Multiple linear regression

Introduction

In multiple linear regression, we have a dependent variable Y which we would like to explain in terms of the multiple independent variables X_1, X_2, ..., X_q simultaneously.

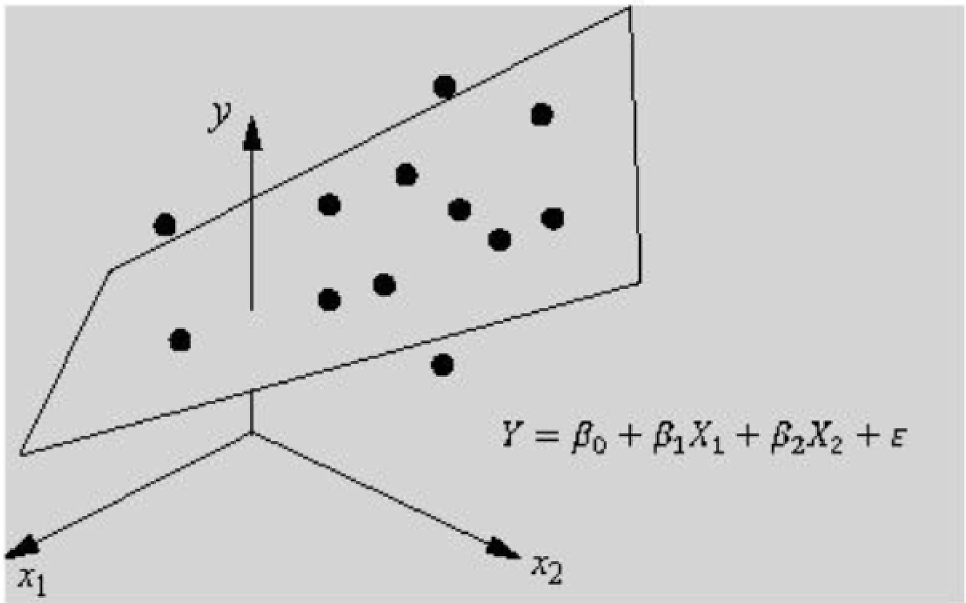


Figure 1: Figure 1: A multiple regression model (with two explanatory variables) represented as a hyperplane in three-dimensional space. The dots surrounding the hyperplane represent the observed data.

The general notation of the model is:

$$Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + ... + \beta_q X_q + \epsilon$$

where

Y is the value of the response variable;

X_j is the value of the j explanatory variable;

β_0 is the intercept, and β_j is the partial slope of the j explanatory variable;

ϵ is that part of Y which is not explained by the regression (i.e. the error).

The parameters, $\beta_0, \beta_1, \beta_2, ...\beta_q$, must be estimated from the data. The parameter estimates, $\beta_0, \beta_1, \beta_2, ...\beta_q$, are estimated by R using the method of least squares.

The formula of the fitted model is: $Y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + ... + \beta_q X_q$

Hypotheses concerning the parameters can be tested. For example, for a particular =1,…, :

0: $\beta_j = 0$ (X_j does not "contribute" to the explanation of Y)

1: $\beta_j \neq 0$ (X_j does "contribute" to the explanation of Y)

Load required packages

```r
library(RcmdrMisc)
```

```
Loading required package: car
```

```
Loading required package: carData
```

```
Loading required package: sandwich
```

```r
library(ggplot2)
library(car)
library(MASS)
```

Importing data

```r
chap7data2 <- read.csv("chap7data2.csv", sep=",", header=T)
dim(chap7data2)
```

```
[1] 10  6
```

```r
head(chap7data2)
```

```
    Detox Enzyme1 Enzyme2 Enzyme3 Enzyme4 Enzyme5
1  56.250 106.329  90.756  94.650 162.791 114.737
2  75.000 144.726 203.361 131.687 255.814 112.632
3 115.625 136.287 672.269 123.457 191.860 153.684
4  68.750 154.430 183.193 113.169 133.721 116.842
5  96.875 385.232 140.336 117.284 174.419  87.368
6 168.750 593.544 146.218 152.263 273.256  94.737
```

```r
chap7data3 <- read.csv("chap7data3.csv", sep=",", header=T)
dim(chap7data3)
```

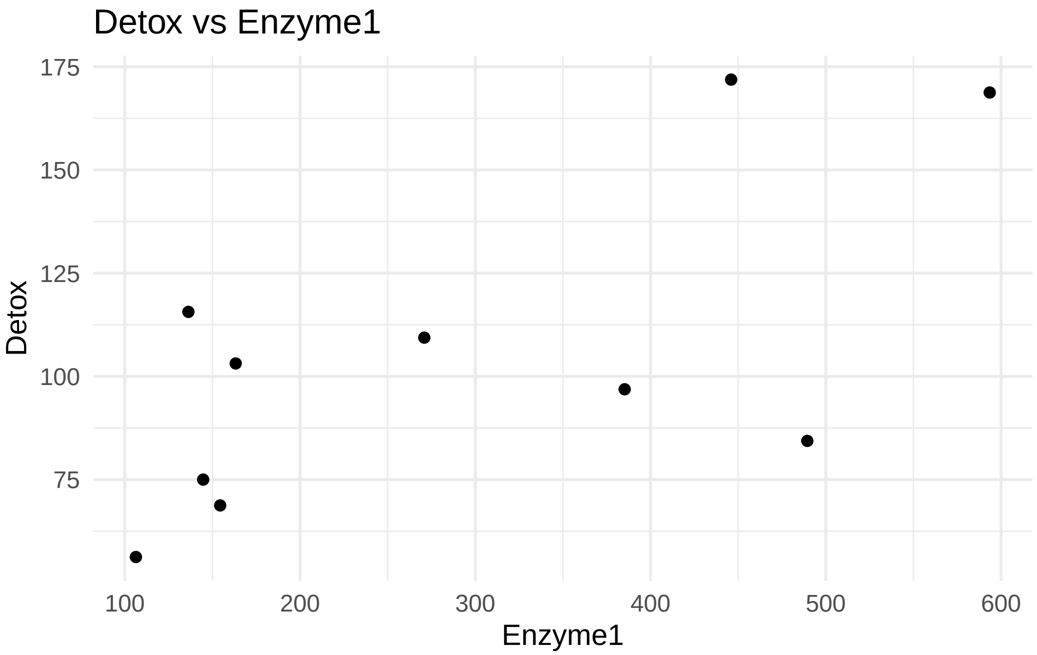
```
[1] 13  5
```

```r
head(chap7data3)
```

