multi_reg_1.R

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```
if(!require(car)) install.packages("car"); library(car)
```

```
## Loading required package: car
```

```
## Warning: package 'car' was built under R version 3.4.4
```

```
## Loading required package: carData
```

```
## Warning: package 'carData' was built under R version 3.4.4
```

```
# 다중회귀모형
# 단순회귀모형은 반응변수와 설명변수가 각각 1 개인 경우
# 설명변수가 여러개와 반응변수 간 선형관계식을 세우는 분석이 다중회귀분석
par(mfrow=c(1,1))

data(iris)
head(iris)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 3          4.7         3.2          1.3         0.2  setosa
## 4          4.6         3.1          1.5         0.2  setosa
## 5          5.0         3.6          1.4         0.2  setosa
## 6          5.4         3.9          1.7         0.4  setosa
```

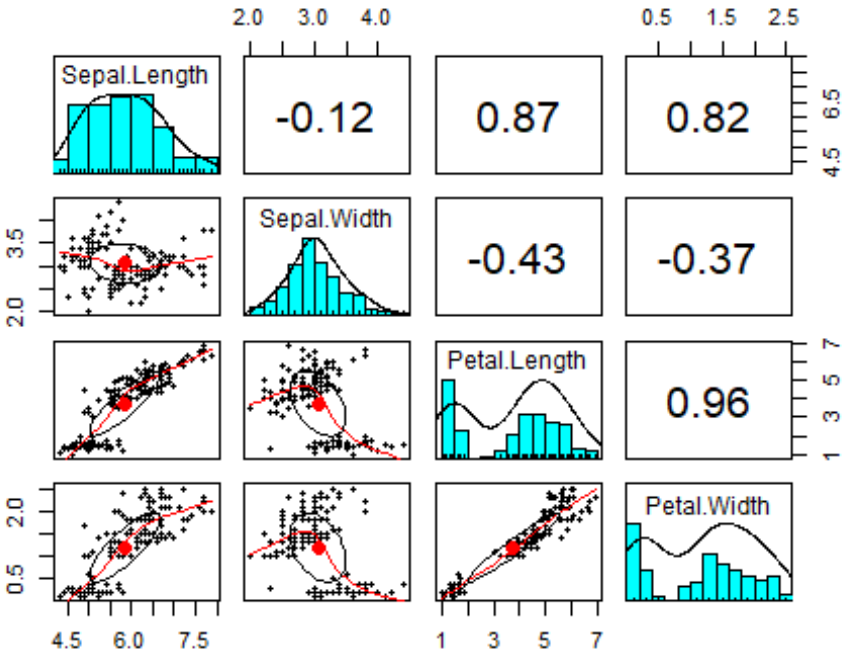
```
# Sepal.Length = Sepal.width + Petal.length+Petal.width + species 로 구성된 회귀식을 세워보자.
# 회귀분석 전 설명변수와 반응변수의 관계를 시각적으로 확인하기 위한 산점도를 그려보자.
# 여러 변수 간 상관성을 살펴보기 위해 pairs.panels() 함수 이용

if (!require(psych)) install.packages("psych"); library(psych)
```

```
## Loading required package: psych
```

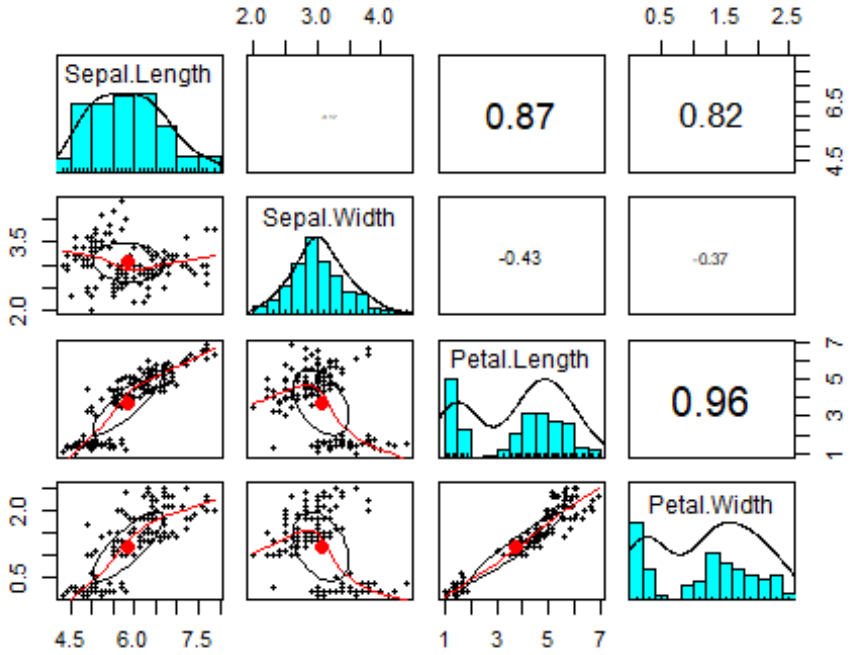
```
## Warning: package 'psych' was built under R version 3.4.4
```

```
##
## Attaching package: 'psych'

