Assignment 1 Submission

Q1

```r
library(Matrix)
library(MASS) # For Moore-Penrose pseudo-inverse ginv()
rankMatrix(matrix(c(1,1,2,2),nrow=2))
```

```
## [1] 1
## attr(,"method")
## [1] "tolNorm2"
## attr(,"useGrad")
## [1] FALSE
## attr(,"tol")
## [1] 4.440892e-16
```

```r
rankMatrix(matrix(c(1,1,2,2,1,2),nrow=3))
```

```
## [1] 2
## attr(,"method")
## [1] "tolNorm2"
## attr(,"useGrad")
## [1] FALSE
## attr(,"tol")
## [1] 6.661338e-16
```

```r
rankMatrix(matrix(c(1,1,2,0),nrow=2))
```

```
## [1] 2
## attr(,"method")
## [1] "tolNorm2"
## attr(,"useGrad")
## [1] FALSE
## attr(,"tol")
## [1] 4.440892e-16
```

```r
rankMatrix(matrix(c(1,2,3,2,0,2),nrow=3))
```

```
## [1] 2
## attr(,"method")
## [1] "tolNorm2"
## attr(,"useGrad")
## [1] FALSE
## attr(,"tol")
## [1] 6.661338e-16
```

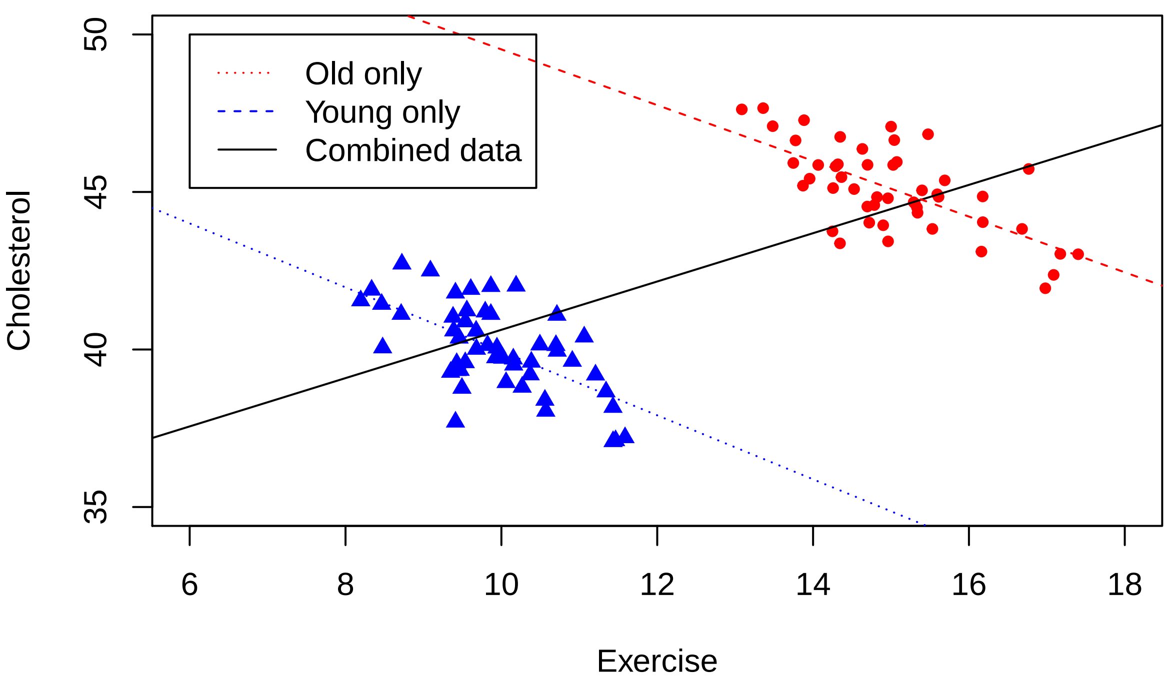
Q2

I. Reproducing the plot

```
df = read.csv("exercise_and_cholesterol.csv")
old_df = df[df$Age=="Old",]
young_df = df[df$Age=="Young",]

attach(df)
plot(Cholesterol ~ Exercise,col=ifelse(Age=="Old","red","blue"),pch=ifelse(Age=="Old",20,17),ylim=c(35,5

all_model = lm(Cholesterol ~ Exercise, data=df)
young_model = lm(Cholesterol ~ Exercise, data=young_df)
old_model = lm(Cholesterol ~ Exercise, data=old_df)
abline(all_model$coefficients[1],all_model$coefficients[2], lty="solid")
abline(young_model$coefficients[1],young_model$coefficients[2], lty="dotted",col="blue")
abline(old_model$coefficients[1],old_model$coefficients[2], lty="dashed",col="red")
legend(6, 50, legend=c("Old only", "Young only","Combined data"),
       col=c("red", "blue","black"), lty=c("dotted","dashed","solid"), cex=1)
```



###

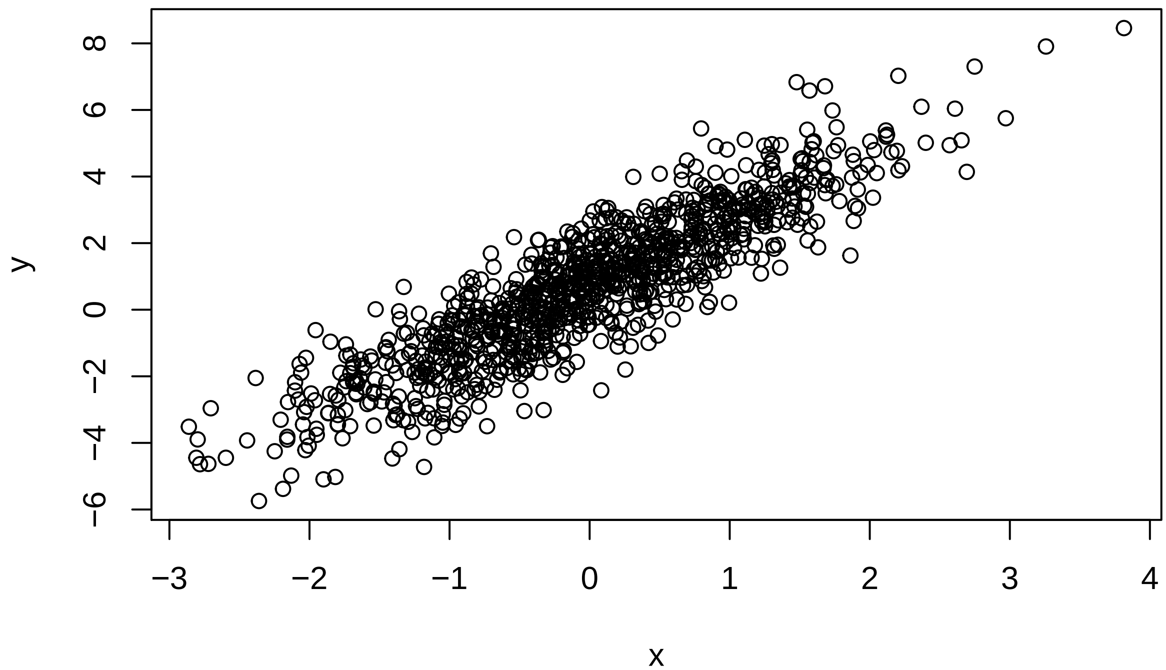
II. Are the three lines giving consistent or conflicting insights? Explain why. The 3 lines are giving conflicting insights. The young and old only lines suggest that Cholesterol and Exercise has negative association while the combined data suggesting positive association. The inconsistency occurs because Cholesterol is positively associated with Age so that the two groups are different. Furthermore, the old only group's exercise data is in the range between 13 - 18 while the young only group's data ranging from 7 - 12.

