Lab 6: Linear Regression Validation

Problem statement:

Calculate following parameter of Simple Liner Regression (drug2.csv) by implementing the formula from scratch.

- R2
- Adjusted- R2
- Residual standard error
- S-value (for slope only)
- P-value (for slope only)

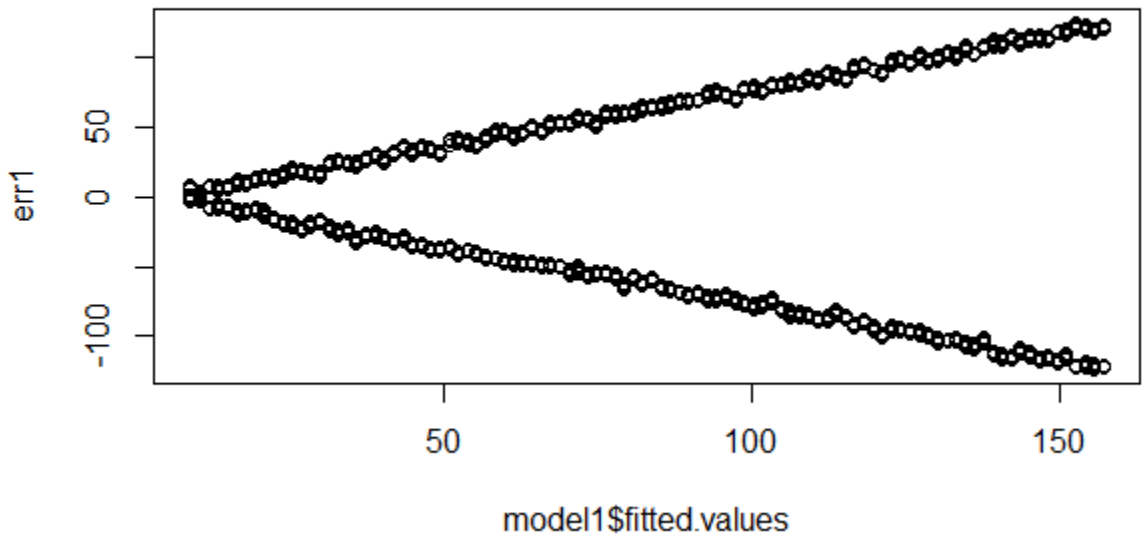
Source Code:

```
#Author: Ashish Upadhyay
#Branch: Computer Science and Engineering
#Semester: 6th
#Dr. SP Mukherjee International Institute of Information Technology, Naya Raipur
#Subject: Machine Learning Lab 6
#Task: Linear Regression Validation

setwd("C:/Users/Ashish Upadhyay/Documents/Semester6/MachineLearning/Lab Programs")
getwd()

drug = read.csv("drug2.csv")
attach(drug)
head(drug)
nrow(drug)

model1 = lm(response~dose)
summary(model1)
err1 = residuals(model1)
plot(model1$fitted.values, err1)
hist(err1)
plot(model1$fitted.values, drug$response)
mean <- mean(response)
sst <- sum((response-mean)**2)
sse <- sum((response-model1$fitted.values)**2)
rsq <- 1 - (sse/sst)
fuv <- sse/sst
fuv
rsq
a <- (nrow(drug)-1)*(1-rsq)
b <- nrow(drug)-2
rad <- 1-(a/b)
rad
```

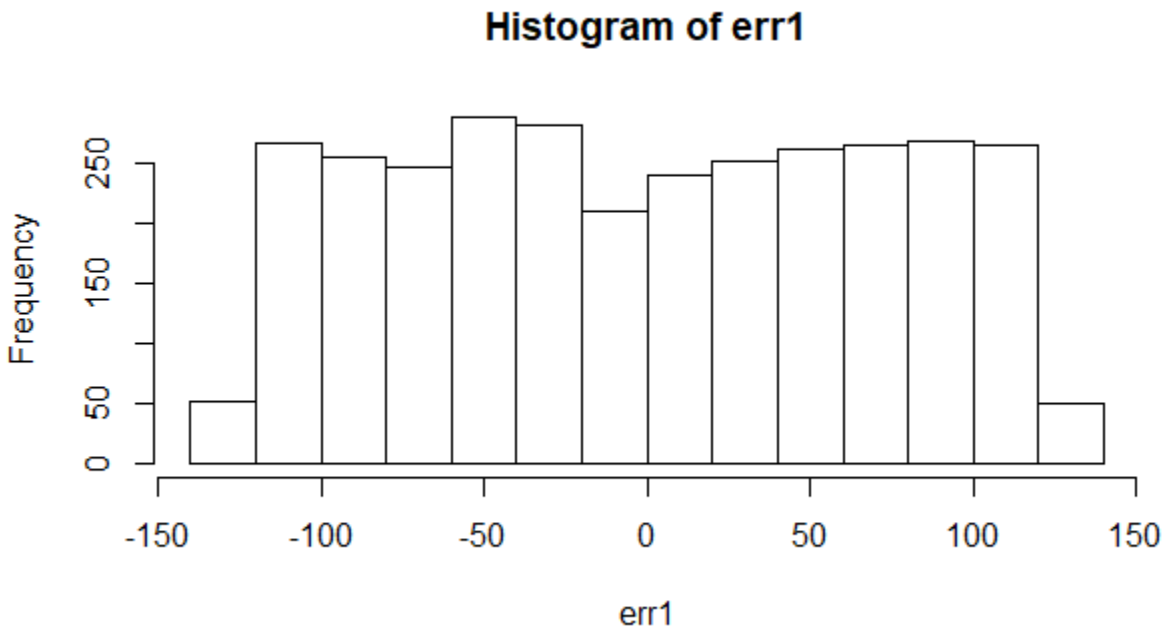
Output:

```
> #Author: Ashish Upadhyay
> #Branch: Computer Science and Engineering
> #Semester: 6th
> #Dr. SP Mukherjee International Institute of Information Technology, Naya Raipur
```