## The following object is masked from 'package:car':
##
##     logit
```

```
pairs.panels(iris[,1:4], scale=FALSE)
```



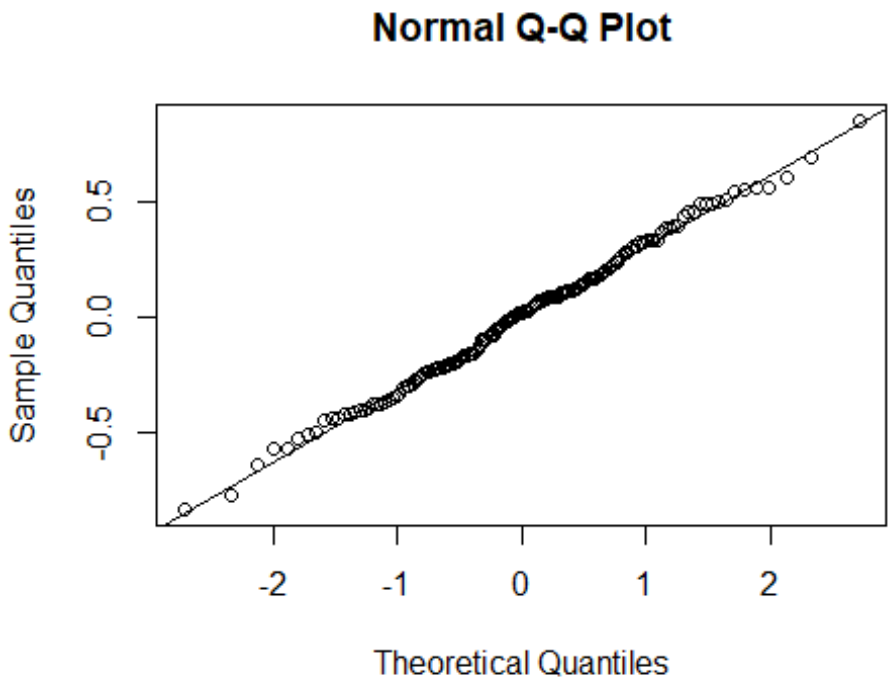

```
pairs.panels(iris[,1:4], scale=TRUE)
```




```
out.i <- lm(Sepal.Length ~ Sepal.Width + Petal.Length+ Petal.Width, data=iris)
summary(out.i)
```

```
##
## Call:
## lm(formula = Sepal.Length ~ Sepal.Width + Petal.Length + Petal.Width,
##     data = iris)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.82816 -0.21989  0.01875  0.19709  0.84570
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.85600    0.25078   7.401 9.85e-12 ***
## Sepal.Width   0.65084    0.06665   9.765  < 2e-16 ***
## Petal.Length  0.70913    0.05672  12.502  < 2e-16 ***
## Petal.Width  -0.55648    0.12755  -4.363 2.41e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3145 on 146 degrees of freedom
## Multiple R-squared:  0.8586, Adjusted R-squared:  0.8557
## F-statistic: 295.5 on 3 and 146 DF,  p-value: < 2.2e-16
```

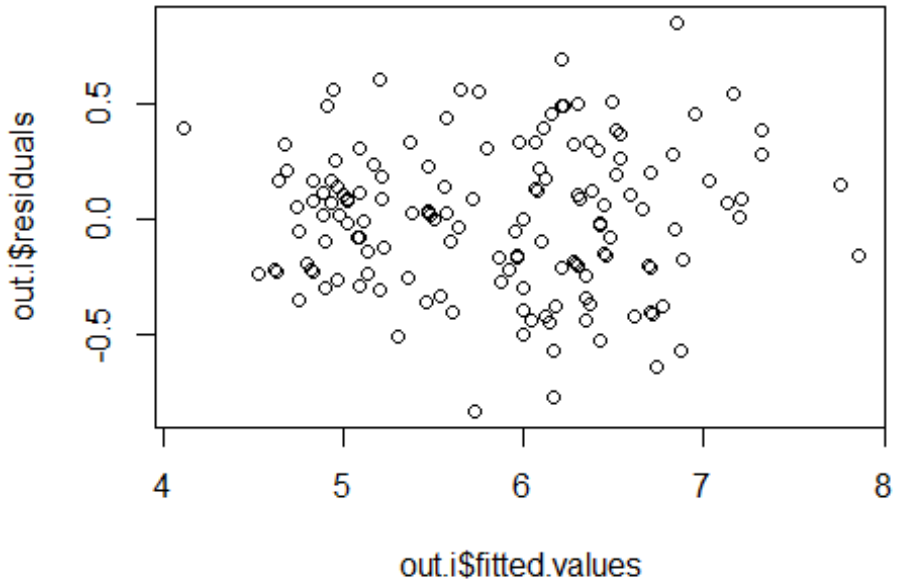
```r
# 다중회귀모형의 경우 설명변수가 증가할 수록 R^2 가 증가한다.
# 불필요한 독립변수가 모형에 반영될 필요가 없으므로 독립변수의 수에 벌점을 준 수정된 R^2 로 최적모형 결정한다.
# adj. R^2 = 1 - (SSE/(n-k-1)) / (SST/(n-1))
# 여기서 n 은 데이터의 수, k 는 독립 변수의 수이다.