III. Can you propose an alternative estimation using all the data in order to obtain the same insight as the two separate regressions using only the old or the young people?

Maybe, collect old only data on the same range as young could solve the problem?

Q3

```
set.seed(37)
# Data generation
x = rnorm(1000) # Sample 1000 points from N(0, 1)
e = rnorm(1000)
y = 0.7 + 2*x + e
plot(y ~ x)
```



Use R's lm() function:

```
# Use lm()
model = lm(y ~ x)
summary(model)
```

```
##
## Call:
## lm(formula = y ~ x)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.3179 -0.6318  0.0383  0.6764  3.2130
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.73407    0.03216   22.82   <2e-16 ***
## x            1.95394    0.03165   61.74   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.017 on 998 degrees of freedom
```

```
## Multiple R-squared:  0.7925, Adjusted R-squared:  0.7923
## F-statistic:  3812 on 1 and 998 DF,  p-value: < 2.2e-16
```

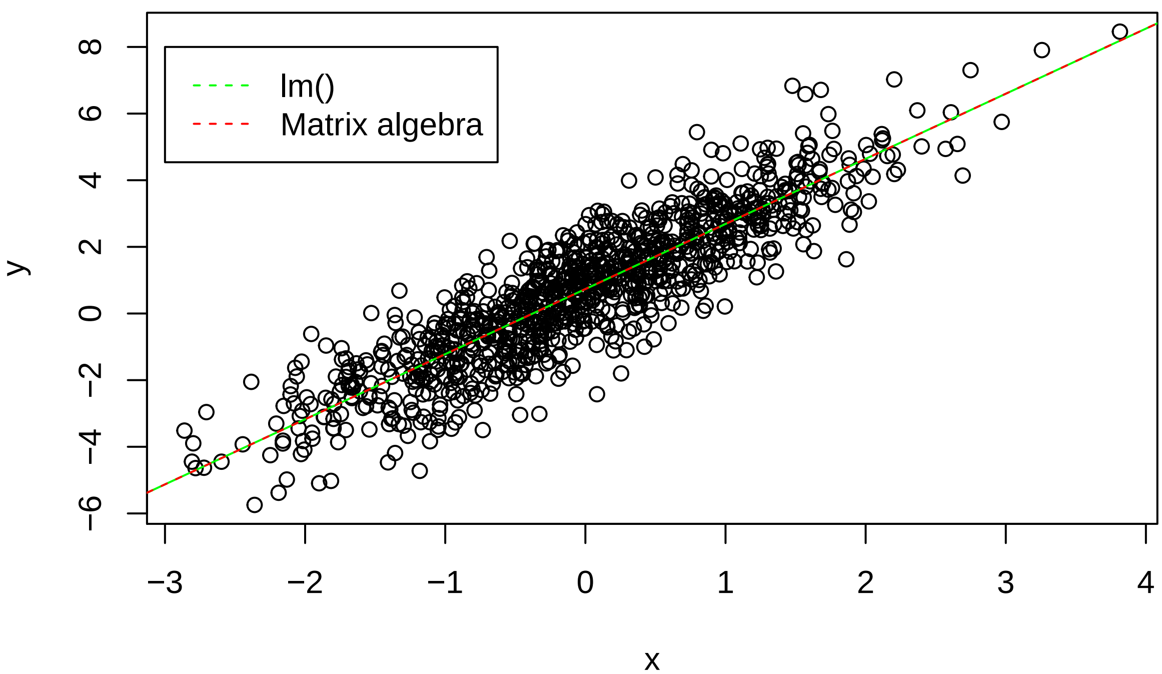
```
# y = 0.734 + 1.954 * x
```

Use matrix algebra: $\hat{\beta} = (X^T X)^{-1} X^T Y$

```
# Use matrix algebra
X = cbind(rep(1,1000),x) # Add bias(constant for intercept) to data matrix
Y = y
beta_h = ginv(t(X)%*%X)%*%t(X)%*%Y
beta_h # \beta0 = 0.734, \beta1 = 1.954
```

```
##           [,1]
## [1,] 0.7340735
## [2,] 1.9539367
```

```
plot(y ~ x)
abline(model$coefficients[1],model$coefficients[2],col="green")
abline(beta_h[1],beta_h[2],col="red",lty="dashed")
legend(-3,8,legend=c("lm()", "Matrix algebra"),col=c("green","red"),lty=c("dashed","dashed"))
```



Use optim(): $\hat{\beta} = argmin_{\beta} \sum_{i=1,...,n} (y_i - \beta_0 - \beta_1 \times x_i)^2$

```
X = cbind(rep(1,1000), x)
Y = y
# Objective function
fun = function(beta) {
  sum((Y - X%*%beta)^2)
}
# Start optimization with random initialization
optim(runif(2),fun) # \beta0 = 0.734, \beta1 = 1.954
```

```
## $par
## [1] 0.734061 1.953818
##
## $value
## [1] 1031.934
##
## $counts
## function gradient
##       57       NA
##
## $convergence
## [1] 0
##
## $message
## NULL
```

Use formula for 1 variable regression: $\bar{y} = \hat{\beta}_0 + \hat{\beta}_1\bar{x}$, $\hat{\beta}_1 = \frac{Cov(x_i,y_i)}{Var(x_i)}$

```
beta1 = cov(x,y)/var(x)
beta0 = mean(y) - beta1*mean(x)
beta0 # 0.734
```

