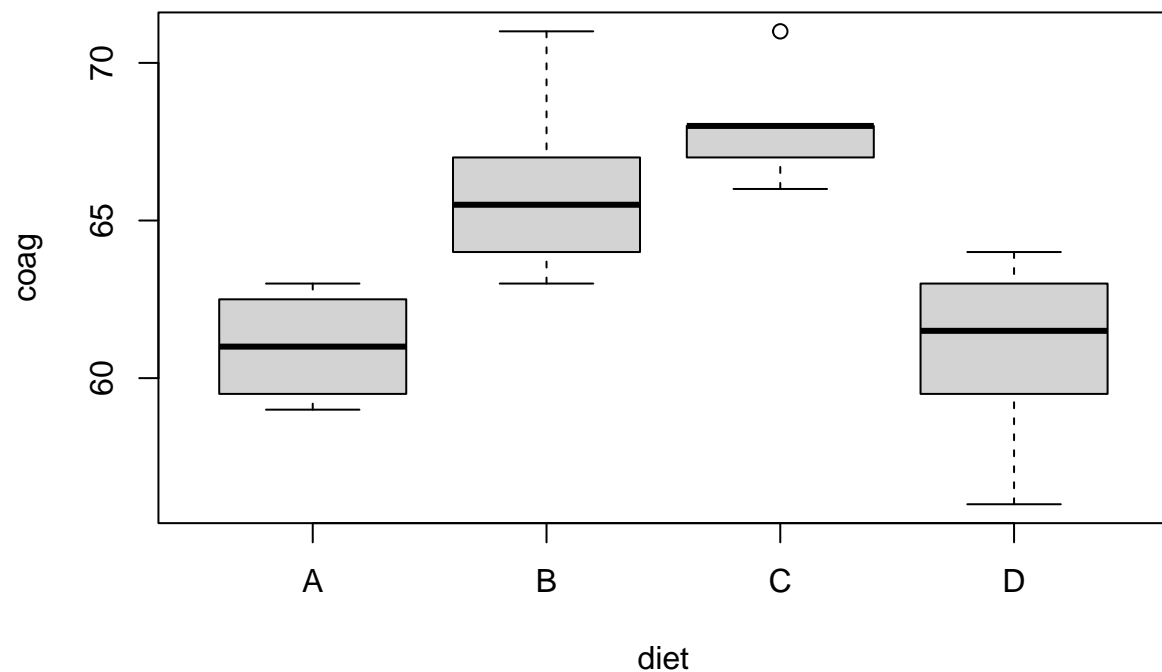# time-series-week-1.R

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```r
library(faraway)
data(package="faraway")
data("coagulation")
ls()
```

```
## [1] "coagulation"
```

```r
coagulation
```

```
##    coag diet
## 1    62    A
## 2    60    A
## 3    63    A
## 4    59    A
## 5    63    B
## 6    67    B
## 7    71    B
## 8    64    B
## 9    65    B
## 10   66    B
## 11   68    C
## 12   66    C
## 13   71    C
## 14   67    C
## 15   68    C
## 16   68    C
## 17   56    D
## 18   62    D
## 19   60    D
## 20   61    D
## 21   63    D
## 22   64    D
## 23   63    D
## 24   59    D
```

```r
plot(coag~diet,
     data = coagulation)
```

```
summary(coagulation)
```

```
##       coag        diet
##  Min.   :56.00   A:4
##  1st Qu.:61.75   B:6
##  Median :63.50   C:6
##  Mean   :64.00   D:8
##  3rd Qu.:67.00
##  Max.   :71.00
```

```
numbers = c(35,8,10,23,42)
numbers
```

```
## [1] 35  8 10 23 42
```

```
print(numbers)
```

```
## [1] 35  8 10 23 42
```

```
summary(numbers)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##     8.0    10.0    23.0    23.6    35.0    42.0
```

```
mean(numbers)
```
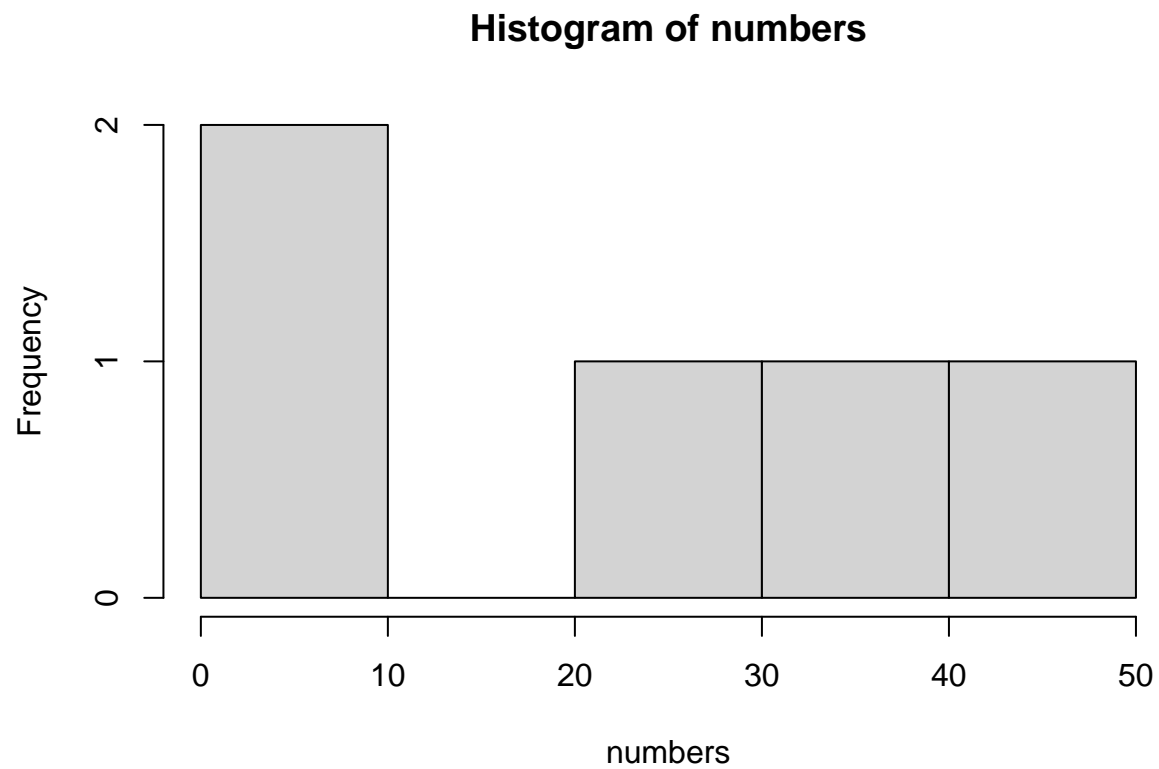
```
## [1] 23.6
```