# 정규성 검정
qqnorm(out.i$residuals)
qqline(out.i$residuals)
```




```r
shapiro.test(out.i$residuals)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  out.i$residuals
## W = 0.99559, p-value = 0.9349
```

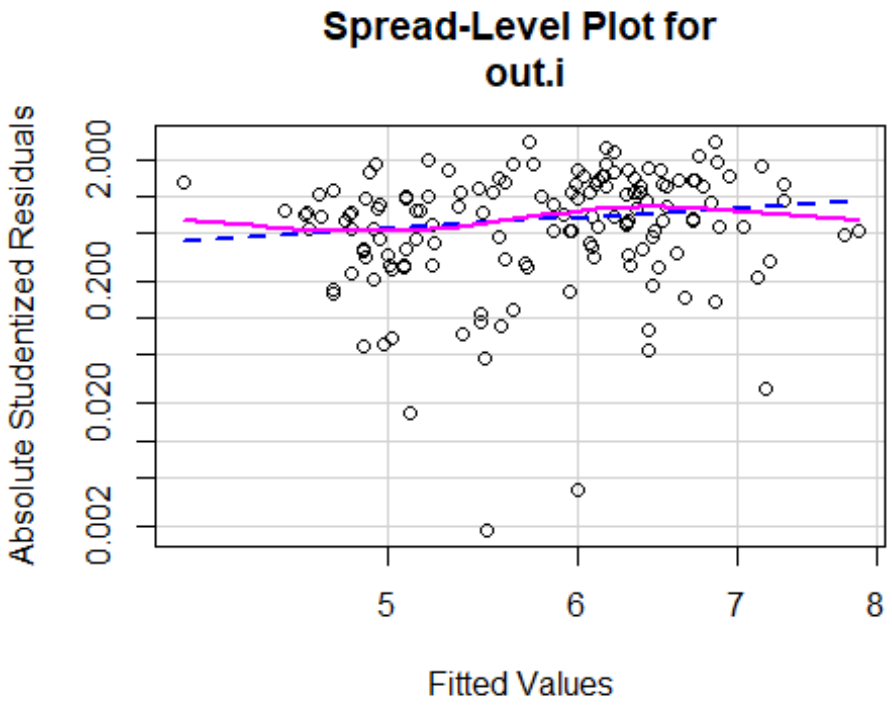
```r
# 독립성 검정
plot(out.i$fitted.values, out.i$residuals)
```




```
durbinWatsonTest(out.i)
```

```
##  lag Autocorrelation D-W Statistic p-value
##    1     -0.03992126      2.060382   0.784
##  Alternative hypothesis: rho != 0
```

```
# 등분산성 검정
spreadLevelPlot(out.i)
```




```
##
## Suggested power transformation:  -0.1805994
```

```
ncvTest(out.i)
```

```
## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
## Chisquare = 4.448612    Df = 1     p = 0.03492962
```

```
# 다중공선성 문제, 독립변수들 간 높은 상관관계가 있는 경우 다중회귀모형 추정이 어려움
# 확인하기 위해 분산팽창지수 (vif)를 확인해야함.
# 만약 vif>5 이상이면 변수선택, 능형회귀모형, 주성분회귀모형 등을 통해 다중공선성 문제 해결이 필요
```

```
vif(out.i) #  Petal.Length 와  Petal.Width 의 vif>5 이상임
```

```
##  Sepal.Width Petal.Length  Petal.Width
##     1.270815    15.097572    14.234335
```

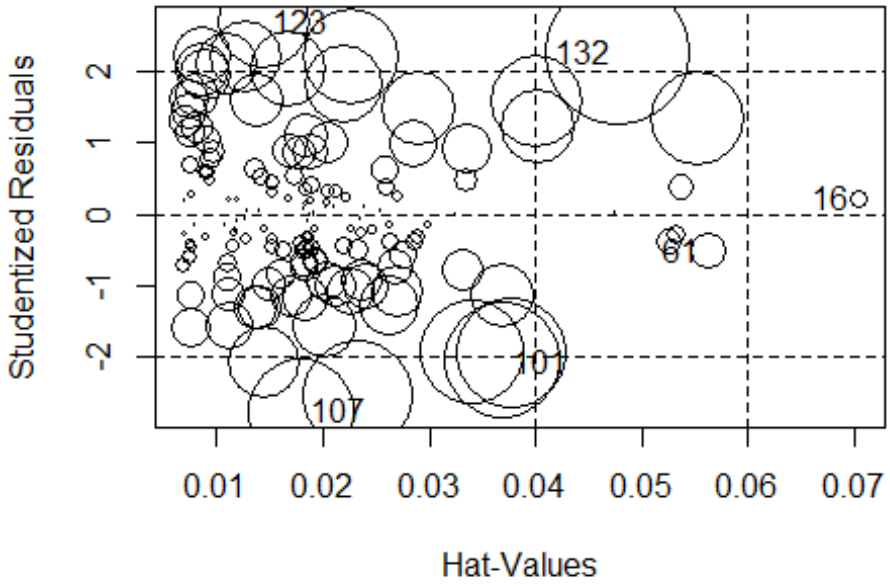
```r
out.i2 <- lm(Sepal.Length ~ Sepal.Width + Petal.Width, data=iris) # 높은 vif 순으로 제거
vif(out.i2) # 다중공선성 문제 해결
```

```
## Sepal.Width Petal.Width
##    1.154799    1.154799
```

```r
summary(out.i2)
```

```
##
## Call:
## lm(formula = Sepal.Length ~ Sepal.Width + Petal.Width, data = iris)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.2076 -0.2288 -0.0450  0.2266  1.1810
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  3.45733    0.30919   11.18  < 2e-16 ***
## Sepal.Width  0.39907    0.09111    4.38 2.24e-05 ***
## Petal.Width  0.97213    0.05210   18.66  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4511 on 147 degrees of freedom
## Multiple R-squared:  0.7072, Adjusted R-squared:  0.7033
## F-statistic: 177.6 on 2 and 147 DF,  p-value: < 2.2e-16
```

```r
# 회귀모형의 진단 및 보정
# 지렛대점, 영향점, 이상점을 알아보자.
influencePlot(out.i2)
```




```
##         StudRes        Hat       CookD
## 16   0.2243801 0.07040119 0.001279224
## 61  -0.5181403 0.05640452 0.005376110
## 101 -2.0661597 0.03702741 0.053525880
## 107 -2.7617060 0.01791588 0.044378518
## 123  2.6926993 0.01440015 0.033871613
## 132  2.2619187 0.04787655 0.083419653