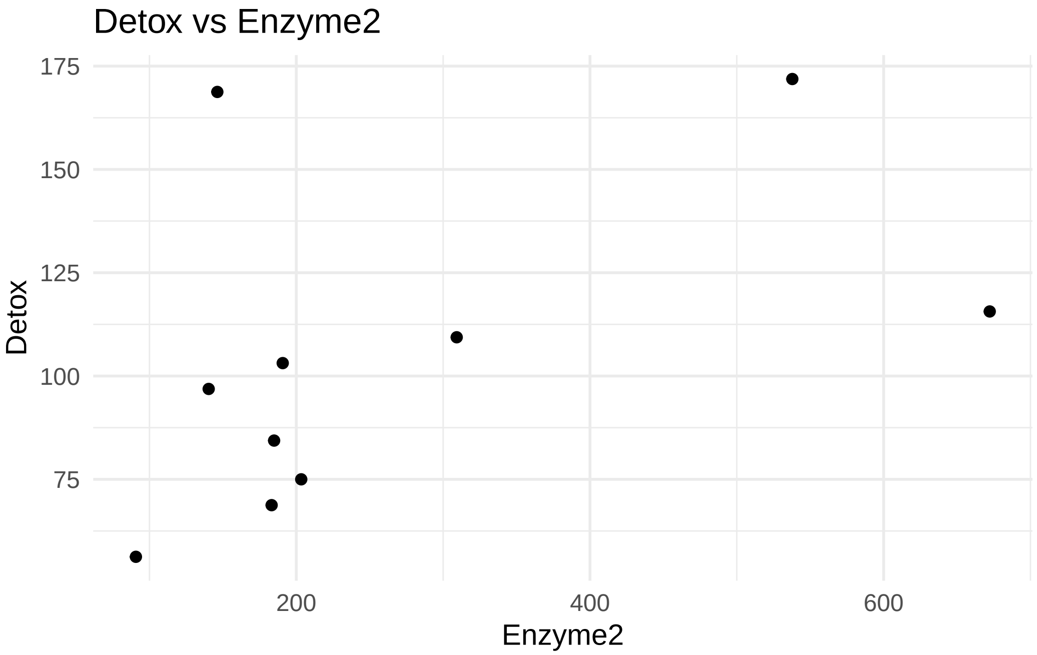
```
  X1 X2 X3 X4     Y
1  7 26  6 60  78.5
2  1 29 15 52  74.3
3 11 56  8 20 104.3
4 11 31  8 47  87.6
5  7 52  6 33  95.9
6 11 55  9 22 109.2
```

#scatter plot

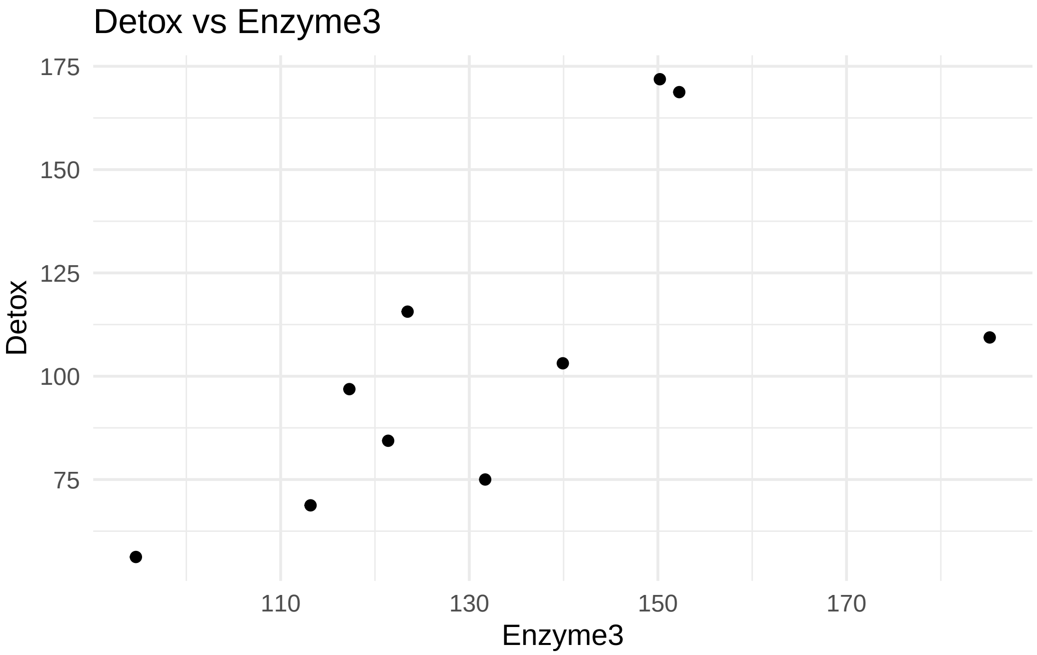
```r
# Scatter plots of 'Detox' against each enzyme
ggplot(chap7data2, aes(x = Enzyme1, y = Detox)) + geom_point() + ggtitle("Detox vs Enzyme1")
  theme_minimal()
```



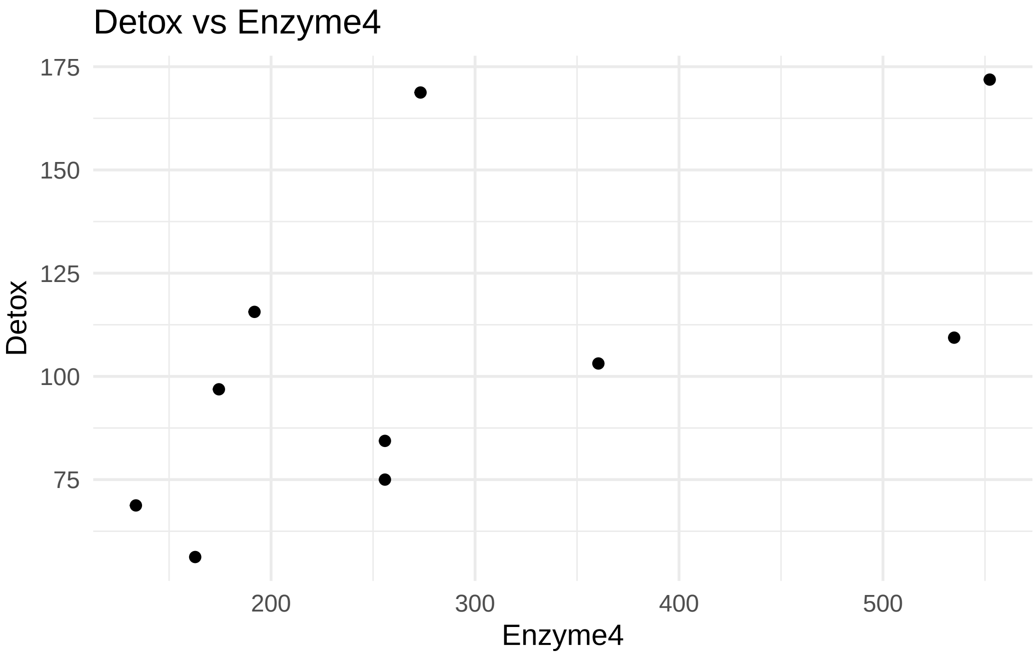
```r
ggplot(chap7data2, aes(x = Enzyme2, y = Detox)) + geom_point() + ggtitle("Detox vs Enzyme2")
  theme_minimal()
```



