use the `leaps` package to perform subset selection.

```
rsubsets <- regsubsets(logY ~ Days+Sex+Weight+Loss+Tumor, data=data)
s <- summary(rsubsets, matrix.logical=TRUE)
s$cp
```

```
## [1] 9.457598 1.430200 2.006538 4.000835 6.000000
```

Part (a): C_p

```
plot(rsubsets, scale='Cp')
```



The way to interpet this plot is to look at first the smallest C_p values, which happens to be around 1.4 and see the `black` dots which in this case are given by `Days, SexMale` So if we were to choose the covarates based only on C_p values, we select: `Days and Sex` Here $p = 5$ and in principle any model with $C_p < p$ is better than the full model, so we can also select these:

- Days, Sex: $C_p = 1.43$
- Days, Sex, Weight: $C_p = 2.006$
- Days, Sex, Weight, Tumor: $C_p = 4.00008$

Part (b): Forward Selection

```
rsubsets <- regsubsets(logY ~ Days+Sex+Weight+Loss+Tumor,
                       data=data,
                       method='forward')
sforward <- summary(rsubsets, matrix.logical=TRUE)
sforward
```

```
## Subset selection object
## Call: regsubsets.formula(logY ~ Days + Sex + Weight + Loss + Tumor,
##     data = data, method = "forward")
## 5 Variables  (and intercept)
##         Forced in Forced out
## Days        FALSE      FALSE
## SexMale     FALSE      FALSE
## Weight      FALSE      FALSE
## Loss        FALSE      FALSE
## Tumor       FALSE      FALSE
## 1 subsets of each size up to 5
## Selection Algorithm: forward
##           Days SexMale Weight  Loss Tumor
## 1  ( 1 ) FALSE    TRUE  FALSE FALSE FALSE
## 2  ( 1 )  TRUE    TRUE  FALSE FALSE FALSE
## 3  ( 1 )  TRUE    TRUE   TRUE FALSE FALSE
## 4  ( 1 )  TRUE    TRUE   TRUE FALSE  TRUE
## 5  ( 1 )  TRUE    TRUE   TRUE  TRUE  TRUE
```

Part (c): Backward Selection

```
rsubsets <- regsubsets(logY ~ Days+Sex+Weight+Loss+Tumor,
                       data=data,
                       method='backward')
sbackward <- summary(rsubsets, matrix.logical=TRUE)
sbackward
```

```
## Subset selection object
## Call: regsubsets.formula(logY ~ Days + Sex + Weight + Loss + Tumor,
##     data = data, method = "backward")
## 5 Variables  (and intercept)
##         Forced in Forced out
```

```
## Days        FALSE      FALSE
## SexMale     FALSE      FALSE
## Weight      FALSE      FALSE
## Loss        FALSE      FALSE
## Tumor       FALSE      FALSE
## 1 subsets of each size up to 5
## Selection Algorithm: backward
##           Days SexMale Weight  Loss Tumor
## 1  ( 1 ) FALSE    TRUE  FALSE FALSE FALSE
## 2  ( 1 )  TRUE    TRUE  FALSE FALSE FALSE
## 3  ( 1 )  TRUE    TRUE   TRUE FALSE FALSE
## 4  ( 1 )  TRUE    TRUE   TRUE FALSE  TRUE
## 5  ( 1 )  TRUE    TRUE   TRUE  TRUE  TRUE
```

Part(d): Stepwise Regression

```
rsubsets <- regsubsets(logY ~ Days+Sex+Weight+Loss+Tumor,
                       data=data,
                       method="seqrep")
sboth <- summary(rsubsets, matrix.logical=TRUE)
sboth
```

```
## Subset selection object
## Call: regsubsets.formula(logY ~ Days + Sex + Weight + Loss + Tumor,
##     data = data, method = "seqrep")
## 5 Variables  (and intercept)
##         Forced in Forced out
## Days        FALSE      FALSE
## SexMale     FALSE      FALSE
## Weight      FALSE      FALSE
## Loss        FALSE      FALSE
## Tumor       FALSE      FALSE
## 1 subsets of each size up to 5
## Selection Algorithm: 'sequential replacement'
##           Days SexMale Weight  Loss Tumor
## 1  ( 1 ) FALSE    TRUE  FALSE FALSE FALSE
## 2  ( 1 )  TRUE    TRUE  FALSE FALSE FALSE
## 3  ( 1 )  TRUE    TRUE   TRUE FALSE FALSE
## 4  ( 1 )  TRUE    TRUE   TRUE FALSE  TRUE
## 5  ( 1 )  TRUE    TRUE   TRUE  TRUE  TRUE
```

Conclusion

From the above, we conclude that the variable selection in this case gives us the same set for all four methods.