# StudRes : 이상점 여부 확인
# Hat : 모자행렬을 이용한 지렛대 점 확인
# CookD : 영향점 확인

# 이상점은 outlierTest()함수를 통해 확인
# 이상점이 많을 수록 모형의 결정계수인 R^2 가 감소됨
outlierTest(out.i2)

## No Studentized residuals with Bonferonni p < 0.05
## Largest |rstudent|:
##      rstudent unadjusted p-value Bonferonni p
## 107 -2.761706          0.0064892      0.97338

# Hat 이 2(k+1)/n 이면 지렛대 점으로 주의깊게 볼 필요가 있음
2*(2+1)/nrow(iris)
```

```
## [1] 0.04
```

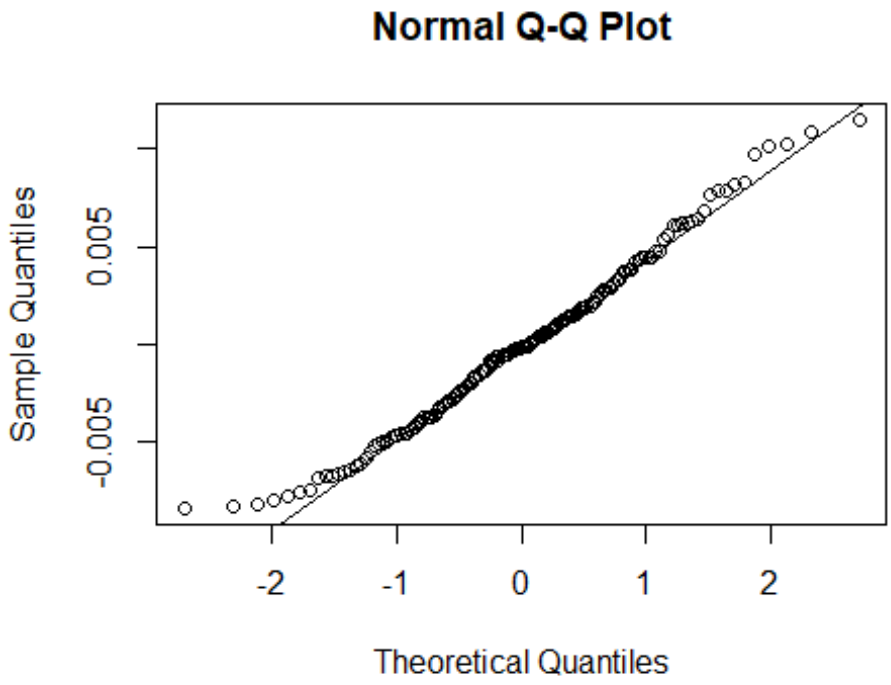
```
# 쿡의 거리는 4/(n-k-1)보다 크면 영향점으로 판단
4/(nrow(iris)-2-1)
```

```
## [1] 0.02721088
```

```
# 영향점 : 101, 107, 123, 132
# 지렛대점 : 16, 61, 132
# 이상점 : 107

# 영향점과 이상점은 회귀모형에 안 좋은 영향을 미치는 자료로 제거시 더 좋은 회귀모형식을 얻을 수 있다.
# 단, 두 개 이상의 이상점이 이웃하면 서로의 이상점 효과가 상쇄될 수 있다.
# 모형이 변하면 이상점을 다시 조사해야 한다.
# 데이터셋이 클 경우 한 두개의 이상점은 문제되지 않지만,
# 이상점이 그룹을 형성하는 경우에는 분석에 주의해야 한다.

# 이 자료의 경우 101, 107, 123, 132 가 회귀모형에 악영향을 미친다고 판단되므로 제거하여 회귀모형을 다시 세우면

iris2 <- iris[c(-101,-107, -123, -132),]

out.i3 <- lm(Sepal.Length^-2 ~ Sepal.Width + Petal.Width, data=iris2)
summary(out.i3)

##
## Call:
## lm(formula = Sepal.Length^-2 ~ Sepal.Width + Petal.Width, data = iris2)
##
## Residuals:
##       Min         1Q     Median         3Q        Max
## -0.0083568 -0.0033739 -0.0001687  0.0028311  0.0114947
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.0543934  0.0031708  17.154  < 2e-16 ***
## Sepal.Width -0.0035895  0.0009328  -3.848 0.000179 ***
## Petal.Width -0.0103619  0.0005343 -19.393  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.004492 on 143 degrees of freedom
```

```
## Multiple R-squared:  0.7328, Adjusted R-squared:  0.7291
## F-statistic: 196.1 on 2 and 143 DF,  p-value: < 2.2e-16
```

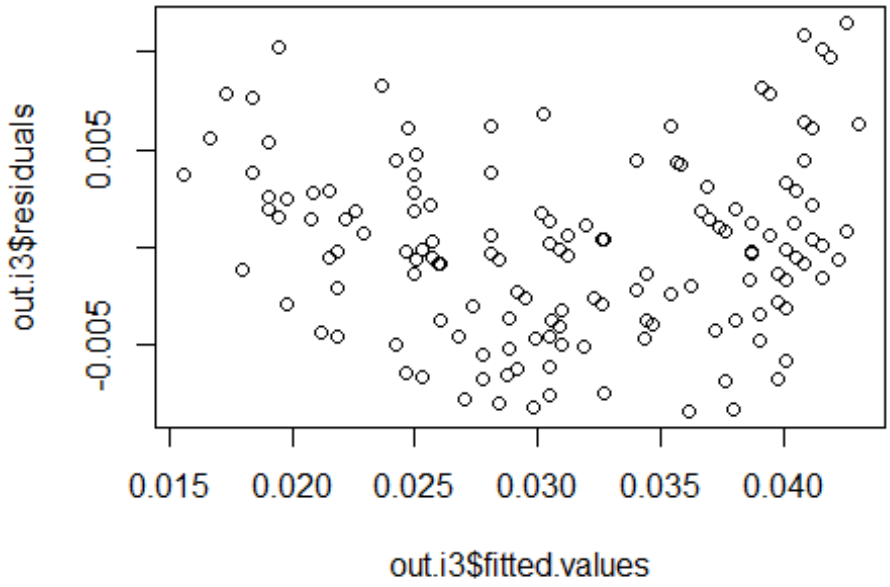
```
# 정규성 검정
qqnorm(out.i3$residuals)
qqline(out.i3$residuals)
```