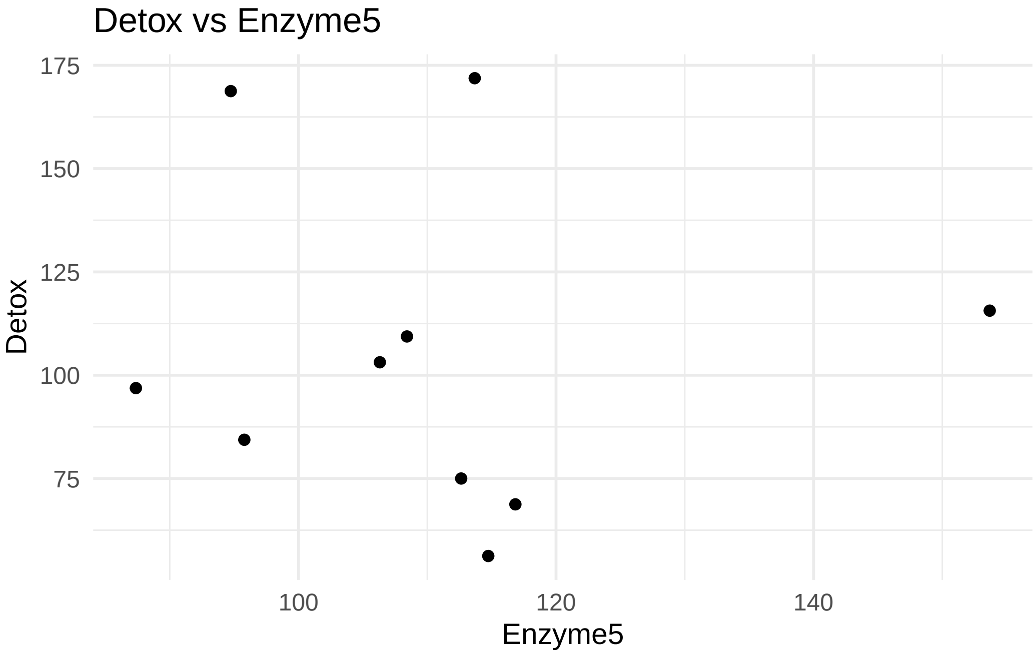
```
ggplot(chap7data2, aes(x = Enzyme3, y = Detox)) + geom_point() + ggtitle("Detox vs Enzyme3")
  theme_minimal()
```



```
ggplot(chap7data2, aes(x = Enzyme4, y = Detox)) + geom_point() + ggtitle("Detox vs Enzyme4")
  theme_minimal()
```

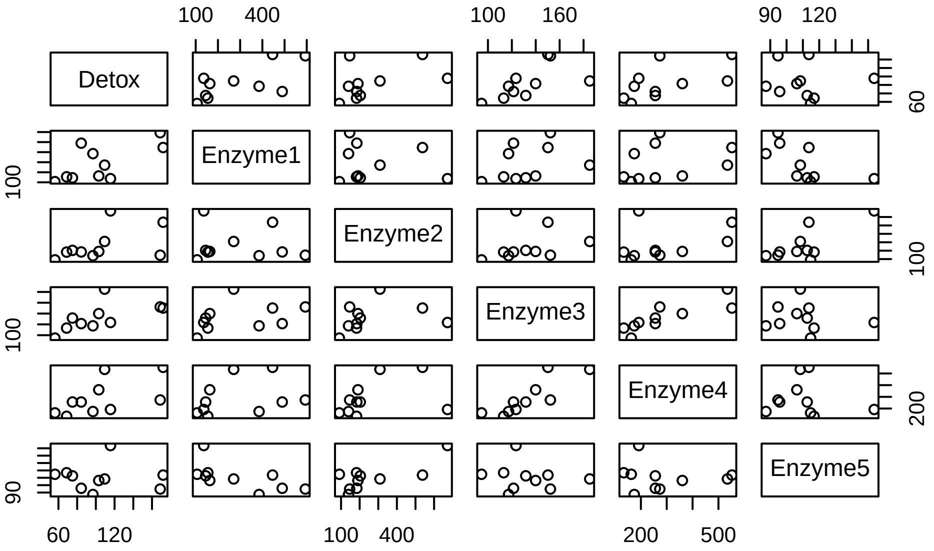


```
ggplot(chap7data2, aes(x = Enzyme5, y = Detox)) + geom_point() + ggtitle("Detox vs Enzyme5")
  theme_minimal()
```



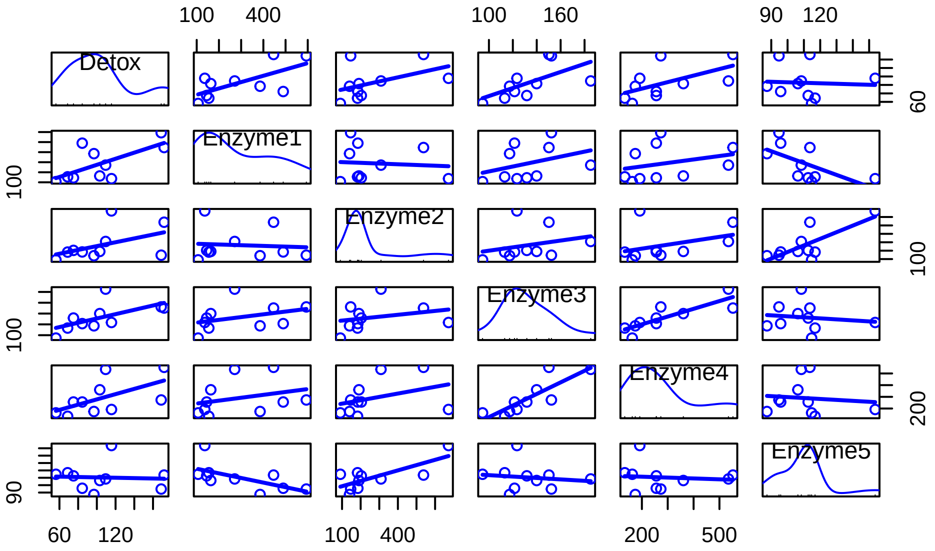
#or

```
plot(chap7data2)
```



#or

```
scatterplotMatrix(~Detox + Enzyme1 + Enzyme2 + Enzyme3 + Enzyme4 + Enzyme5,
                  reg.line = lm,
                  smooth = FALSE,
                  spread = FALSE,
                  span = 0.5,
                  ellipse = FALSE,
                  levels = c(0.5, 0.9),
                  id.n = 0,
                  diagonal = 'density',
                  data = chap7data2) |> suppressWarnings()
```