```
sum(numbers)
```

```
## [1] 118
```
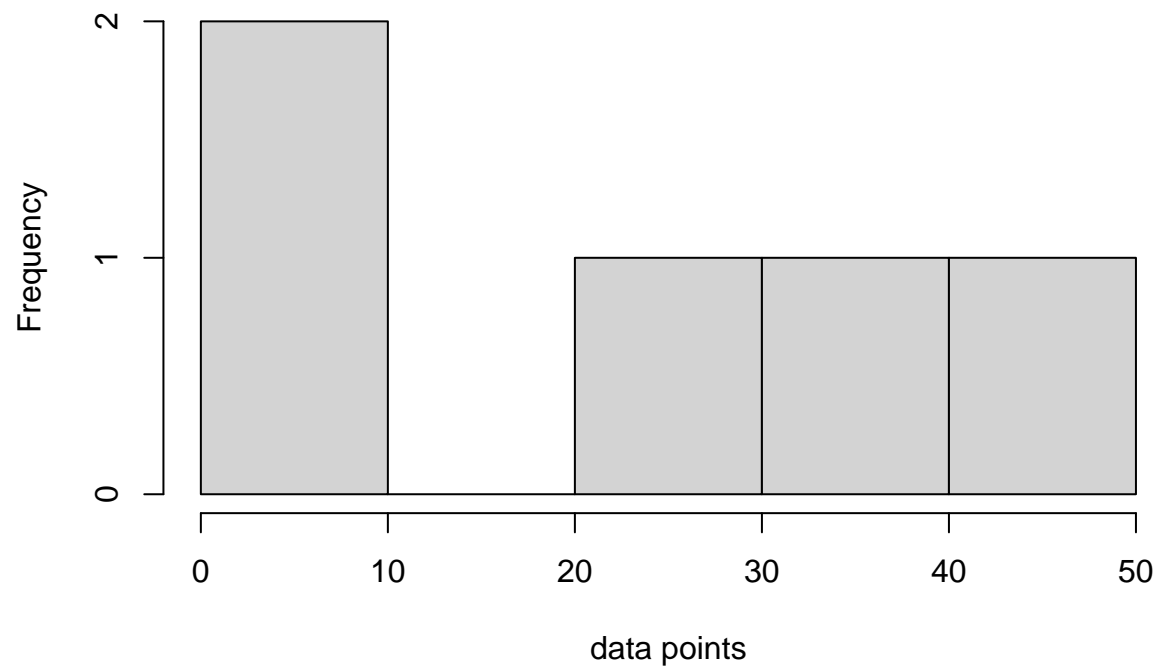
```
sd(numbers)
```

```
## [1] 14.97665
```
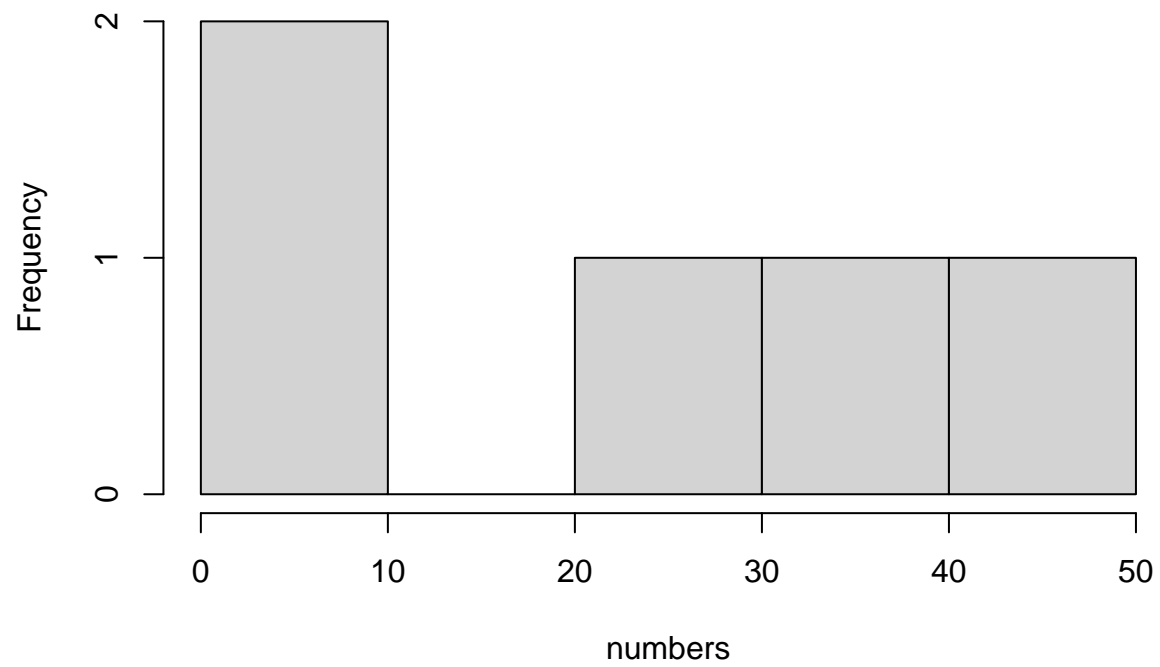
```
hist(numbers)
```

Histogram of numbers