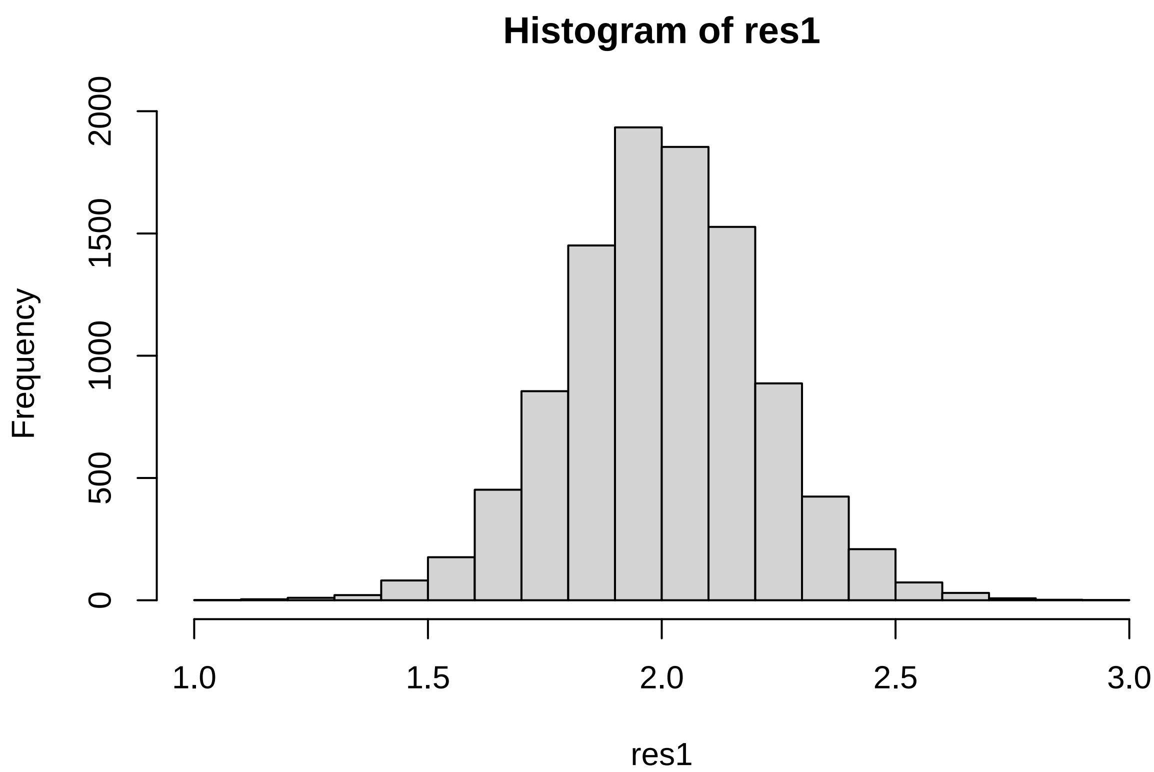
```
## [1] 0.7340735
```

```
beta1 # 1.954
```

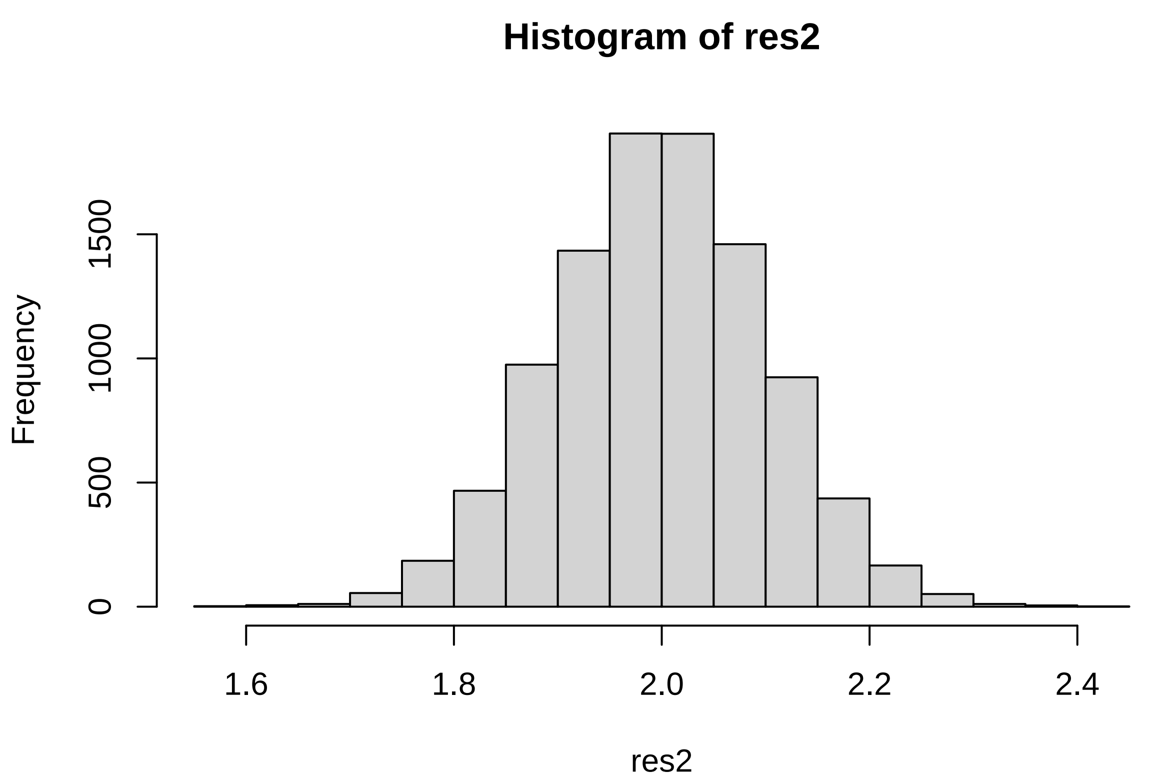
```
## [1] 1.953937
```

```
set.seed(37)
S = 10000
single_loop = function(N) {
  x = rnorm(N)
  e = rnorm(N)
  Y = 0.7 + 2*x + e
  X = cbind(rep(1,N),x)
  beta_h = ginv(t(X)%*%X)%*%t(X)%*%Y
  beta1 = beta_h[2]
}
vec_loop = Vectorize(single_loop)


res1 = vec_loop(rep(25,S))
hist(res1)
```




```r
res2 = vec_loop(rep(100,S))
hist(res2)
```



```r
mean(res1) # 2.002271
```

```
## [1] 2.002271
```

```r
mean(res2) # 1.998513
```

```
## [1] 1.998513
```

```r
var(res1) # 0.04465469
```

```
## [1] 0.04465469
```

```r
var(res2) # 0.01046778
```

```
## [1] 0.01046778
```