```
shapiro.test(out.i3$residuals)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  out.i3$residuals
## W = 0.98497, p-value = 0.1126
```

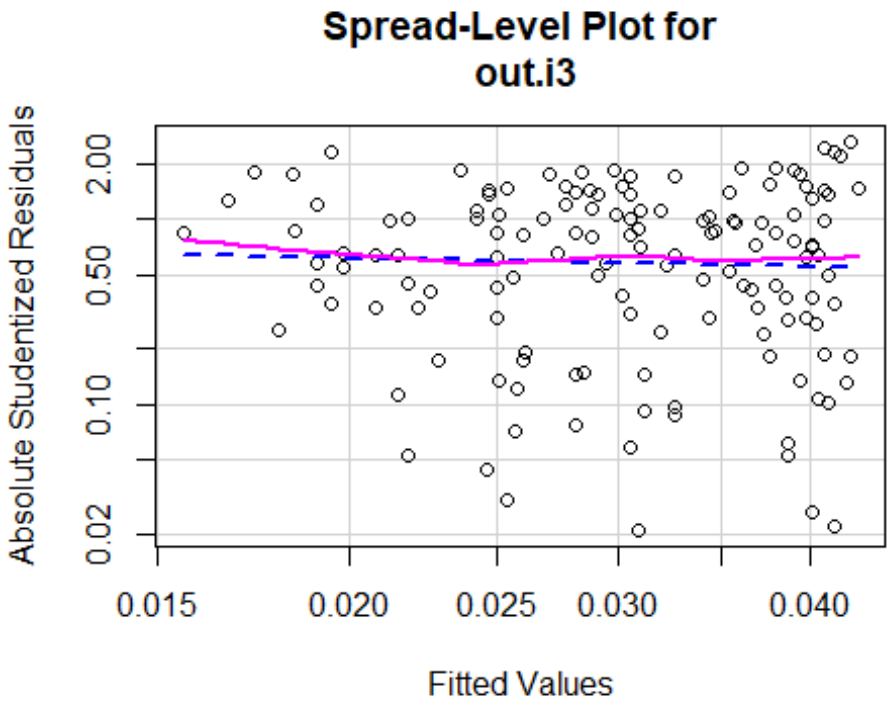
```
# 독립성 검정
plot(out.i3$fitted.values, out.i3$residuals)
```



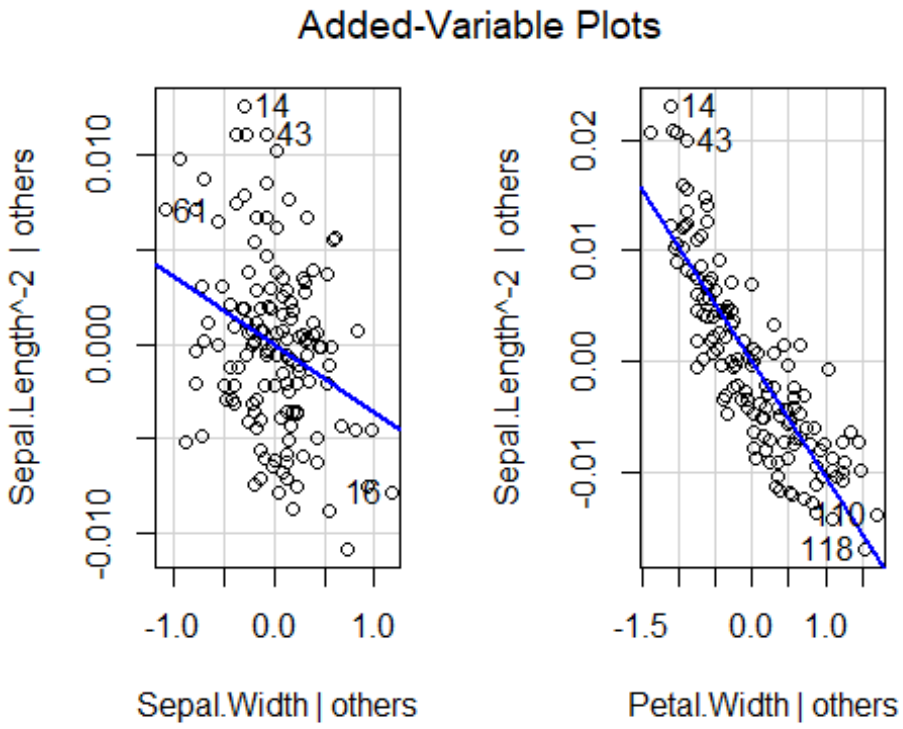

```
durbinWatsonTest(out.i3)
```

```
##  lag Autocorrelation D-W Statistic p-value
##    1       0.1525169      1.689486   0.058
##  Alternative hypothesis: rho != 0
```