```
hist(numbers,xlab = "data points")
```

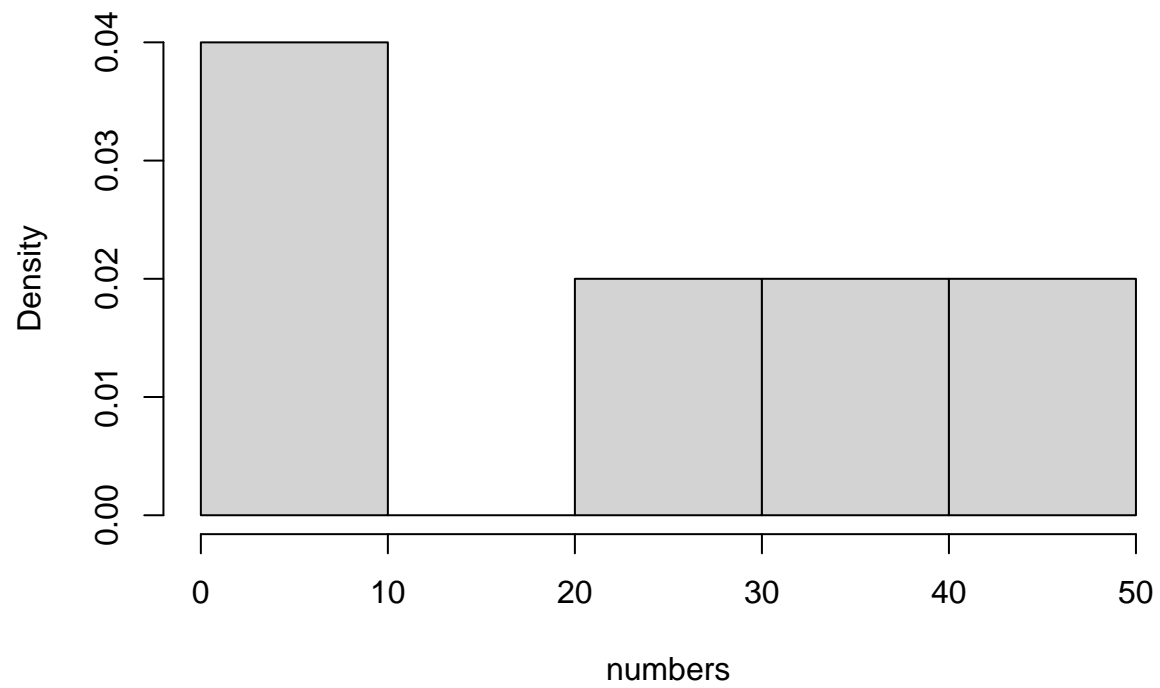## Histogram of numbers


```r
hist(numbers,main = "histo of data")
```
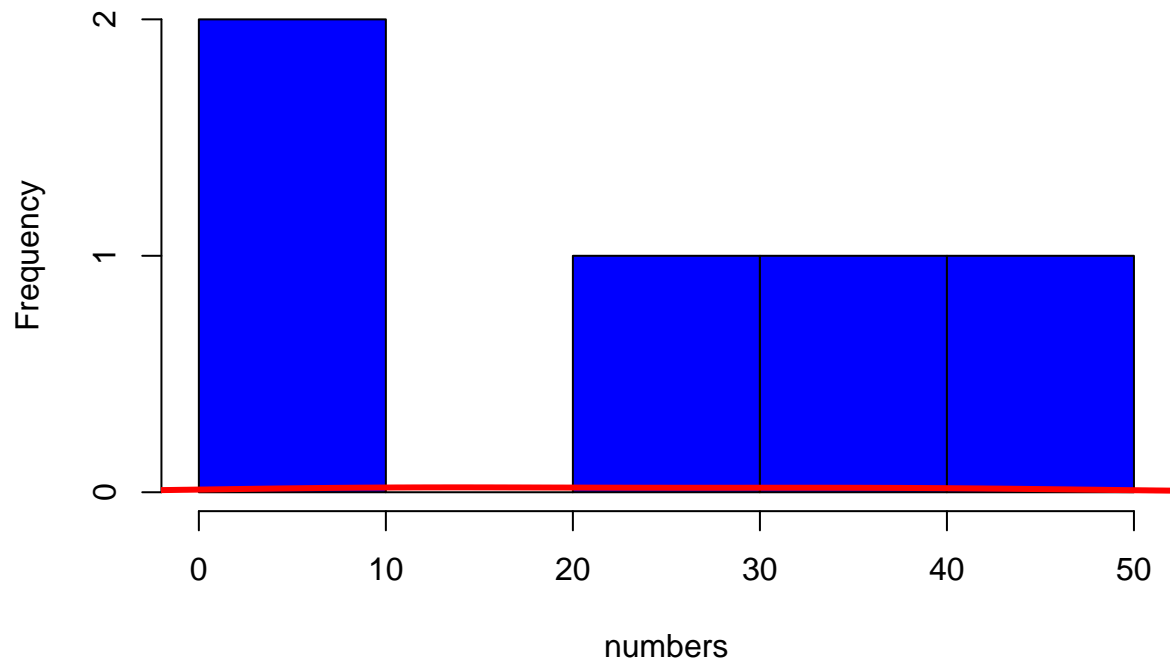
histo of data


```
hist(numbers,freq = F)
```

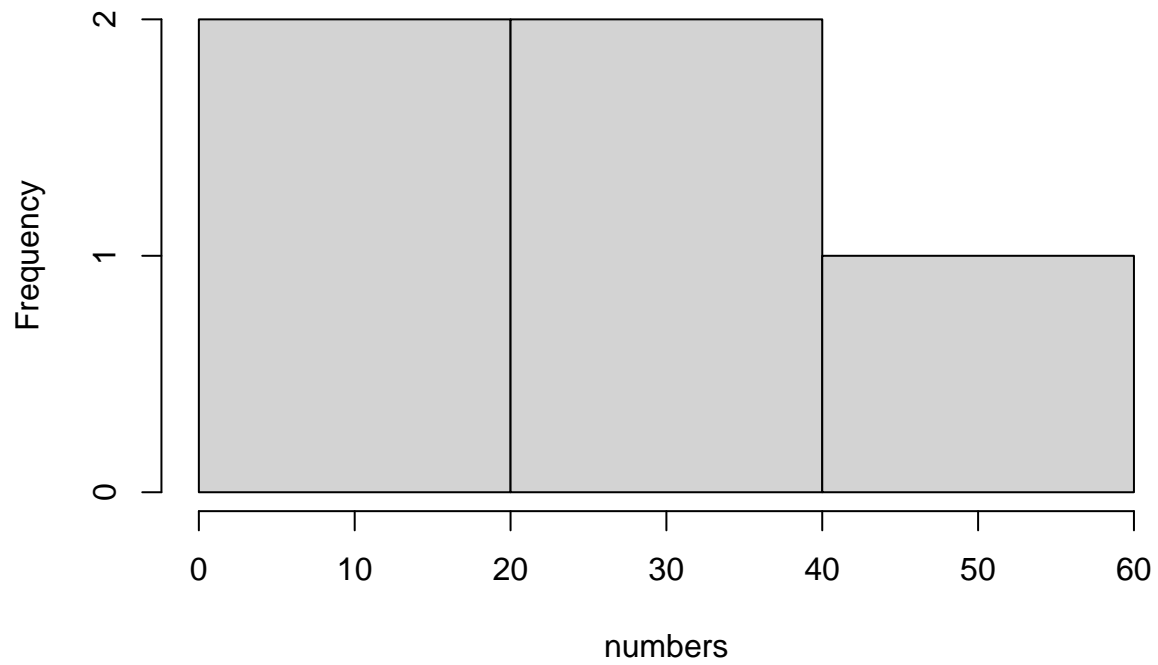## Histogram of numbers