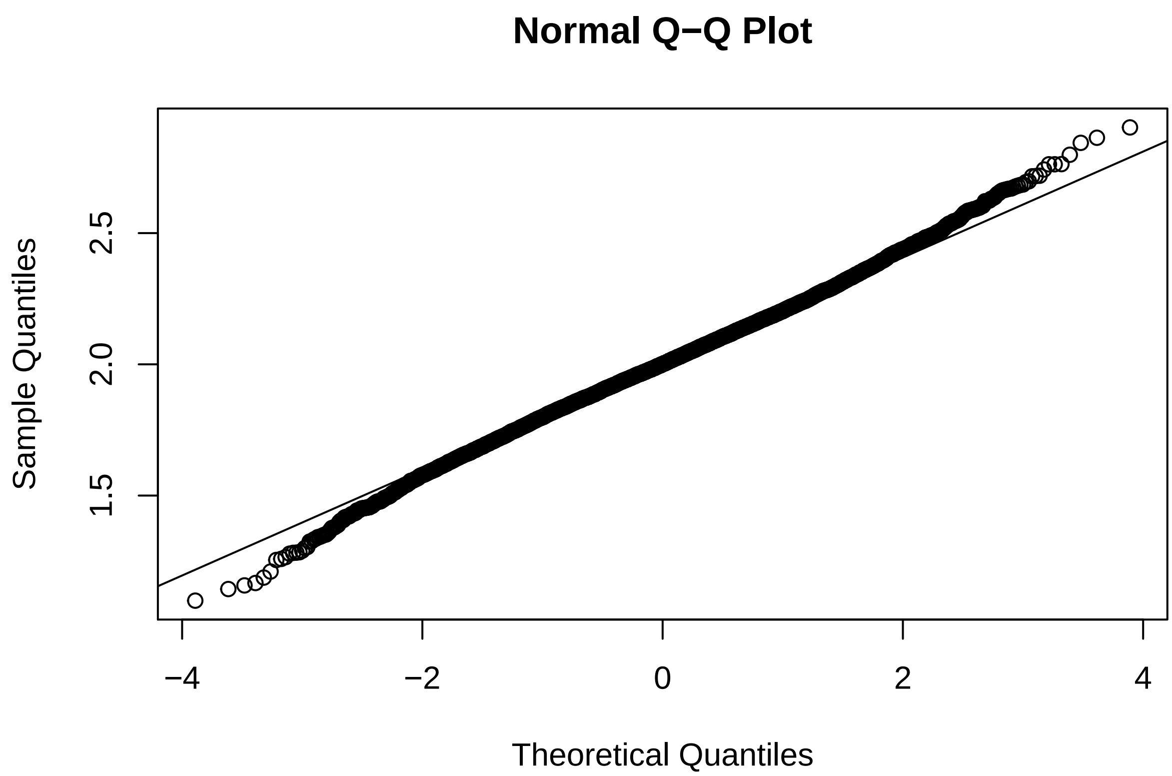
```r
t.test(res1, res2, alternative = "two.sided", var.equal = FALSE) # p-value = 0.1095
```

```
##
##  Welch Two Sample t-test
##
## data:  res1 and res2
## t = 1.6006, df = 14443, p-value = 0.1095
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.0008440232  0.0083600243
## sample estimates:
## mean of x mean of y
##  2.002271  1.998513
```

```r
# Test normality
library(nortest)
#Anderson-Darling normality test
ad.test(res1) # p-value = 2.064e-08
```

```
##
##  Anderson-Darling normality test
##
## data:  res1
## A = 3.3628, p-value = 2.064e-08
```

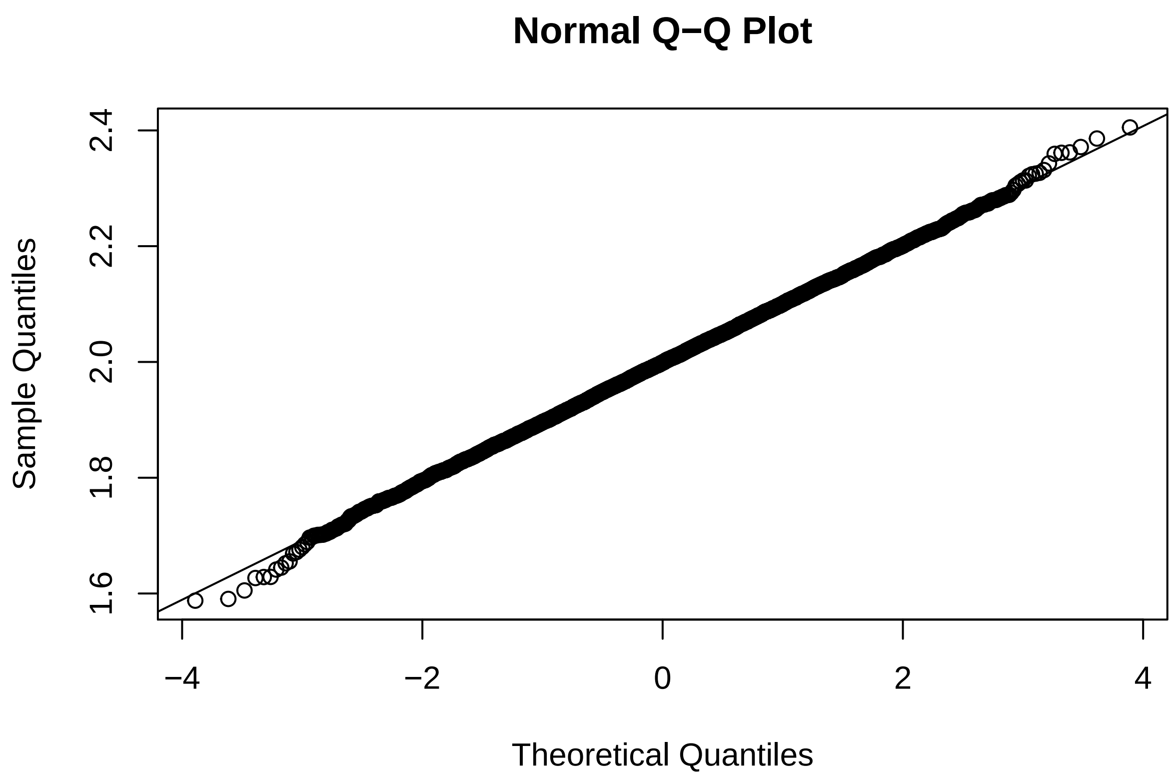
```r
qqnorm(res1)
qqline(res1)
```




```r
ad.test(res1) # p-value = 2.064e-08
```

```
##
##  Anderson-Darling normality test
##
## data:  res1
## A = 3.3628, p-value = 2.064e-08
```