Interpretation

This document provides an interpretation of the scatterplot matrix that includes the response variable (`Detox`) and explanatory variables (`Enzyme1`, `Enzyme2`, `Enzyme3`, `Enzyme4`, and `Enzyme5`). The scatterplot matrix is used to visualize the relationships between these variables and identify potential correlations.

1. Relationships Between `Detox` and Each Enzyme

Examine row-wise.

- **`Detox vs. Enzyme1`**:
  There is a positive linear relationship, as indicated by the upward trend in the scatter plot. The regression line is slightly upward, and the points are moderately scattered around it, suggesting a moderate positive correlation.

- **`Detox vs. Enzyme2`**:
  The plot shows a positive linear relationship, as evidenced by the upward trend and a moderately steep regression line. The points are widely scattered without any discernible pattern, suggesting little to no linear relationship between `Detox` and `Enzyme2`.

- **Detox vs. Enzyme3**:
  The plot shows a positive linear relationship, as evidenced by the upward trend and a moderately steep regression line. Points are somewhat dispersed, but there is a noticeable trend suggesting a moderate positive correlation.

- **Detox vs. Enzyme4**:
  The plot shows a positive linear relationship, as evidenced by the upward trend and a moderately steep regression line. The points are widely scattered. This suggests a moderately correlation between Detox and Enzyme4.

- **Detox vs. Enzyme5**:
  The scatter plot indicates a weak relationship with a relatively flat, slightly negative, regression line. The points are fairly scattered, with no clear trend, suggesting little to no linear correlation between Detox and Enzyme5.

2. Relationships Among Explanatory Variables (Enzyme1 to Enzyme5)

- **Enzyme1 vs. Enzyme2**:
  There is a slight negative linear relationship with an downward trend. The regression line is mildy flat, and points are dispersed, indicating a slight negative correlation to little correlation.

- **Enzyme1 vs. Enzyme3, Enzyme4, Enzyme5**:
  All these plots show relatively moderate positive linear relationships, with upward trends and points moderately clustered around the regression lines.

- **Enzyme1 vs. Enzyme5**:
  There is a strong negative linear relationship with an downward trend. The regression line is steep and downwards sloping, and points are relatively clustered, indicating a strong negative correlation.

- **Enzyme2 vs. Enzyme3**:
  The relationship appears to be non-linear, with points forming a curved pattern. This suggests a non-linear relationship between Enzyme2 and Enzyme3.

- **Enzyme2 vs. Enzyme4, Enzyme5**:
  These plots show no clear pattern, suggesting little to no linear relationship between Enzyme2 and either Enzyme4 or Enzyme5.

- **Enzyme3 vs. Enzyme4**:
  There seems to be a positive relationship with an upward trend in the scatter plot, though the points are somewhat scattered, indicating a moderate positive correlation.

- **Enzyme3 vs. Enzyme5**:
  Shows a weak or no discernible relationship, with the points widely scattered around a flat regression line.

- **Enzyme4 vs. Enzyme5**:
  No clear relationship is observed here, as the points are scattered without any noticeable pattern.

3. Diagonal Plots (Density Plots)

- The diagonal plots display the distribution of each variable. For example:
  - **Detox** appears to have a somewhat skewed distribution, possibly slightly left-skewed.
  - **Enzyme1** and **Enzyme3** appear to be normally distributed with slight variation.
  - **Enzyme2** shows a highly skewed distribution with a long tail.
  - **Enzyme4** and **Enzyme5** show more uniform distributions with less obvious skewness.

Conclusion

- `Detox` has a moderate positive relationship with `Enzyme1` and `Enzyme3`, suggesting these enzymes might be more influential in predicting `Detox` levels.
- `Enzyme2` and `Enzyme5` appear to have little to no linear relationship with `Detox`.
- The relationships among explanatory variables vary, with some moderate positive linear correlations (like `Enzyme1` with `Enzyme2`), and some non-linear or weak relationships.

Multiple linear regression

```r
chap7data2.model1 <- lm(Detox~.,data=chap7data2)
# the `.` is shorthand to denote all predictor (i.e., X_j) variables
# to be included in the model

# Alternatively, you can specify the variables independently:
# chap7data2.model1 <- lm(Detox ~ Enzyme1 + Enzyme2 + Enzyme3 +
# Enzyme4 + Enzyme5, data=chap7data2)

summary(chap7data2.model1)
```

```
Call:
lm(formula = Detox ~ ., data = chap7data2)

Residuals:
       1         2         3         4         5         6         7         8 
  2.7526   -3.0631   -0.8577   -2.1760    6.2696   21.6524  -36.4182   11.8682 
       9        10 
-19.7684   19.7406 

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -87.96535  189.66881  -0.464    0.667
Enzyme1       0.17063    0.10045   1.699    0.165
Enzyme2       0.03305    0.14039   0.235    0.825
Enzyme3       0.31844    0.67350   0.473    0.661
Enzyme4       0.04325    0.13468   0.321    0.764
Enzyme5       0.72460    1.69421   0.428    0.691

Residual standard error: 26.35 on 4 degrees of freedom
Multiple R-squared:  0.798, Adjusted R-squared:  0.5455 
F-statistic: 3.161 on 5 and 4 DF,  p-value: 0.1439
```