```
hist(numbers,col="blue")
lines(density(numbers),col="red",lwd=3)
```
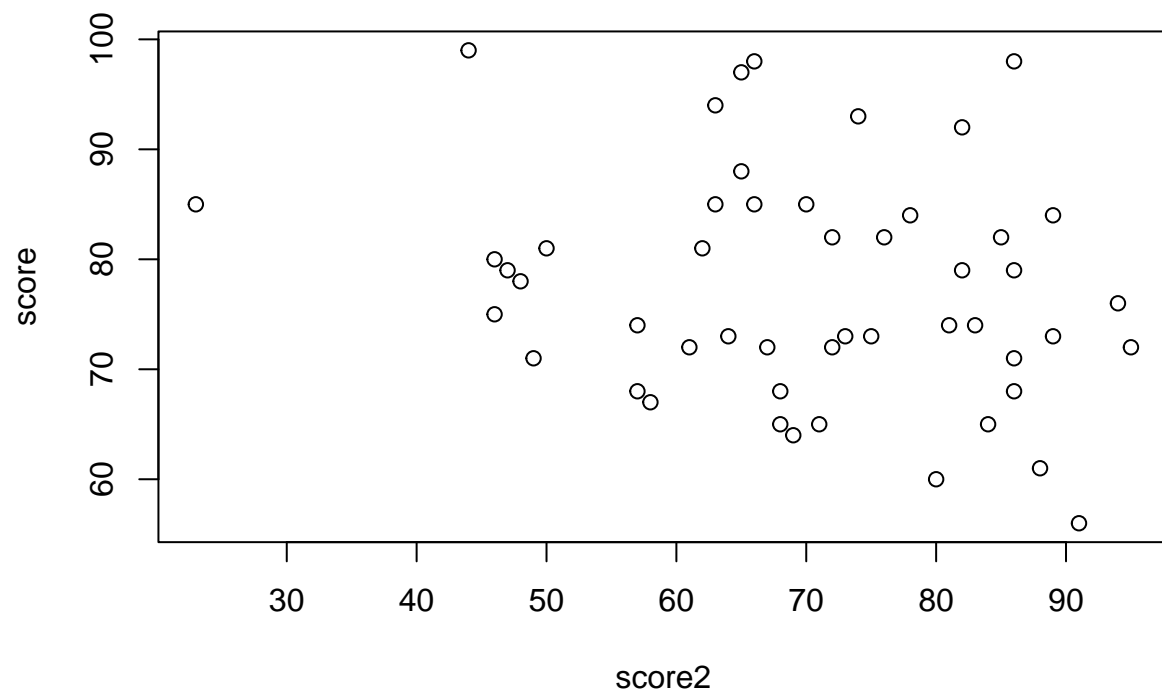
Histogram of numbers


```
hist(numbers,breaks =2)
```
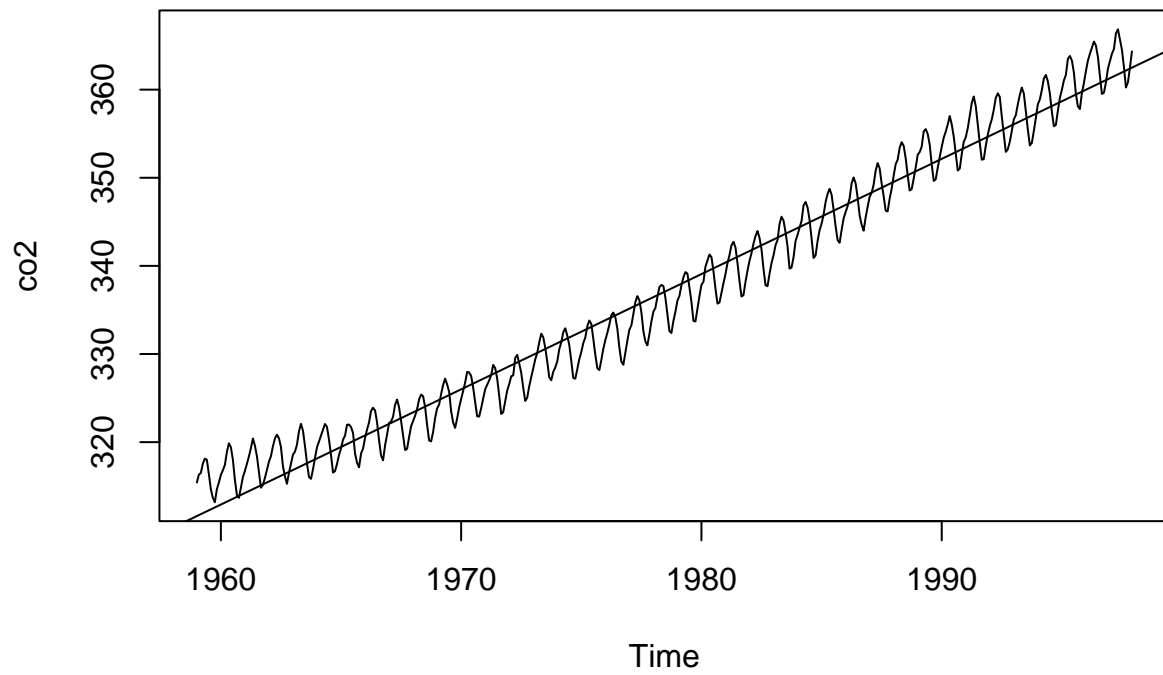
Histogram of numbers