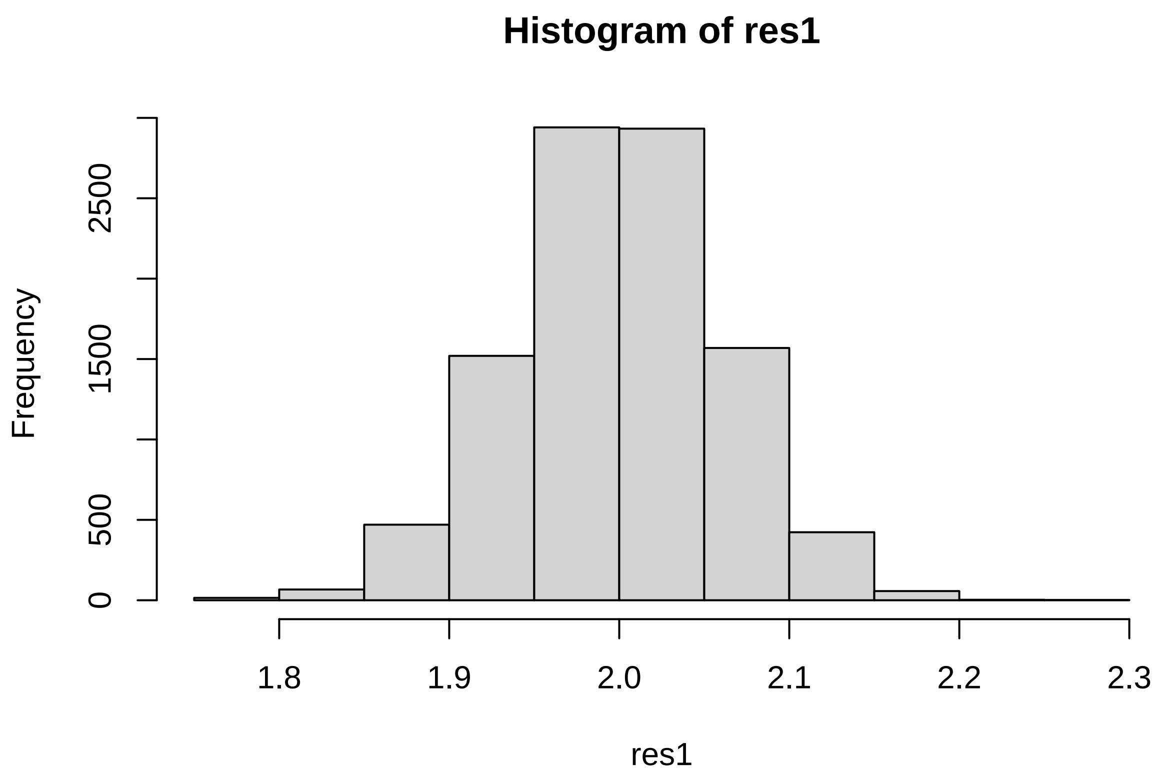
```r
qqnorm(res2)
qqline(res2)
```



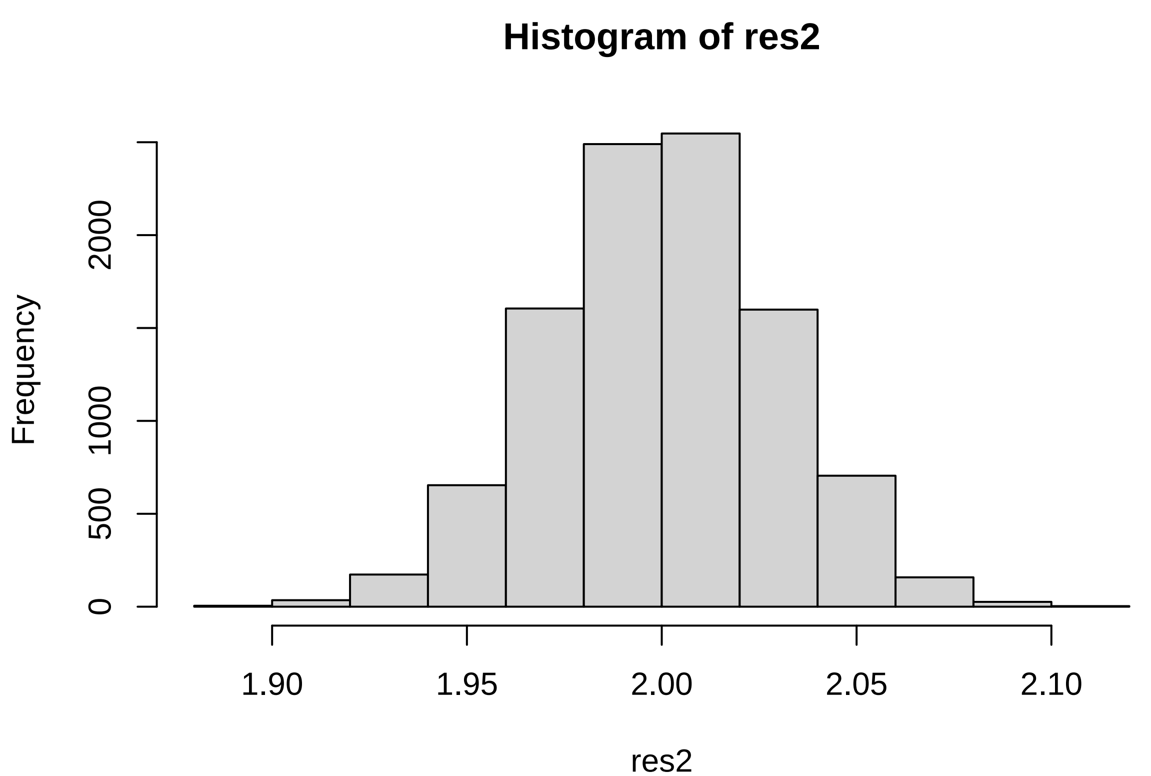
Use uniformly distributed error

```
set.seed(37)
S = 10000
single_loop = function(N) {
  x = rnorm(N)
  e = runif(N)
  Y = 0.7 + 2*x + e
  X = cbind(rep(1,N),x)
  beta_h = ginv(t(X)%*%X)%*%t(X)%*%Y
  beta1 = beta_h[2]
}
vec_loop = Vectorize(single_loop)

res1 = vec_loop(rep(25,S))
hist(res1)
```




```r
res2 = vec_loop(rep(100,S))
hist(res2)
```



```r
mean(res1) # 1.999372
```

```
## [1] 1.999372
```

```r
mean(res2) # 2.000016
```

```
## [1] 2.000016
```

```r
var(res1) # 0.003772373
```

```
## [1] 0.003772373
```

```r
var(res2) # 0.0008630136
```

```
## [1] 0.0008630136
```