```
# 등분산성 검정
spreadLevelPlot(out.i3)
```




```
##
## Suggested power transformation:  1.130383

ncvTest(out.i3)

## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
## Chisquare = 0.8141326    Df = 1     p = 0.3669013

# 추가그림은 반응변수와 설명변수의 관계를 2 차식으로 표현한 그림이다.
avPlots(out.i3)
```




```
# 다중공선선, 영향점, 이상점, 지렛대점을 확인


################################################################################
summary(iris) # Species 는 범주형 변수임

##   Sepal.Length    Sepal.Width     Petal.Length    Petal.Width
##  Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100
##  1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300
##  Median :5.800   Median :3.000   Median :4.350   Median :1.300
##  Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199
##  3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800
##  Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500
##        Species
##  setosa    :50
##  versicolor:50
##  virginica :50
##
##
##

# 범주형 자료는 factor 로 변환하여 분석
# factor 로 변환시 가변수로 처리하여 회귀모형을 세움
```

```r
out.i2 <- lm(Sepal.Length ~ Sepal.Width + Petal.Length+ Petal.Width+as.factor
(Species), data=iris)
summary(out.i2)
```

```
##
## Call:
## lm(formula = Sepal.Length ~ Sepal.Width + Petal.Length + Petal.Width +
##     as.factor(Species), data = iris)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.79424 -0.21874  0.00899  0.20255  0.73103
##
## Coefficients:
##                                Estimate Std. Error t value Pr(>|t|)
## (Intercept)                     2.17127    0.27979   7.760 1.43e-12 ***
## Sepal.Width                     0.49589    0.08607   5.761 4.87e-08 ***
## Petal.Length                    0.82924    0.06853  12.101  < 2e-16 ***
## Petal.Width                    -0.31516    0.15120  -2.084  0.03889 *
## as.factor(Species)versicolor -0.72356    0.24017  -3.013  0.00306 **
## as.factor(Species)virginica  -1.02350    0.33373  -3.067  0.00258 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3068 on 144 degrees of freedom
## Multiple R-squared:  0.8673, Adjusted R-squared:  0.8627
## F-statistic: 188.3 on 5 and 144 DF,  p-value: < 2.2e-16
```

```r
# 범주형 결과에 대한 해석
# default : setosa
# versicolor : setosa 종에 비해 versicolor 종의  Sepal.Length 가 -0.72356 작다
# virginica  : setosa 종에 비해 virginica 종의  Sepal.Length 가 -1.02350 작다

# 아이리스의 종별 Sepal.Length 의 식을 다시 정리하면 아래와 같다.
# setosa : 2.17+Sepal.width*0.49 + petal.length*0.82+Petal.width*-0.31
# versicolor : 2.17 -0.72356 +Sepal.width*0.49 + petal.length*0.82+Petal.widt
h*-0.31
# virginica : 2.17 - 1.02350 +Sepal.width*0.49 + petal.length*0.82+Petal.widt
h*-0.31

################################################################################
# 회귀모형의 설명변수가 많은 경우 중요한 설명변수를 선택해야한다.
# 1. 전진선택법
# 2. 후진제거법
# 3. 단계적 방법
```

```r
# 위의 세가지 방법은 step()함수를 통해 진행할 수 있다.

if(!require(mlbench)) install.packages("mlbench"); library(mlbench)

## Loading required package: mlbench

data("BostonHousing")

m <- lm (medv ~ ., data=BostonHousing) # 여기서 .은  medv 를 제외한 모든 변수를 설명변수로 간
m2 <- step(m, ddirection="forward") # 전진선택법

## Start:  AIC=1589.64
## medv ~ crim + zn + indus + chas + nox + rm + age + dis + rad +
##     tax + ptratio + b + lstat
##
##           Df Sum of Sq   RSS    AIC
## - age      1      0.06 11079 1587.7
## - indus    1      2.52 11081 1587.8
## <none>                 11079 1589.6
## - chas     1    218.97 11298 1597.5
## - tax      1    242.26 11321 1598.6
## - crim     1    243.22 11322 1598.6
## - zn       1    257.49 11336 1599.3
## - b        1    270.63 11349 1599.8
## - rad      1    479.15 11558 1609.1
## - nox      1    487.16 11566 1609.4
## - ptratio  1   1194.23 12273 1639.4
## - dis      1   1232.41 12311 1641.0
## - rm       1   1871.32 12950 1666.6
## - lstat    1   2410.84 13490 1687.3
##
## Step:  AIC=1587.65
## medv ~ crim + zn + indus + chas + nox + rm + dis + rad + tax +
##     ptratio + b + lstat
##
##           Df Sum of Sq   RSS    AIC
## - indus    1      2.52 11081 1585.8
## <none>                 11079 1587.7
## - chas     1    219.91 11299 1595.6
## - tax      1    242.24 11321 1596.6
## - crim     1    243.20 11322 1596.6
## - zn       1    260.32 11339 1597.4
## - b        1    272.26 11351 1597.9
## - rad      1    481.09 11560 1607.2
## - nox      1    520.87 11600 1608.9
## - ptratio  1   1200.23 12279 1637.7
```