```
set.seed=2016
score <- round(rnorm(50,78,10))
score2 <- round(rnorm(50,70,14))
plot(score~score2)
```
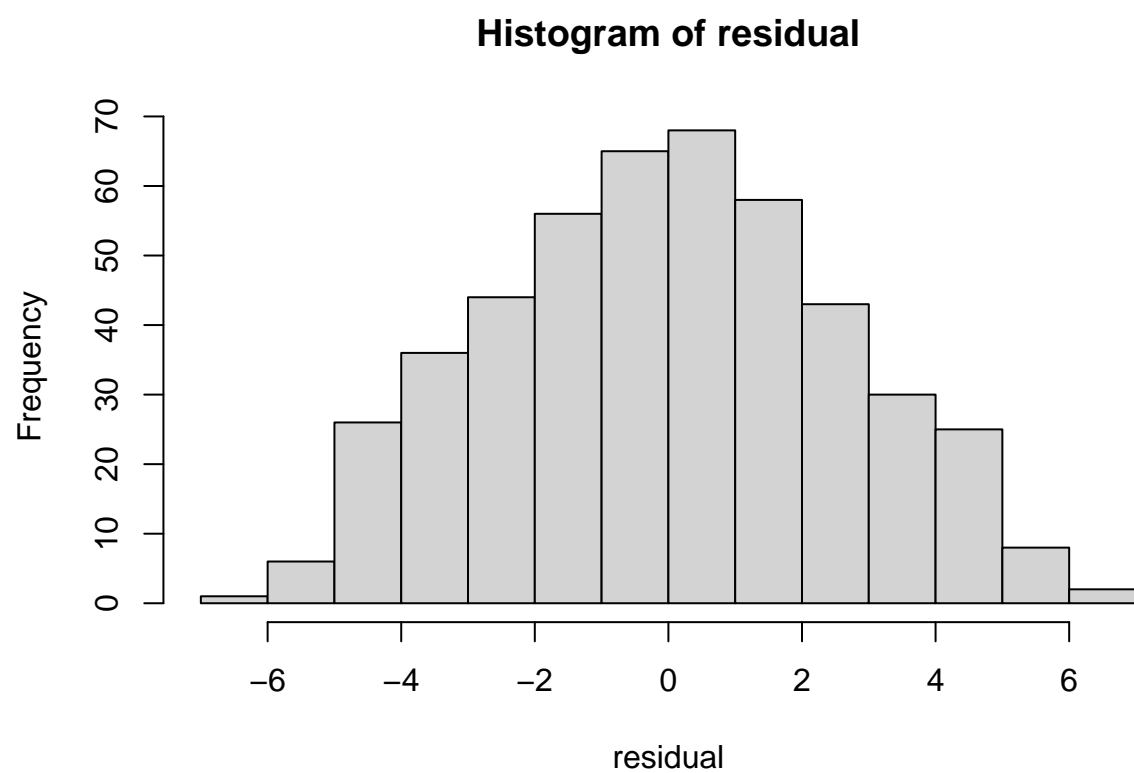
```
plot(co2)
model <- lm(co2~time(co2))
model
```

```
##
## Call:
## lm(formula = co2 ~ time(co2))
##
## Coefficients:
## (Intercept)     time(co2)
##   -2249.774         1.307
```

```
abline(model)
```

```
residual <- resid(model)
hist(residual)
```
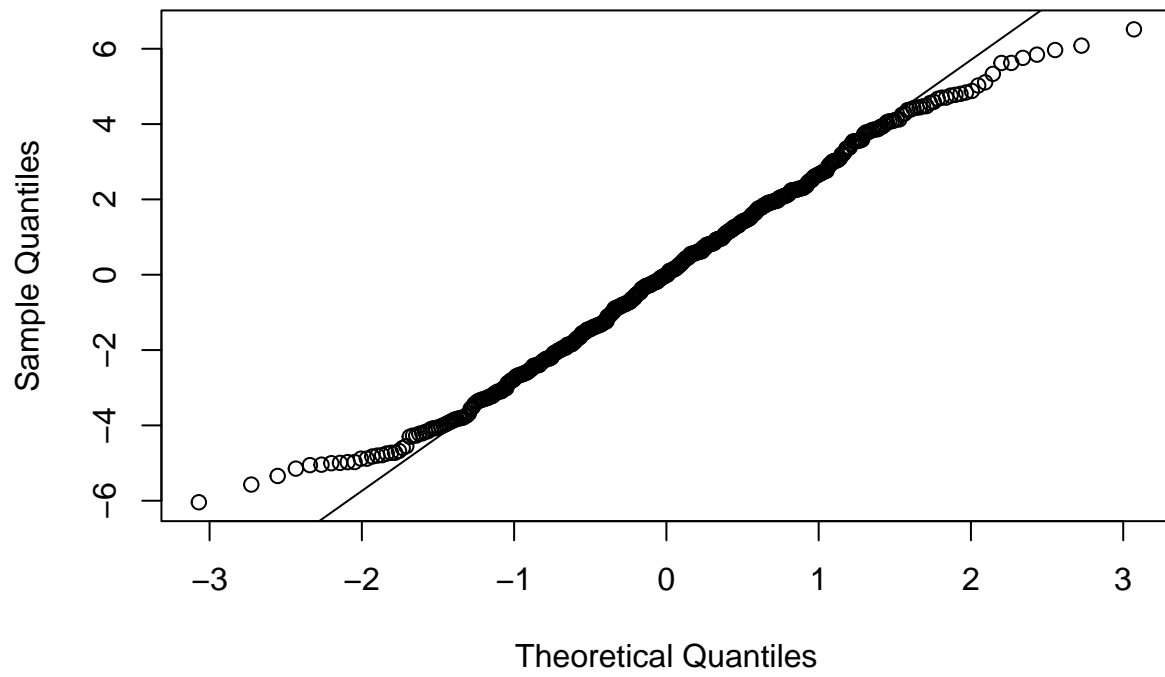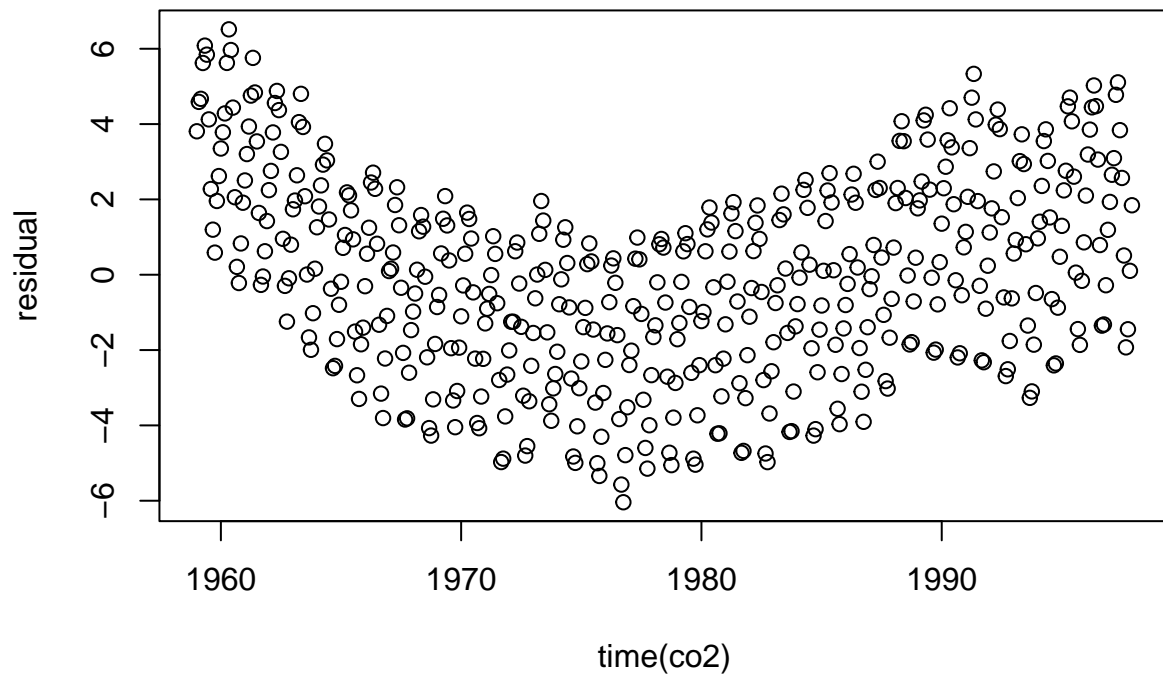
Histogram of residual