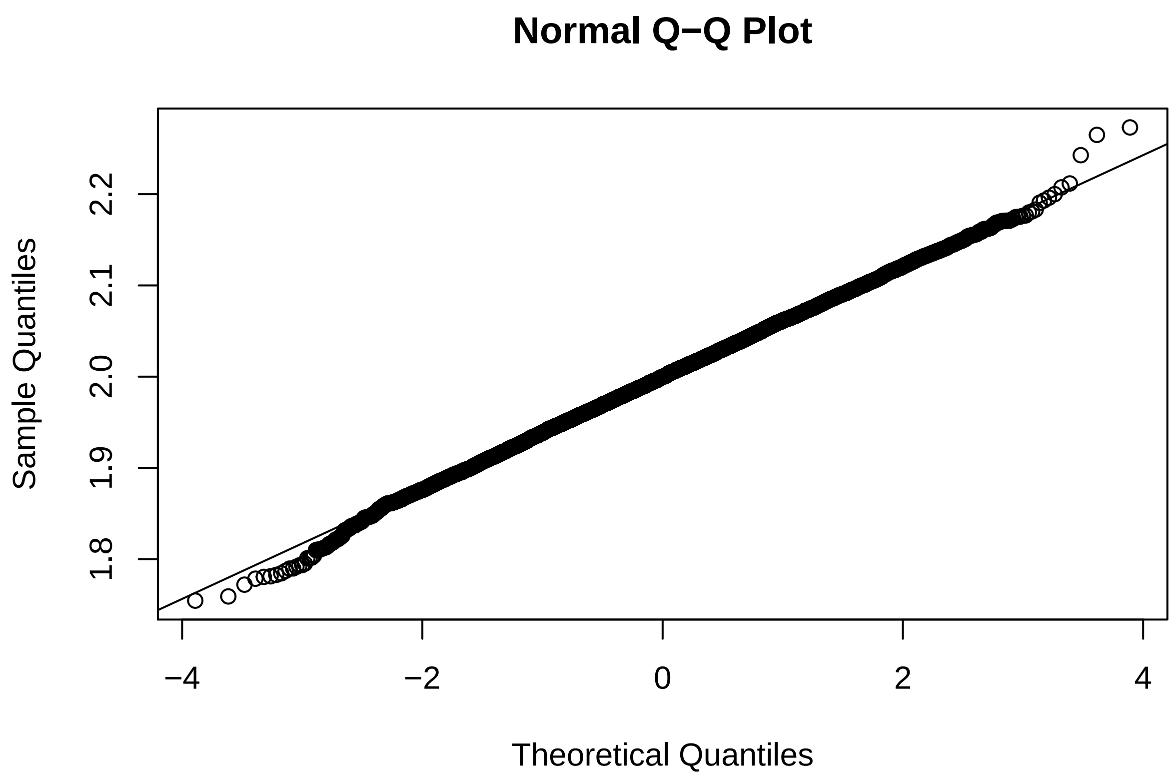
```r
t.test(res1, res2, alternative = "two.sided", var.equal = TRUE) # p-value = 0.3446
```

```
##
##  Two Sample t-test
##
## data:  res1 and res2
## t = -0.94514, df = 19998, p-value = 0.3446
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.0019779794  0.0006910131
## sample estimates:
## mean of x mean of y
##  1.999372  2.000016
```

```r
#Anderson-Darling normality test
ad.test(res1) # p-value = 0.4207
```

```
##
##  Anderson-Darling normality test
##
## data:  res1
## A = 0.37211, p-value = 0.4207
```

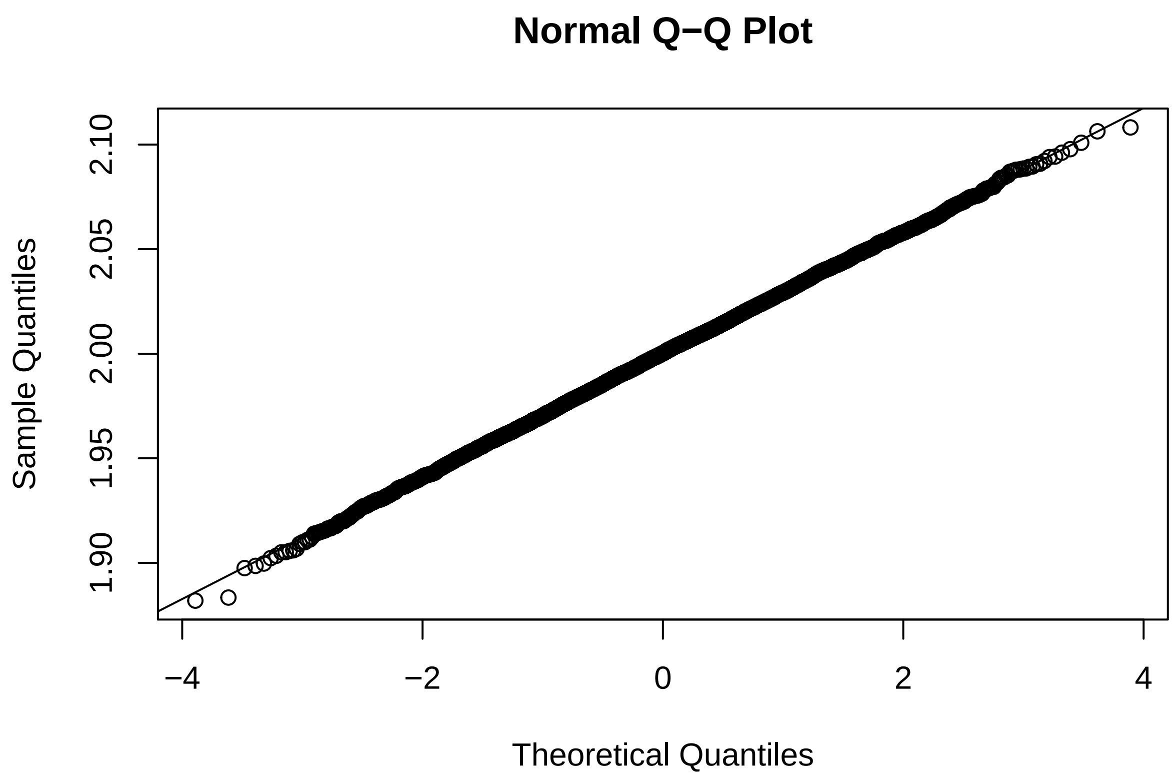
```r
qqnorm(res1)
qqline(res1)
```




```r
ad.test(res1) # p-value = 0.4207
```

```
##
##  Anderson-Darling normality test
##
## data:  res1
## A = 0.37211, p-value = 0.4207
```