```
## - dis      1   1352.26 12431 1643.9
## - rm       1   1959.55 13038 1668.0
## - lstat    1   2718.88 13798 1696.7
##
## Step:  AIC=1585.76
## medv ~ crim + zn + chas + nox + rm + dis + rad + tax + ptratio +
##     b + lstat
##
##           Df Sum of Sq   RSS    AIC
## <none>                  11081 1585.8
## - chas     1    227.21 11309 1594.0
## - crim     1    245.37 11327 1594.8
## - zn       1    257.82 11339 1595.4
## - b        1    270.82 11352 1596.0
## - tax      1    273.62 11355 1596.1
## - rad      1    500.92 11582 1606.1
## - nox      1    541.91 11623 1607.9
## - ptratio  1   1206.45 12288 1636.0
## - dis      1   1448.94 12530 1645.9
## - rm       1   1963.66 13045 1666.3
## - lstat    1   2723.48 13805 1695.0

m3 <- step(m, ddirection="bacward") # 후진제거법

## Start:  AIC=1589.64
## medv ~ crim + zn + indus + chas + nox + rm + age + dis + rad +
##     tax + ptratio + b + lstat
##
##           Df Sum of Sq   RSS    AIC
## - age      1      0.06 11079 1587.7
## - indus    1      2.52 11081 1587.8
## <none>                  11079 1589.6
## - chas     1    218.97 11298 1597.5
## - tax      1    242.26 11321 1598.6
## - crim     1    243.22 11322 1598.6
## - zn       1    257.49 11336 1599.3
## - b        1    270.63 11349 1599.8
## - rad      1    479.15 11558 1609.1
## - nox      1    487.16 11566 1609.4
## - ptratio  1   1194.23 12273 1639.4
## - dis      1   1232.41 12311 1641.0
## - rm       1   1871.32 12950 1666.6
## - lstat    1   2410.84 13490 1687.3
##
## Step:  AIC=1587.65
## medv ~ crim + zn + indus + chas + nox + rm + dis + rad + tax +
##     ptratio + b + lstat
##
##           Df Sum of Sq   RSS    AIC
```

```
## - indus    1      2.52 11081 1585.8
## <none>                 11079 1587.7
## - chas     1    219.91 11299 1595.6
## - tax      1    242.24 11321 1596.6
## - crim     1    243.20 11322 1596.6
## - zn       1    260.32 11339 1597.4
## - b        1    272.26 11351 1597.9
## - rad      1    481.09 11560 1607.2
## - nox      1    520.87 11600 1608.9
## - ptratio  1   1200.23 12279 1637.7
## - dis      1   1352.26 12431 1643.9
## - rm       1   1959.55 13038 1668.0
## - lstat    1   2718.88 13798 1696.7
##
## Step:  AIC=1585.76
## medv ~ crim + zn + chas + nox + rm + dis + rad + tax + ptratio +
##     b + lstat
##
##           Df Sum of Sq   RSS    AIC
## <none>                 11081 1585.8
## - chas     1    227.21 11309 1594.0
## - crim     1    245.37 11327 1594.8
## - zn       1    257.82 11339 1595.4
## - b        1    270.82 11352 1596.0
## - tax      1    273.62 11355 1596.1
## - rad      1    500.92 11582 1606.1
## - nox      1    541.91 11623 1607.9
## - ptratio  1   1206.45 12288 1636.0
## - dis      1   1448.94 12530 1645.9
## - rm       1   1963.66 13045 1666.3
## - lstat    1   2723.48 13805 1695.0
```

```
m4 <- step(m, ddirection="both")    # 단계적방법
```

```
## Start:  AIC=1589.64
## medv ~ crim + zn + indus + chas + nox + rm + age + dis + rad +
##     tax + ptratio + b + lstat
##
##           Df Sum of Sq   RSS    AIC
## - age      1      0.06 11079 1587.7
## - indus    1      2.52 11081 1587.8
## <none>                 11079 1589.6
## - chas     1    218.97 11298 1597.5
## - tax      1    242.26 11321 1598.6
## - crim     1    243.22 11322 1598.6
## - zn       1    257.49 11336 1599.3
## - b        1    270.63 11349 1599.8
## - rad      1    479.15 11558 1609.1
## - nox      1    487.16 11566 1609.4
```

```
## - ptratio  1   1194.23 12273 1639.4
## - dis      1   1232.41 12311 1641.0
## - rm       1   1871.32 12950 1666.6
## - lstat    1   2410.84 13490 1687.3
##
## Step:  AIC=1587.65
## medv ~ crim + zn + indus + chas + nox + rm + dis + rad + tax +
##     ptratio + b + lstat
##
##           Df Sum of Sq   RSS    AIC
## - indus    1      2.52 11081 1585.8
## <none>                 11079 1587.7
## - chas     1    219.91 11299 1595.6
## - tax      1    242.24 11321 1596.6
## - crim     1    243.20 11322 1596.6
## - zn       1    260.32 11339 1597.4
## - b        1    272.26 11351 1597.9
## - rad      1    481.09 11560 1607.2
## - nox      1    520.87 11600 1608.9
## - ptratio  1   1200.23 12279 1637.7
## - dis      1   1352.26 12431 1643.9
## - rm       1   1959.55 13038 1668.0
## - lstat    1   2718.88 13798 1696.7
##
## Step:  AIC=1585.76
## medv ~ crim + zn + chas + nox + rm + dis + rad + tax + ptratio +
##     b + lstat
##
##           Df Sum of Sq   RSS    AIC
## <none>                 11081 1585.8
## - chas     1    227.21 11309 1594.0
## - crim     1    245.37 11327 1594.8
## - zn       1    257.82 11339 1595.4
## - b        1    270.82 11352 1596.0
## - tax      1    273.62 11355 1596.1
## - rad      1    500.92 11582 1606.1
## - nox      1    541.91 11623 1607.9
## - ptratio  1   1206.45 12288 1636.0
## - dis      1   1448.94 12530 1645.9
## - rm       1   1963.66 13045 1666.3
## - lstat    1   2723.48 13805 1695.0
```

```
formula(m2)
```

```
## medv ~ crim + zn + chas + nox + rm + dis + rad + tax + ptratio +
##     b + lstat
```