#the allSubsets() function

```
allSubsets <- function(data,y.name="Y",
                       perf.measure=c("adj.r.squared","r.squared",
                                      "AIC","perc.error")
                       )
 {

  Cols <- names(data)
  Cols <- Cols[! Cols %in% y.name]
  n <- length(Cols)

  id <- unlist(
    lapply(1:n,
           function(i)combn(1:n,i,simplify=F)
    )
    ,recursive=F)

  Formulas <- sapply(id,function(i)
    paste(y.name,"~",paste(Cols[i],collapse="+"))
  )

  result.mat <- matrix(0,nrow=length(Formulas),6)
  result.mat[,1] <- Formulas

  #get all adjusted R2 values
  for(i in 1:length(Formulas)){
   result.mat[i,2] <- summary(
    lm(
    as.formula(Formulas[i]), data=data)
   )$adj.r.squared
  }

  #get all R2 values
  for(i in 1:length(Formulas)){
   result.mat[i,3] <- summary(
    lm(
     as.formula(Formulas[i]), data=data)
    )$r.squared
  }

  #get all AIC's
  for(i in 1:length(Formulas)){
   result.mat[i,4] <- AIC(
    lm(
     as.formula(Formulas[i]), data=data)
   )
  }

  #get all sigma's
  for(i in 1:length(Formulas)){
   result.mat[i,5] <- summary(
    lm(
     as.formula(Formulas[i]), data=data
     )
   )$sigma/mean(data[,y.name])
  }

  #get all mallows cp's
  for(i in 1:length(Formulas)){
   result.mat[i,6] <- mallows.cp(data=data,model=lm(
    as.formula(Formulas[i]), data=data), y.name=y.name)
   }

  colnames(result.mat) <- c("Model",
                            "adj.r.squared",
                            "r.squared",
                            "AIC","perc.error",
                            "mallows.cp")


  final.output <- data.frame(
   result.mat[order(result.mat[,perf.measure],decreasing=T),]
   )

  return(final.output)

}
```

calculating the Mallow's Cp statistic (function)

Goal: Choose models where Cp ≈ p

Interpretation: Helps select models with a good balance of fit and complexity.

```
mallows.cp <- function(data,model,y.name)
{

  n <- nrow(data)
  p <- length(model$coefficients)

  mean.sq.error <- summary(
   lm(
    as.formula(paste(y.name,"~.")),data=data
    )
   )$sigma^2

  sse <- summary(model)$sigma^2*summary(model)$df[2]

  cp <- sse/mean.sq.error-(n-2*p)
  cp/100
}
```

Variable selection

```
stepwise(chap7data2.model1, direction='backward/forward', criterion='AIC')
```

```
Direction:  backward/forward
Criterion:  AIC

Start:  AIC=68.27
Detox ~ Enzyme1 + Enzyme2 + Enzyme3 + Enzyme4 + Enzyme5

          Df Sum of Sq    RSS    AIC
- Enzyme2  1     38.50 2816.7 66.407
- Enzyme4  1     71.60 2849.8 66.524
- Enzyme5  1    127.05 2905.2 66.717
- Enzyme3  1    155.27 2933.4 66.813
<none>                 2778.2 68.270
- Enzyme1  1   2004.15 4782.3 71.701

Step:  AIC=66.41
Detox ~ Enzyme1 + Enzyme3 + Enzyme4 + Enzyme5

          Df Sum of Sq    RSS    AIC
- Enzyme3  1     130.4 2947.1 64.860
- Enzyme4  1     221.1 3037.8 65.163
<none>                 2816.7 66.407
+ Enzyme2  1      38.5 2778.2 68.270
- Enzyme5  1    2216.4 5033.0 70.212
- Enzyme1  1    5478.4 8295.1 75.208

Step:  AIC=64.86
Detox ~ Enzyme1 + Enzyme4 + Enzyme5

          Df Sum of Sq    RSS    AIC
<none>                 2947.1 64.860
+ Enzyme3  1     130.4 2816.7 66.407
+ Enzyme2  1      13.6 2933.4 66.813
- Enzyme4  1    1837.7 4784.8 67.706
- Enzyme5  1    2262.8 5209.8 68.557
- Enzyme1  1    6029.0 8976.1 73.997
```

```

Call:
lm(formula = Detox ~ Enzyme1 + Enzyme4 + Enzyme5, data = chap7data2)

Coefficients:
(Intercept)      Enzyme1      Enzyme4      Enzyme5
  -102.4349       0.1938       0.1008       1.1069
```

```r
#or
allSubsets(chap7data2,y.name="Detox",perf.measure="mallows.cp")
```

```
                                             Model      adj.r.squared
1                                  Detox ~ Enzyme5 -0.121740174648695
2                  Detox ~ Enzyme3+Enzyme4+Enzyme5 0.0953356909980044
3                                  Detox ~ Enzyme2  0.121913336927653
4                          Detox ~ Enzyme4+Enzyme5   0.16091426388108
5                  Detox ~ Enzyme2+Enzyme3+Enzyme4  0.220935843219152
6                          Detox ~ Enzyme3+Enzyme5  0.202661735249138
7                          Detox ~ Enzyme3+Enzyme4  0.223753049711396
8                          Detox ~ Enzyme2+Enzyme4  0.255553133684301
9                                  Detox ~ Enzyme4  0.265785404743971
10         Detox ~ Enzyme2+Enzyme3+Enzyme4+Enzyme5  0.374128029592512
11                         Detox ~ Enzyme2+Enzyme3  0.329335344543953
12                                 Detox ~ Enzyme3  0.301375192960427
13 Detox ~ Enzyme1+Enzyme2+Enzyme3+Enzyme4+Enzyme5   0.54551810809289
14                 Detox ~ Enzyme2+Enzyme4+Enzyme5  0.404467243817661
15                 Detox ~ Enzyme1+Enzyme3+Enzyme4  0.451096799223505
16                 Detox ~ Enzyme2+Enzyme3+Enzyme5   0.46270944285908
17                                 Detox ~ Enzyme1  0.384163301765189
18         Detox ~ Enzyme1+Enzyme2+Enzyme4+Enzyme5  0.616094255366656
19         Detox ~ Enzyme1+Enzyme2+Enzyme3+Enzyme4  0.619787416838814
20         Detox ~ Enzyme1+Enzyme2+Enzyme3+Enzyme5  0.627043441524617
21                         Detox ~ Enzyme2+Enzyme5  0.476586035306095
22         Detox ~ Enzyme1+Enzyme3+Enzyme4+Enzyme5  0.631375639659066
23                         Detox ~ Enzyme1+Enzyme3  0.505130867699246
24                         Detox ~ Enzyme1+Enzyme4  0.512984256086067
25                 Detox ~ Enzyme1+Enzyme2+Enzyme5  0.589864494082874
26                         Detox ~ Enzyme1+Enzyme5  0.552720532095238
27                 Detox ~ Enzyme1+Enzyme2+Enzyme4  0.658170511105981
28                 Detox ~ Enzyme1+Enzyme3+Enzyme5  0.668698598042593
29                 Detox ~ Enzyme1+Enzyme4+Enzyme5  0.678591090390398
30                 Detox ~ Enzyme1+Enzyme2+Enzyme3  0.682256480210184
```

```
31                       Detox ~ Enzyme1+Enzyme2  0.646870701721216
            r.squared              AIC        perc.error         mallows.cp
1  0.0028976225344936 106.614682983029  0.39431982572297  0.137453882255527
2   0.396890460665336 105.587136855917 0.354116533733155 0.0994323899514434
3   0.219478521713469 104.165771062923 0.348876057988313 0.0945648667123251
4   0.347377760796396 104.376133095174 0.341040255742936 0.0892372756191775
5   0.480623895479435 104.092431403323 0.328616289784617 0.0828508511322706
6   0.379848016304885 103.865794310814 0.332448041968861 0.0828072658700512
7   0.396252371997752 103.597711242751 0.328021590110949 0.0795587491774218
8   0.420985770643346 103.179419011073 0.321232390178822  0.074660851334314
9   0.347364804216863 102.376331624279 0.319017114715357 0.0692398413807154
10  0.652293349773618 102.079740132558 0.294540640692888 0.0688555453531038
11  0.478371934645297 102.135696635339 0.304898428354942 0.0632968017381836
12   0.37900017152038 101.879456538239 0.311189172259715 0.0629751626156955
13  0.798008048041284 98.6484270290975 0.250992513755551               0.06
14  0.602978162545108 101.406061334488 0.287313017352848 0.0586213180485603
15   0.63406453281567 100.590718467776  0.27583562615466 0.0524653558987582
16  0.641806295239386 100.376887629136 0.272902227212976 0.0509322725558538
17  0.452589601569056 100.618136405545 0.292169756597092 0.0484024176453974
18  0.786719030759254 97.1922524896298 0.230682570166493 0.0422355380345724
19  0.788770787132675 97.0955870885837  0.22957030910281 0.0418292334558949
20   0.79280191195812 96.9029013083644 0.227369182566776  0.041030959111525
21  0.592900249682518 99.6567309027967 0.269355054023775 0.0406170238704733
22  0.795208688699481 96.7860631506573 0.226044785017069 0.0405543506688574
23  0.615101785988302 99.0959376823384 0.261907333353099 0.0362205048823659
24   0.62120997695583 98.9359687073529 0.259820836463091 0.0350109139242518
25  0.726576329388583 97.6763734731404 0.238432888587324  0.034145458363074
26  0.652115969407407 98.0848402690308 0.248995763195505 0.0288906715775875
27  0.772113674070654 95.8546178223231  0.21767434129564 0.0251278031069124
28  0.779132398695062 95.5417828096502 0.214296023808806 0.0237379012704586
29  0.785727393593599 95.2386391415135 0.211072391978277 0.0224319096535481
30  0.788170986806789 95.1239425579172 0.209865392142655 0.0219480105299455
31  0.725343879116501 95.7213469375342 0.221242904754148 0.0143895176456604
```