```
qqnorm(residual)
qqline(residual)
```
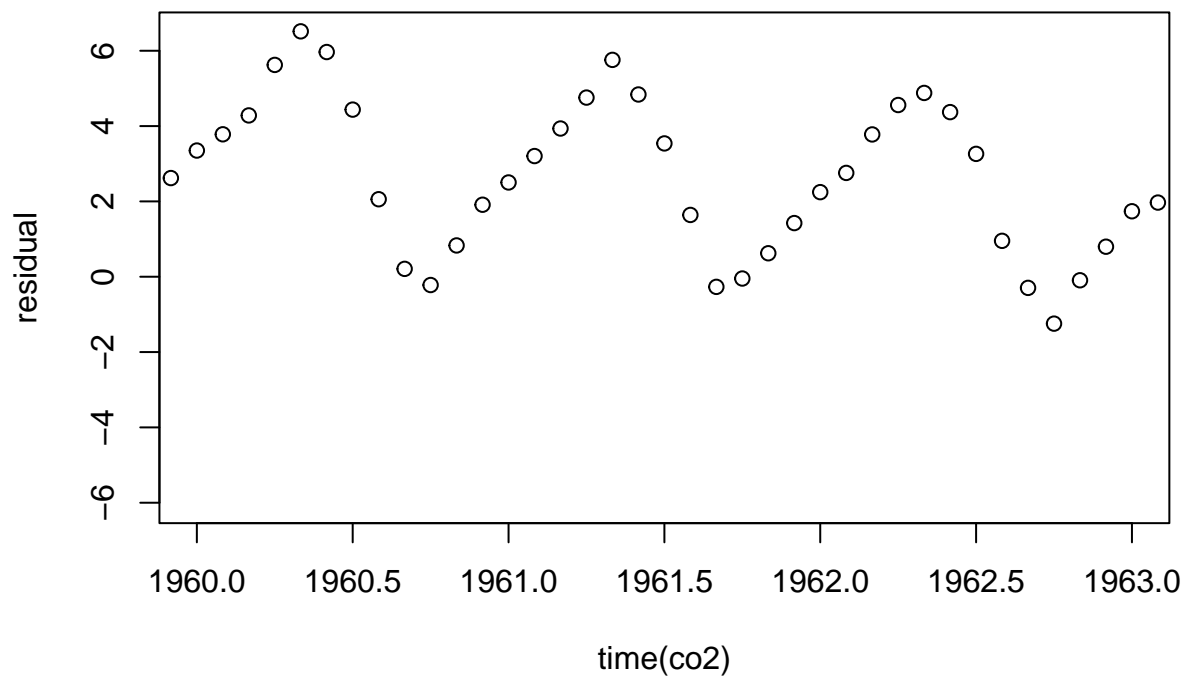
Normal Q-Q Plot


```
plot(residual~time(co2))
```

```
plot(residual~time(co2),xlim=c(1960,1963))
```

```
help(sleep)
```

```
## starting httpd help server ... done
```

```
plot(extra~group,data = sleep)
```
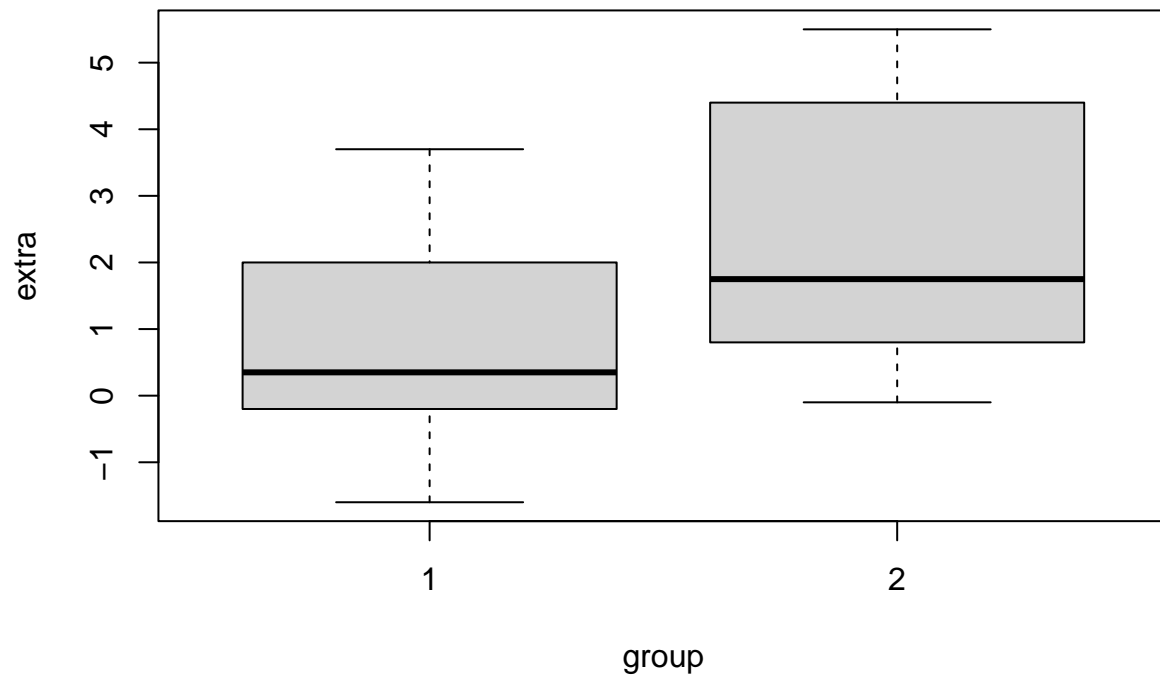
```
attach(sleep)
extra1 <- extra[group==1]
extra2 <- extra[group==2]
t.test(extra1,extra2,paired = TRUE,alternative = "two.sided")
```