```
formula(m3)
```

```
## medv ~ crim + zn + chas + nox + rm + dis + rad + tax + ptratio +
##     b + lstat
```

```
formula(m4)
```

```
## medv ~ crim + zn + chas + nox + rm + dis + rad + tax + ptratio +
##     b + lstat
```

```
# 모든 가능한 경우를 고려한 최적모형 찾기
# leaps::regsubsets()함수는 2N 개의 회귀 모형을 만들어 비교를 수행하는 함수
```

```
if(!require(leaps)) install.packages("leaps"); library(leaps)
```

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

```
m5 <- regsubsets(medv ~., data=BostonHousing)
summary(m5)
```

```
## Subset selection object
## Call: regsubsets.formula(medv ~ ., data = BostonHousing)
## 13 Variables  (and intercept)
##         Forced in Forced out
## crim        FALSE      FALSE
## zn          FALSE      FALSE
## indus       FALSE      FALSE
## chas1       FALSE      FALSE
## nox         FALSE      FALSE
## rm          FALSE      FALSE
## age         FALSE      FALSE
## dis         FALSE      FALSE
## rad         FALSE      FALSE
## tax         FALSE      FALSE
## ptratio     FALSE      FALSE
## b           FALSE      FALSE
## lstat       FALSE      FALSE
## 1 subsets of each size up to 8
## Selection Algorithm: exhaustive
##          crim zn  indus chas1 nox rm  age dis rad tax ptratio b   lstat
## 1  ( 1 ) " "  " " " "   " "   " " " " " " " " " " " " "     " " "*"
## 2  ( 1 ) " "  " " " "   " "   " " "*" " " " " " " " " "     " " "*"
## 3  ( 1 ) " "  " " " "   " "   " " "*" " " " " " " " "*"     " " "*"
## 4  ( 1 ) " "  " " " "   " "   " " "*" " " "*" " " " " "*"     " " "*"
## 5  ( 1 ) " "  " " " "   " "   "*" "*" " " "*" " " " " "*"     " " "*"
## 6  ( 1 ) " "  " " " "   "*"   "*" "*" " " "*" " " " " "*"     " " "*"
## 7  ( 1 ) " "  " " " "   "*"   "*" "*" " " "*" " " " " "*"     "*" "*"
## 8  ( 1 ) " "  "*" " "   "*"   "*" "*" " " "*" " " " " "*"     "*" "*"
```

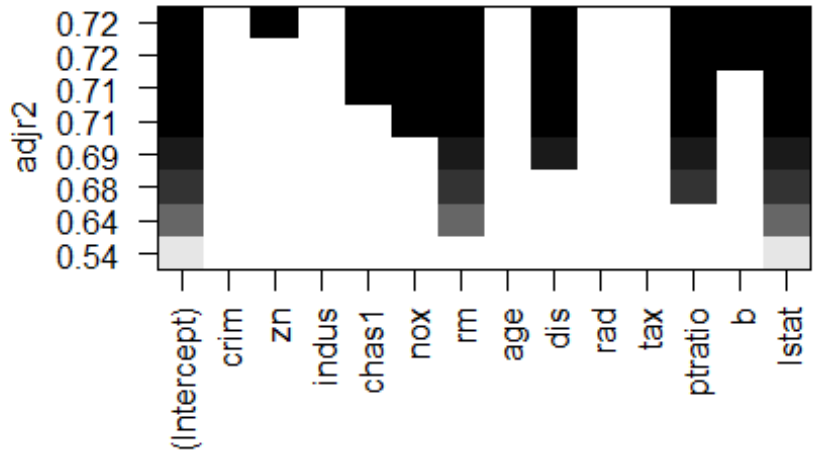
```
summary(m5)$bic
```

```
## [1] -385.0521 -496.2582 -549.4767 -561.9884 -585.6823 -592.9553 -598.2295
## [8] -600.1663
```

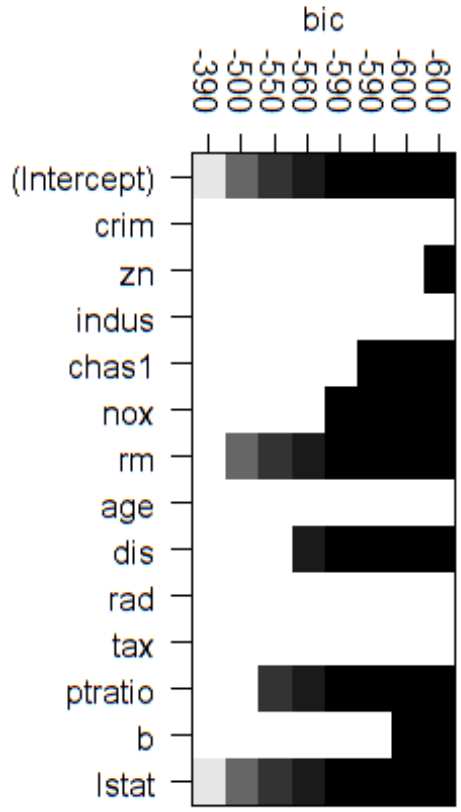
```
summary(m5)$adjr2
```

```
## [1] 0.5432418 0.6371245 0.6767036 0.6878351 0.7051702 0.7123567 0.7182560
## [8] 0.7222072
```

```
plot(m5, scale="adjr2")
```




```
plot(m5, scale="bic")
```


bic
-390
-500
-550
-560
-590
-590
-600
-600
(Intercept)
crim
zn
indus
chas1
nox
rm
age
dis
rad
tax
ptratio
b
lstat