Interpretation 1

The stepwise regression analysis identified that the best model for predicting `Detox` includes the variables `Enzyme1`, `Enzyme4`, and `Enzyme5`. This model was chosen because it has the lowest Akaike Information Criterion (AIC) value (64.86), indicating the best balance between model complexity and fit.

- **Enzyme1** and **Enzyme4** have small positive effects on `Detox`, while **Enzyme5** has a

larger positive effect.
- The variables `Enzyme2` and `Enzyme3` were excluded from the final model as they did not significantly improve the model's fit.

This suggests that `Enzyme1`, `Enzyme4`, and `Enzyme5` are the most important predictors of `Detox` in this dataset.

Interpretation 2

Based on the regression analysis and the adjusted R-squared values for various models, the following conclusions can be drawn:

1. **Best Model**: The model `Detox ~ Enzyme1 + Enzyme2 + Enzyme3` has the highest adjusted R-squared value of 0.6823. This indicates that it explains about 68.23% of the variability in `Detox` and is the best model among all those considered in terms of fit.
2. **Other Notable Models**:
    - The models `Detox ~ Enzyme1 + Enzyme2 + Enzyme5` (Adjusted R-squared: 0.6687) and `Detox ~ Enzyme1 + Enzyme2 + Enzyme4` (Adjusted R-squared: 0.6582) also have high adjusted R-squared values. These models provide a good fit and are close in performance to the best model.
3. **Poorly Performing Models**:
    - Models with adjusted R-squared values close to or below 0, such as `Detox ~ Enzyme5` (-0.1217) and `Detox ~ Enzyme3` (0.3014), indicate a poor fit. These models do not explain much of the variability in `Detox` and are not suitable for prediction.
4. **Model Selection**:
    - The top models to consider for predicting `Detox` are:
        - `Detox ~ Enzyme1 + Enzyme2 + Enzyme3` (Adjusted R-squared: 0.6823)
        - `Detox ~ Enzyme1 + Enzyme2 + Enzyme5` (Adjusted R-squared: 0.6687)
        - `Detox ~ Enzyme1 + Enzyme2 + Enzyme4` (Adjusted R-squared: 0.6582)
    - These models provide a good balance between complexity (number of variables) and explanatory power.

Conclusion:

The best model based on adjusted R-squared is `Detox ~ Enzyme1 + Enzyme2 + Enzyme3`, which explains 68.23% of the variance in `Detox`. Models with fewer variables generally have lower adjusted R-squared values and may not provide sufficient explanatory power, while models with negative adjusted R-squared values should be discarded as they do not fit the data well.