```
##
##  Paired t-test
##
## data:  extra1 and extra2
## t = -4.0621, df = 9, p-value = 0.002833
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -2.4598858 -0.7001142
## sample estimates:
## mean difference
##           -1.58
```

```
help(trees)
pairs(trees,pch=21,bg=c("red"))
```
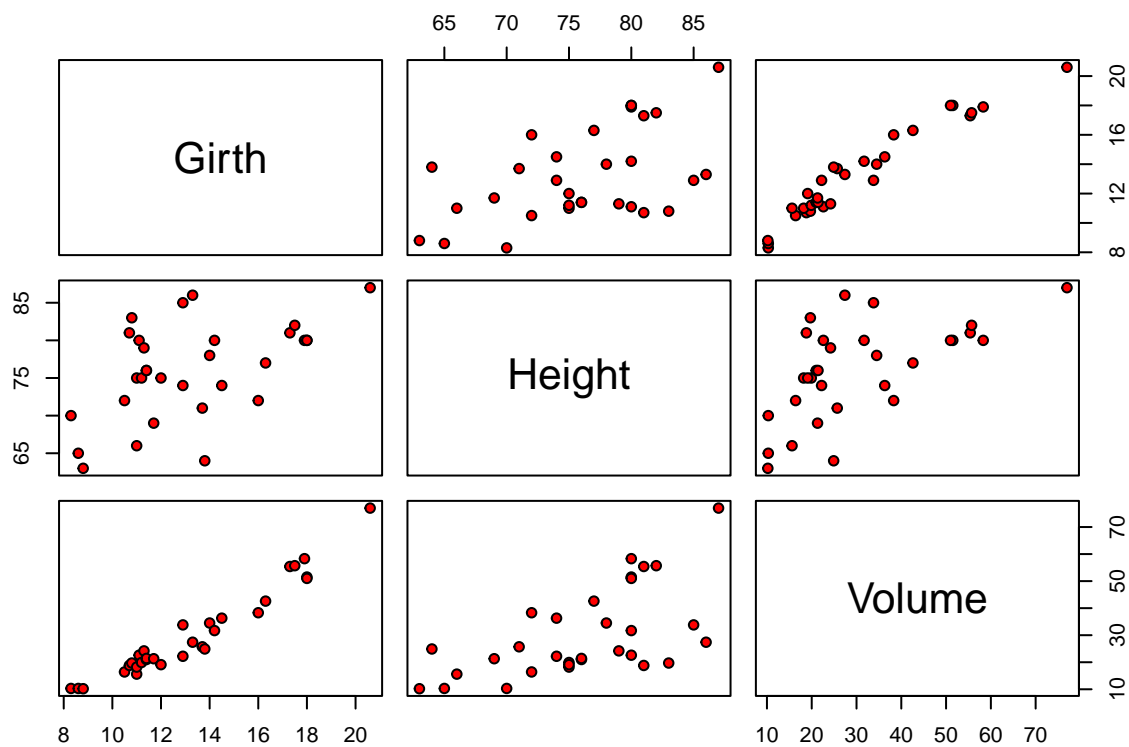
```
cov(trees)
```

```
##            Girth    Height    Volume
## Girth    9.847914 10.38333  49.88812
## Height 10.383333 40.60000  62.66000
## Volume 49.888118 62.66000 270.20280
```

```
cor(trees)
```

```
##            Girth    Height    Volume
## Girth  1.0000000 0.5192801 0.9671194
## Height 0.5192801 1.0000000 0.5982497
## Volume 0.9671194 0.5982497 1.0000000
```