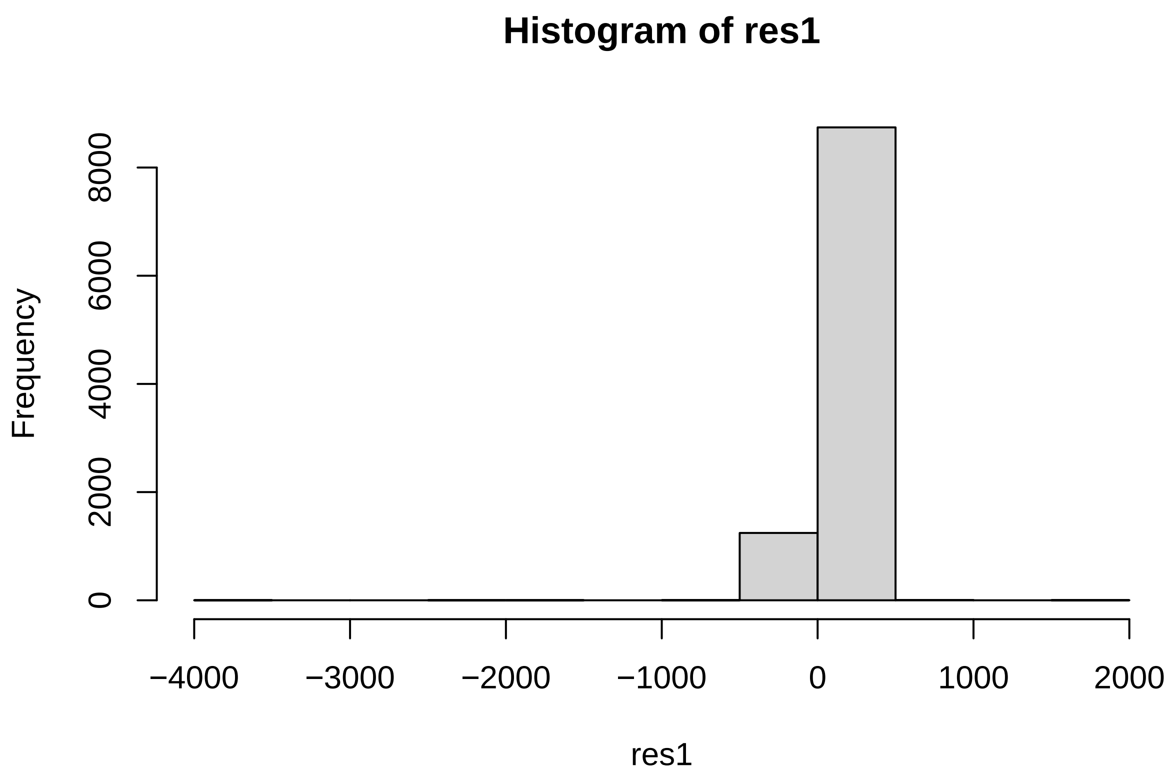
```r
qqnorm(res2)
qqline(res2)
```



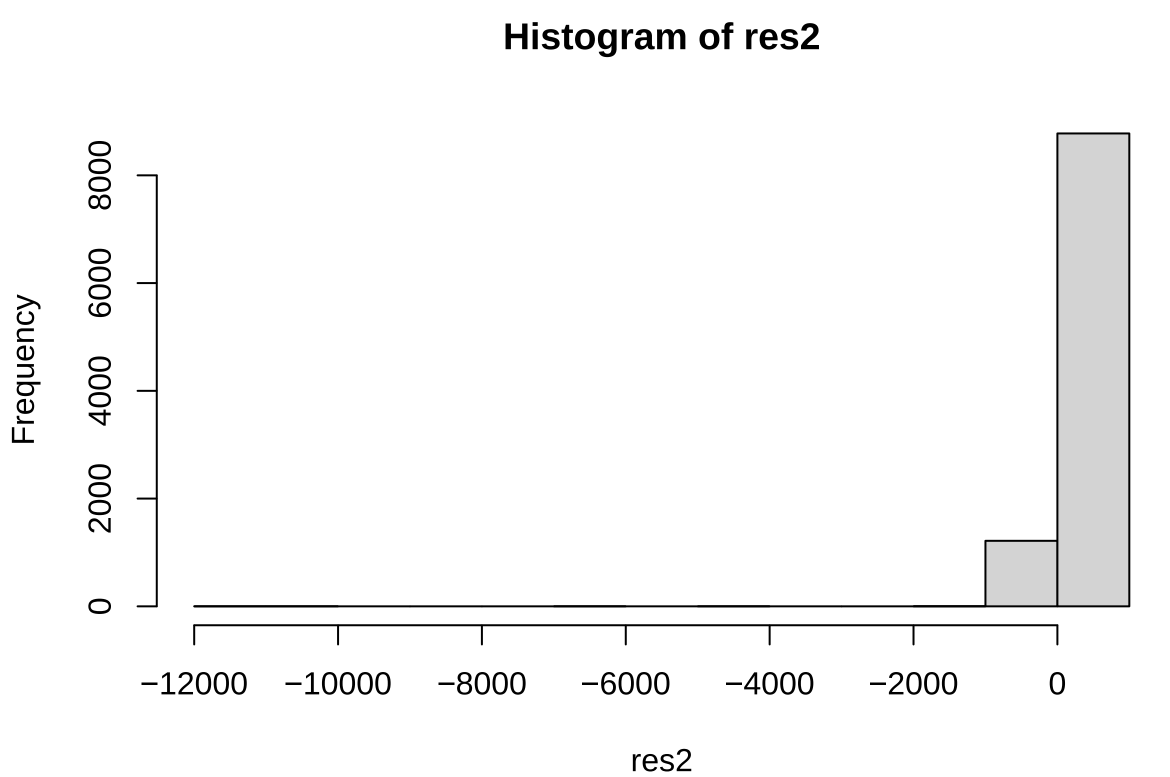
Use Cauchy distributed error

```
set.seed(37)
S = 10000
single_loop = function(N) {
  x = rnorm(N)
  e = rcauchy(N)
  Y = 0.7 + 2*x + e
  X = cbind(rep(1,N),x)
  beta_h = ginv(t(X)%*%X)%*%t(X)%*%Y
  beta1 = beta_h[2]
}
vec_loop = Vectorize(single_loop)

res1 = vec_loop(rep(25,S))
hist(res1)
```




```
res2 = vec_loop(rep(100,S))
hist(res2)
```



```r
mean(res1) # 1.907382
```

```
## [1] 1.907382
```

```r
mean(res2) # -1.599096
```

```
## [1] -1.599096
```

```r
var(res1) # 3427.213
```

```
## [1] 3427.213
```

```r
var(res2) # 29851.75
```

```
## [1] 29851.75
```