Another example with data 3

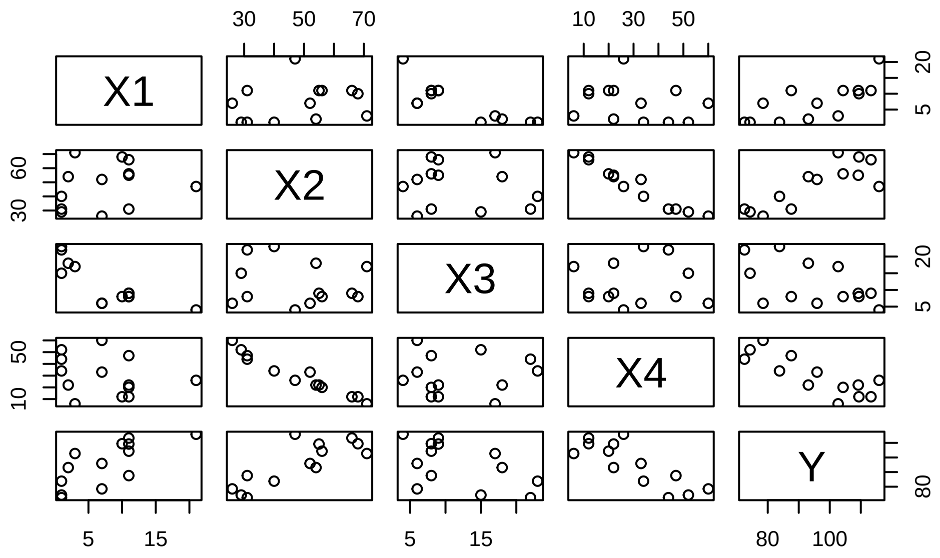
```r
chap7data3.model1 <- lm(Y~.,data=chap7data3)
#chap7data3.model1 <- lm(Y~X1+X2+X3+X4,data=chap7data3)
summary(chap7data3.model1)
```

```
Call:
lm(formula = Y ~ ., data = chap7data3)

Residuals:
    Min      1Q  Median      3Q     Max 
-3.1750 -1.6709  0.2508  1.3783  3.9254 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)  
(Intercept)  62.4054    70.0710   0.891   0.3991  
X1            1.5511     0.7448   2.083   0.0708 .
X2            0.5102     0.7238   0.705   0.5009  
X3            0.1019     0.7547   0.135   0.8959  
X4           -0.1441     0.7091  -0.203   0.8441  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.446 on 8 degrees of freedom
Multiple R-squared:  0.9824,    Adjusted R-squared:  0.9736 
F-statistic: 111.5 on 4 and 8 DF,  p-value: 4.756e-07
```

```r
# Test for multicollinearity and variable influence using Variable Influence Factor [vif()]
# VIF equal to 1 = variables are not correlated
# VIF between 1 and 5 = variables are moderately correlated
# VIF greater than 5 = variables are highly correlated
vif(chap7data3.model1)
```

```
       X1        X2        X3        X4 
 38.49621 254.42317  46.86839 282.51286 
```

```
base::plot(chap7data3)
```



```
stepwise(chap7data3.model1, direction='backward', criterion='AIC')
```

```
Direction:  backward
Criterion:  AIC 

Start:  AIC=26.94
Y ~ X1 + X2 + X3 + X4

       Df Sum of Sq    RSS    AIC
- X3    1    0.1091 47.973 24.974
- X4    1    0.2470 48.111 25.011
- X2    1    2.9725 50.836 25.728
```

```
<none>                 47.864 26.944
- X1    1   25.9509 73.815 30.576

Step:  AIC=24.97
Y ~ X1 + X2 + X4

       Df Sum of Sq    RSS    AIC
<none>                 47.97 24.974
- X4    1      9.93  57.90 25.420
- X2    1     26.79  74.76 28.742
- X1    1    820.91 868.88 60.629


Call:
lm(formula = Y ~ X1 + X2 + X4, data = chap7data3)

Coefficients:
(Intercept)           X1           X2           X4
    71.6483       1.4519       0.4161      -0.2365
```

```
stepwise(chap7data3.model1, direction='forward', criterion='AIC')
```

```
Direction:  forward
Criterion:  AIC

Start:  AIC=71.44
Y ~ 1

       Df Sum of Sq     RSS    AIC
+ X4    1   1831.90  883.87 58.852
+ X2    1   1809.43  906.34 59.178
+ X1    1   1450.08 1265.69 63.519
+ X3    1    776.36 1939.40 69.067
<none>              2715.76 71.444

Step:  AIC=58.85
Y ~ X4

       Df Sum of Sq    RSS    AIC
+ X1    1    809.10  74.76 28.742
+ X3    1    708.13 175.74 39.853
```

```
<none>              883.87 58.852
+ X2    1      14.99 868.88 60.629

Step:  AIC=28.74
Y ~ X4 + X1

       Df Sum of Sq    RSS    AIC
+ X2    1     26.789 47.973 24.974
+ X3    1     23.926 50.836 25.728
<none>              74.762 28.742

Step:  AIC=24.97
Y ~ X4 + X1 + X2

       Df Sum of Sq    RSS    AIC
<none>              47.973 24.974
+ X3    1    0.10909 47.864 26.944


Call:
lm(formula = Y ~ X4 + X1 + X2, data = chap7data3)

Coefficients:
(Intercept)           X4           X1           X2
    71.6483      -0.2365       1.4519       0.4161
```

```
stepwise(chap7data3.model1, direction='backward/forward', criterion='AIC')
```

```
Direction:  backward/forward
Criterion:  AIC

Start:  AIC=26.94
Y ~ X1 + X2 + X3 + X4

       Df Sum of Sq    RSS    AIC
- X3    1     0.1091 47.973 24.974
- X4    1     0.2470 48.111 25.011
- X2    1     2.9725 50.836 25.728
<none>              47.864 26.944
- X1    1    25.9509 73.815 30.576
```

```
Step:  AIC=24.97
Y ~ X1 + X2 + X4

       Df Sum of Sq    RSS    AIC
<none>              47.97 24.974
- X4    1      9.93  57.90 25.420
+ X3    1      0.11  47.86 26.944
- X2    1     26.79  74.76 28.742
- X1    1    820.91 868.88 60.629


Call:
lm(formula = Y ~ X1 + X2 + X4, data = chap7data3)

Coefficients:
(Intercept)           X1           X2           X4
    71.6483       1.4519       0.4161      -0.2365
```

```
allSubsets(chap7data3,y.name="Y",perf.measure="adj.r.squared")
```

```
             Model     adj.r.squared         r.squared              AIC
1      Y ~ X1+X2+X4 0.976447268267236 0.982335451200427 63.8662854718626
2      Y ~ X1+X2+X3 0.976379572292115 0.982284679219087 63.9035968705951
3      Y ~ X1+X3+X4 0.975041456783125 0.981281092587343 64.6199522325816
4         Y ~ X1+X2 0.974414049442758 0.978678374535632 64.3123927621906
5   Y ~ X1+X2+X3+X4  0.97356343061152  0.98237562040768 65.8366897916517
6         Y ~ X1+X4 0.966965257260317 0.972471047716931 67.6341062672404
7      Y ~ X2+X3+X4 0.963759945848363 0.972819959386272  69.468286610933
8         Y ~ X3+X4 0.922347568738969 0.935289640615807  78.744985808948
9         Y ~ X2+X3 0.816430499370665 0.847025416142221 89.9295421295082
10           Y ~ X4 0.644954869961756 0.674541964131609 97.7440447788562
11           Y ~ X2  0.63592900832723 0.666268257633294 98.0703964203777
12        Y ~ X2+X4  0.61607248954006  0.68006040795005 99.5217275129777
13           Y ~ X1 0.491579662365491 0.533948023835033  102.41187201392
14        Y ~ X1+X3 0.457800098613821 0.548166748844851 104.009080451406
15           Y ~ X3 0.220952070432522 0.285872731229812 107.959804394717
           perc.error         mallows.cp
1  0.0241948282253226 0.0301823347348734
2  0.0242295740305319 0.0304127972306419
3  0.0249064320090681 0.0349682444234851
4  0.0252175376870345 0.0267824159831842
5  0.0256332957861164               0.05
```

```
6  0.0286541391065289 0.0549585082475868
7  0.0300120954747619 0.0733747399565644
8  0.0439318436492178  0.223731119646975
9  0.0675463931752181  0.624377163435314
10 0.0939385128212314   1.38730833491677
11  0.095125058915528   1.42486406936961
12 0.0976846931820687   1.38225919754642
13  0.112412176793213    2.0254876912345
14  0.116086473289248   1.98094652569577
15  0.139150249457931   3.15154284140081
```

```
chap7data3.model2 <- lm(Y ~ X1 + X2 + X4,data=chap7data3)
summary(chap7data3.model2)
```

```

Call:
lm(formula = Y ~ X1 + X2 + X4, data = chap7data3)

Residuals:
    Min      1Q  Median      3Q     Max 
-3.0919 -1.8016  0.2562  1.2818  3.8982 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)  71.6483    14.1424   5.066 0.000675 ***
X1            1.4519     0.1170  12.410 5.78e-07 ***
X2            0.4161     0.1856   2.242 0.051687 .  
X4           -0.2365     0.1733  -1.365 0.205395    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.309 on 9 degrees of freedom
Multiple R-squared:  0.9823,    Adjusted R-squared:  0.9764 
F-statistic: 166.8 on 3 and 9 DF,  p-value: 3.323e-08
```

```
vif(chap7data3.model2)
```

```
      X1       X2       X4 
 1.06633 18.78031 18.94008 
```

```r
chap7data3.model3 <- lm(Y ~ X1 + X2,data=chap7data3)
summary(chap7data3.model3)
```

```

Call:
lm(formula = Y ~ X1 + X2, data = chap7data3)

Residuals:
   Min     1Q Median     3Q    Max 
-2.893 -1.574 -1.302  1.363  4.048 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 52.57735    2.28617   23.00 5.46e-10 ***
X1           1.46831    0.12130   12.11 2.69e-07 ***
X2           0.66225    0.04585   14.44 5.03e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.406 on 10 degrees of freedom
Multiple R-squared:  0.9787,	Adjusted R-squared:  0.9744 
F-statistic: 229.5 on 2 and 10 DF,  p-value: 4.407e-09
```

```r
vif(chap7data3.model3)
```

```
      X1       X2 
1.055129 1.055129 
```