```
#Quiz
quiz_data=c(37, 86, 79, 95, 61, 93, 19, 98, 121, 26, 39, 11, 26, 75, 29,130, 42, 8)
hist(quiz_data,breaks = 10,main = "Histogram",xlab = "quiz data")
```

Histogram
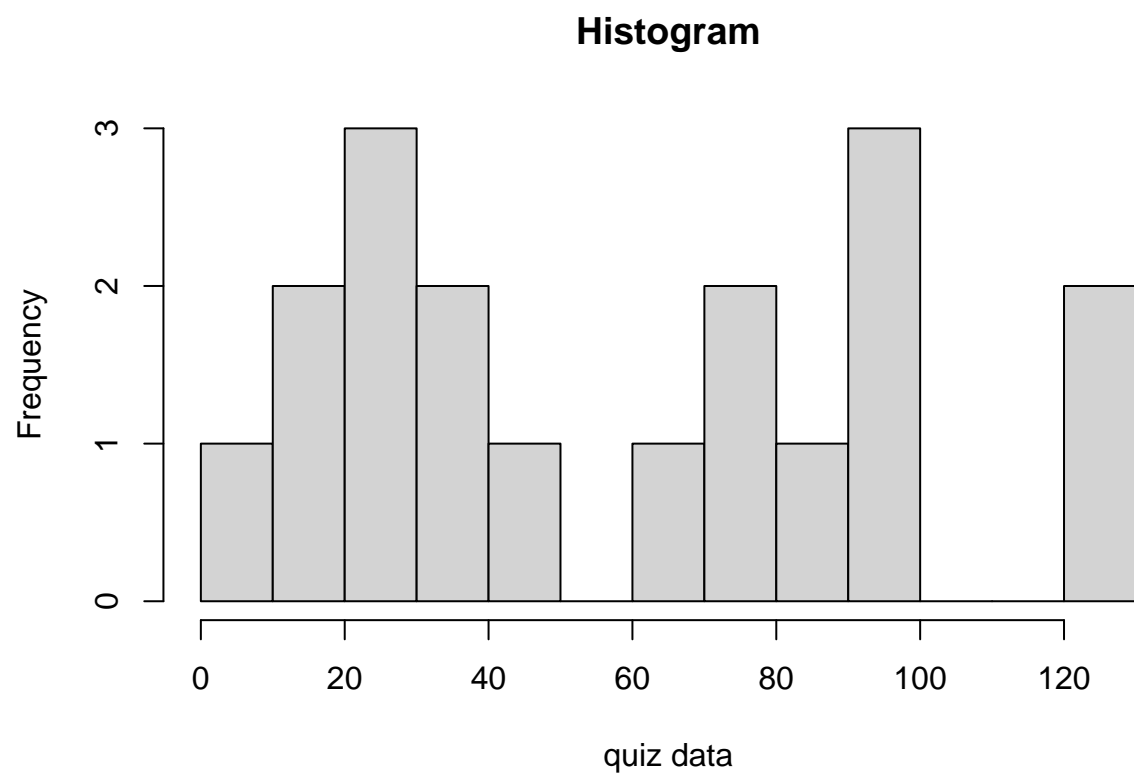
quiz data

```
hist(quiz_data, freq=F, breaks=10, main='Histogram', xlab='Quiz data', col='blue')
lines(density(quiz_data), col='red', lwd=5)
```

Histogram
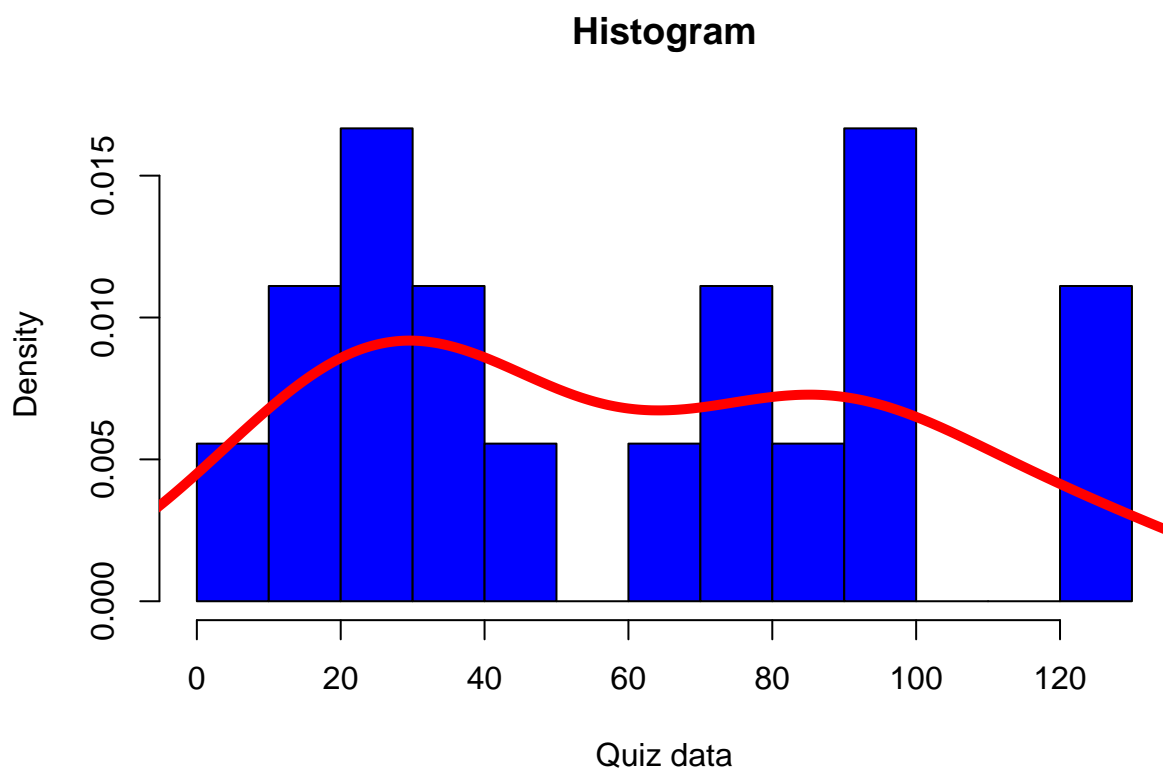

```r
#Quiz2
data <- c(37,86,79,95,61,93,19,98,121,26,39,11,26,75,29,130,42,8)
summary(data)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    8.00   26.75   51.50   59.72   91.25  130.00
```

```r
help("cheddar")
model <- lm(taste~H2S,data = cheddar)
summary(model)
```

```
##
## Call:
## lm(formula = taste ~ H2S, data = cheddar)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -15.426  -7.611  -3.491   6.420  25.687
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -9.7868     5.9579  -1.643    0.112
## H2S           5.7761     0.9458   6.107 1.37e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## 
## Residual standard error: 10.83 on 28 degrees of freedom
## Multiple R-squared:  0.5712, Adjusted R-squared:  0.5558
## F-statistic: 37.29 on 1 and 28 DF,  p-value: 1.374e-06
```

```
residual <- resid(model)
sum(residual)
```

```
## [1] 1.332268e-15
```

```
model
```

```
## 
## Call:
## lm(formula = taste ~ H2S, data = cheddar)
## 
## Coefficients:
## (Intercept)           H2S
##      -9.787         5.776
```

```
sum(model$fitted.values)
```

```
## [1] 736
```

```
sum(model$residuals)
```

```
## [1] 1.332268e-15
```

```
data = c(7,  5,  1,  7,  2,  5,  2,  4, 10,  6)
t.test(data, alternative = "two.sided", paired=FALSE)
```

```
## 
##  One Sample t-test
## 
## data:  data
## t = 5.6003, df = 9, p-value = 0.0003342
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  2.920702 6.879298
## sample estimates:
## mean of x
##       4.9
```