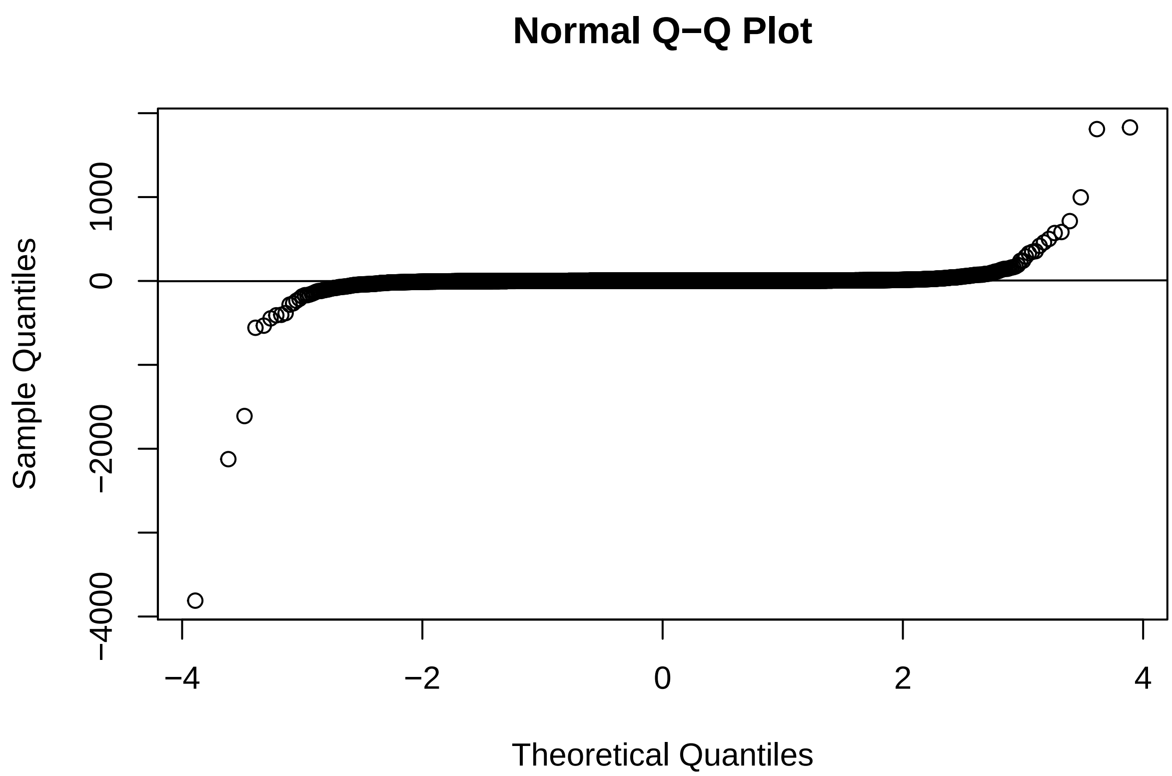
```r
t.test(res1, res2, alternative = "two.sided", var.equal = FALSE) # p-value = 0.05461
```

```
## 
##  Welch Two Sample t-test
## 
## data:  res1 and res2
## t = 1.9221, df = 12265, p-value = 0.05461
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.06934377  7.08229918
## sample estimates:
## mean of x mean of y 
##  1.907382 -1.599096
```

```r
#Anderson-Darling normality test
ad.test(res1) # p-value = 2.2e-16
```

```
## 
##  Anderson-Darling normality test
## 
## data:  res1
## A = 3277, p-value < 2.2e-16
```

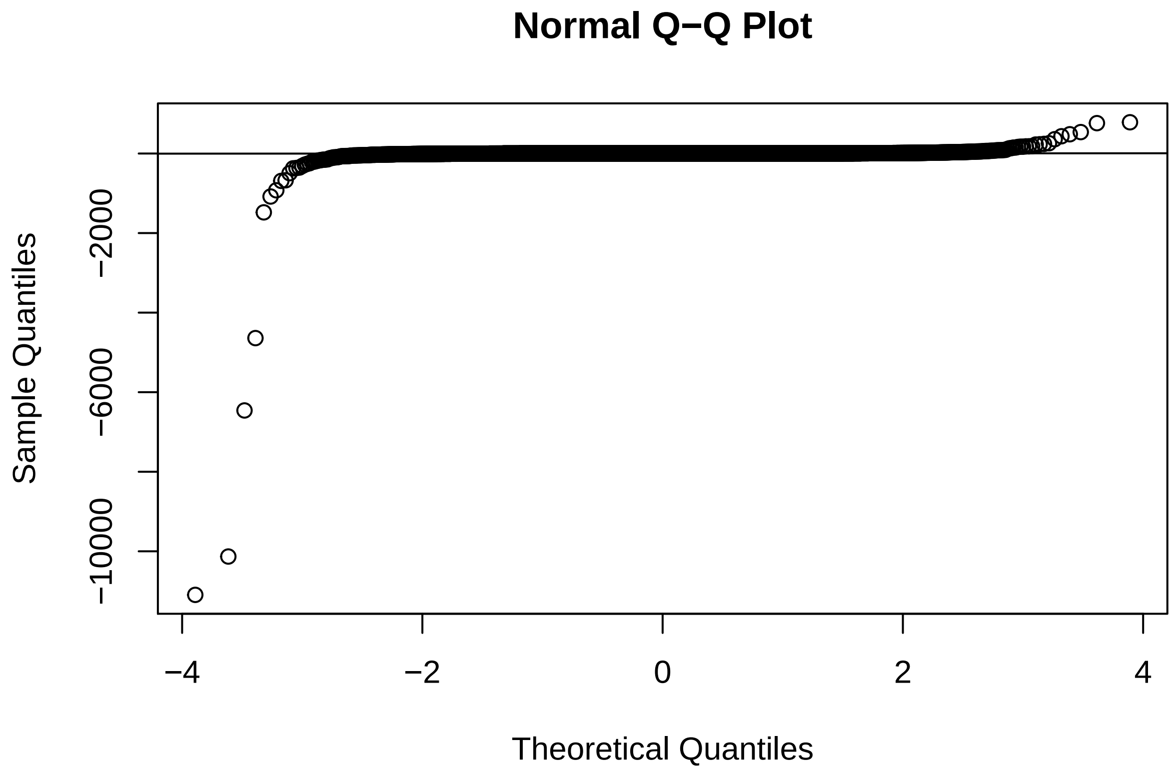
```r
qqnorm(res1)
qqline(res1)
```




```r
ad.test(res1) # p-value = 2.2e-16
```

```
##
##  Anderson-Darling normality test
##
## data:  res1
## A = 3277, p-value < 2.2e-16
```

```r
qqnorm(res2)
qqline(res2)
```


Normal Q−Q Plot
Sample Quantiles
−2000
−6000
−10000
−4
−2
0
2
4
Theoretical Quantiles