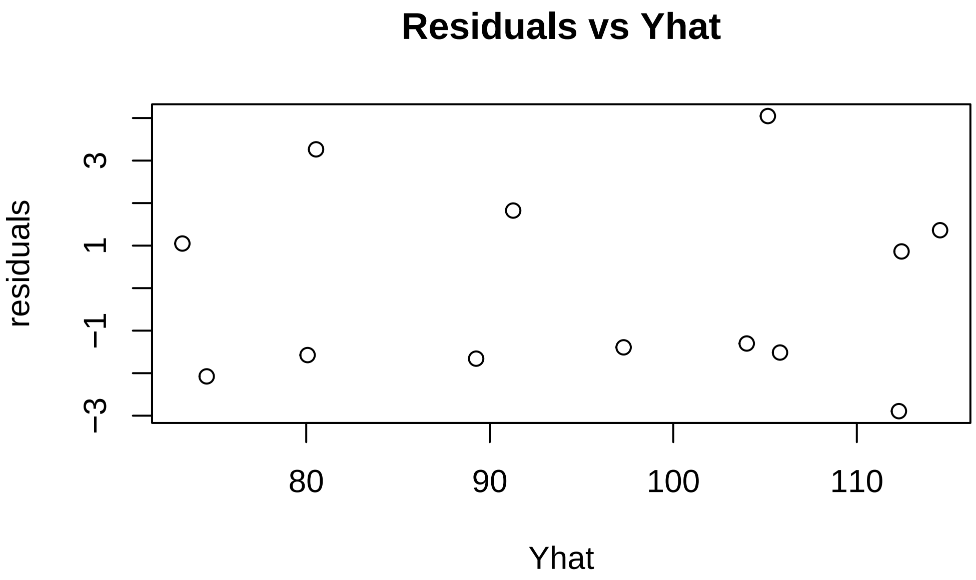
#Assess normality

```r
shapiro.test(chap7data3.model3$residuals)
```

```

	Shapiro-Wilk normality test

data:  chap7data3.model3$residuals
W = 0.90527, p-value = 0.158
```

#Assess homoscedasticity

```
plot(y=chap7data3.model3$residuals,x=chap7data3.model3$fitted.values,
     main="Residuals vs Yhat",ylab="residuals",xlab="Yhat")
```



Exercises

Exercise 1

Use the `swiss` dataset in R (do this by running the code `data(swiss)`) to fit a multiple linear regression model of `Fertility` on the other variables, and find the best fitting model according to Mallows' Cp criterion. Do this using all department observations (i.e., rownames) except `Moutier` (i.e.m the 4th observation/row).

To know more about the dataset, you can type and run `?swiss` in the R console.

For this final model:

- Test the model assumptions
- Interpret the regression coefficients (parameter estimates)
- Interpret the coefficient of determination (R^2)

- Predict Fertility for Moutier using the collected data for the department. What is the prediction? How does the predicted value and observed value compare to the predicted interval?

Exercise 2 and further reading

Polynomial regression

See pdf file Biometry 721-821 Workbook (2024), Chapter 7, Section 2, pages 52-54 on polynomial regression.

With the data from C&S Example 8.1, p. 90 (chap8exer1.csv): Fit a quadratic regression model of wheat yield (Y) on nitrogen fertilizer (X) and give the equation of the regression line, as well as the coefficient of determination R^2. Also check that the assumptions of this polynomial regression model are justified. Does the quadratic model fit the data better than the simple linear regression (straight-line) model?