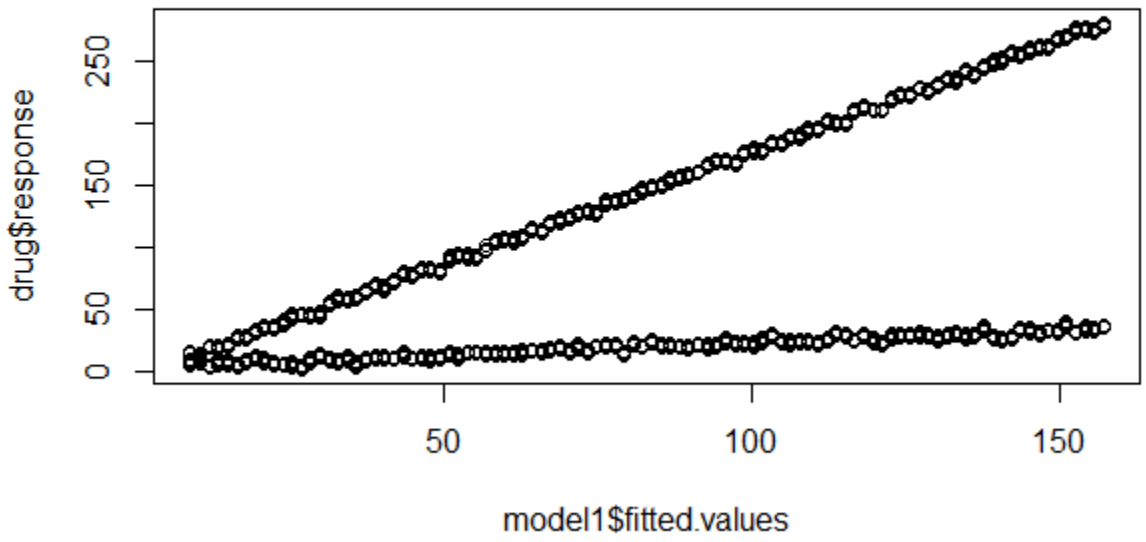
```
> #Subject: Machine Learning Lab 6
> #Task: Linear Regression Validation
>
> setwd("C:/Users/Ashish Upadhyay/Documents/Semester6/MachineLearning/Lab Programs")
> getwd()
[1] "C:/Users/Ashish Upadhyay/Documents/Semester6/MachineLearning/Lab Programs"
>
> drug = read.csv("drug2.csv")
> attach(drug)
> head(drug)
  sex dose response
1   1  0.1    13.75
2   1  0.2    12.90
3   1  0.3    19.26
4   1  0.4    20.34
5   1  0.5    19.97
6   1  0.6    26.80
> nrow(drug)
[1] 3200
>
> model1 = lm(response~dose)
> summary(model1)

Call:
lm(formula = response ~ dose)

Residuals:
    Min      1Q  Median      3Q     Max
-123.514  -62.764    0.401   63.669  124.707

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   7.2534     2.5778   2.814  0.00493 **
dose         15.0020     0.4432  33.852  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 72.36 on 3198 degrees of freedom
Multiple R-squared:  0.2638,      Adjusted R-squared:  0.2636
F-statistic:  1146 on 1 and 3198 DF,  p-value: < 2.2e-16

> err1 = residuals(model1)
> plot(model1$fitted.values, err1)
```




```
> hist(err1)
```




```
> plot(model1$fitted.values, drug$response)
```




```
> mean <- mean(response)
> sst <- sum((response-mean)**2)
> sse <- sum((response-model1$fitted.values)**2)
> rsq <- 1 - (sse/sst)
> fuv <- sse/sst
> fuv
[1] 0.7361931
> rsq
[1] 0.2638069
> a <- (nrow(drug)-1)*(1-rsq)
> b <- nrow(drug)-2
> rad <- 1-(a/b)
> rad
[1] 0.2635767
```