M1_A12

Sofia Cantu

2024-09-04

El Validez del modelo

```
M = read.csv("~/Downloads/ArchivosCodigos/Estatura-peso_HyM.csv")

# Fitting the linear model
modelo <- lm(Peso ~ Estatura, data=M)

MM = subset(M,M$Sexo=="M")
MH = subset(M,M$Sexo=="H")
Modelo1H = lm(Estatura~Peso, MH)
Modelo1M = lm(Estatura~Peso, MM)
Modelo2 = lm(Estatura~Peso, M)
Modelo3 = lm(Peso~Estatura*Sexo, M)
```

Analiza si el (los) modelo(s) obtenidos anteriormente son apropiados para el conjunto de datos. Realiza el análisis de los residuos:

- Normalidad de los residuos
- Verificación de media cero
- Homocedasticidad e independencia

```
# Anderson-Darling Test for normality
library(nortest)
ad.test(Modelo1H$residuals)

##
##  Anderson-Darling normality test
##
## data:  Modelo1H$residuals
## A = 0.38581, p-value = 0.3884

ad.test(Modelo1M$residuals)

##
##  Anderson-Darling normality test
##
## data:  Modelo1M$residuals
## A = 0.19471, p-value = 0.8909

ad.test(Modelo2$residuals)

##
##  Anderson-Darling normality test
```

```
##
## data:  Modelo2$residuals
## A = 0.25276, p-value = 0.7341
```

```
ad.test(Modelo3$residuals)
```

```
##
##  Anderson-Darling normality test
##
## data:  Modelo3$residuals
## A = 0.8138, p-value = 0.03516
```

Hipótesis nula (H_0): Los datos siguen una distribución normal. Hipótesis alternativa (H_1): Los datos no siguen una distribución normal.

Si el valor p es bajo (< 0.05), se rechaza la hipótesis nula, lo que sugiere que los datos no son normales.

Entonces solo hay normalidad en los modelos: -Modelo1H -Modelo1M -Modelo2

```
t.test(Modelo1H$residuals)
```

```
##
##  One Sample t-test
##
## data:  Modelo1H$residuals
## t = 1.5745e-15, df = 219, p-value = 1
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  -0.004362545  0.004362545
## sample estimates:
##    mean of x
## 3.485217e-18
```

```
t.test(Modelo1M$residuals)
```

```
##
##  One Sample t-test
##
## data:  Modelo1M$residuals
## t = -9.0273e-16, df = 219, p-value = 1
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  -0.00569816  0.00569816
## sample estimates:
##    mean of x
## -2.60997e-18
```

```
t.test(Modelo2$residuals)
```

```
##
##  One Sample t-test
```

```
##
## data:  Modelo2$residuals
## t = -4.6486e-16, df = 439, p-value = 1
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  -0.003867162  0.003867162
## sample estimates:
##     mean of x
## -9.146724e-19
```

```
t.test(Modelo3$residuals)
```

```
##
##  One Sample t-test
##
## data:  Modelo3$residuals
## t = -3.1626e-16, df = 439, p-value = 1
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  -0.5017741  0.5017741
## sample estimates:
##     mean of x
## -8.074349e-17
```

Hipótesis nula (H_0): La media de los residuos es igual a 0. Hipótesis alternativa (H_1): La media de los residuos es diferente de 0.

Si el valor p resultante es menor que el nivel de significancia (0.05), se rechaza la hipótesis nula, lo que sugiere que la media de los residuos es significativamente diferente de 0.

Entonces, todos los modelos tienen media de 0.

```
library(lmtest)
```

```
## Loading required package: zoo
```

```
##
## Attaching package: 'zoo'
```

```
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
```

```
dwtest(Modelo1H)
```

```
##
##  Durbin-Watson test
##
## data:  Modelo1H
## DW = 1.9884, p-value = 0.4659
## alternative hypothesis: true autocorrelation is greater than 0
```

```r
bgtest(Modelo1H)
```

```
##
##  Breusch-Godfrey test for serial correlation of order up to 1
##
## data:  Modelo1H
## LM test = 0.0010484, df = 1, p-value = 0.9742
```

```r
dwtest(Modelo1M)
```

```
##
##  Durbin-Watson test
##
## data:  Modelo1M
## DW = 2.0825, p-value = 0.7297
## alternative hypothesis: true autocorrelation is greater than 0
```

```r
bgtest(Modelo1M)
```

```
##
##  Breusch-Godfrey test for serial correlation of order up to 1
##
## data:  Modelo1M
## LM test = 0.39351, df = 1, p-value = 0.5305
```

```r
dwtest(Modelo2)
```

```
##
##  Durbin-Watson test
##
## data:  Modelo2
## DW = 1.9578, p-value = 0.3184
## alternative hypothesis: true autocorrelation is greater than 0
```

```r
bgtest(Modelo2)
```

```
##
##  Breusch-Godfrey test for serial correlation of order up to 1
##
## data:  Modelo2
## LM test = 0.16657, df = 1, p-value = 0.6832
```

```r
dwtest(Modelo3)
```

```
##
##  Durbin-Watson test
##
## data:  Modelo3
## DW = 1.8646, p-value = 0.07113
## alternative hypothesis: true autocorrelation is greater than 0
```

```r
bgtest(Modelo3)
```

```
##
##  Breusch-Godfrey test for serial correlation of order up to 1
##
## data:  Modelo3
## LM test = 1.3453, df = 1, p-value = 0.2461
```

```
bptest(Modelo1H)
```

```
##
##  studentized Breusch-Pagan test
##
## data:  Modelo1H
## BP = 0.45776, df = 1, p-value = 0.4987
```

```
gqtest(Modelo1H)
```

```
##
##  Goldfeld-Quandt test
##
## data:  Modelo1H
## GQ = 0.91478, df1 = 108, df2 = 108, p-value = 0.6778
## alternative hypothesis: variance increases from segment 1 to 2
```

```
bptest(Modelo1M)
```

```
##
##  studentized Breusch-Pagan test
##
## data:  Modelo1M
## BP = 1.9859, df = 1, p-value = 0.1588
```

```
gqtest(Modelo1M)
```

```
##
##  Goldfeld-Quandt test
##
## data:  Modelo1M
## GQ = 0.94892, df1 = 108, df2 = 108, p-value = 0.6071
## alternative hypothesis: variance increases from segment 1 to 2
```

```
bptest(Modelo2)
```

```
##
##  studentized Breusch-Pagan test
##
## data:  Modelo2
## BP = 9.9492, df = 1, p-value = 0.001609
```

```
gqtest(Modelo2)
```

```
##
##  Goldfeld-Quandt test
```

```
##
## data:  Modelo2
## GQ = 1.706, df1 = 218, df2 = 218, p-value = 4.502e-05
## alternative hypothesis: variance increases from segment 1 to 2
```

```
bptest(Modelo3)
```

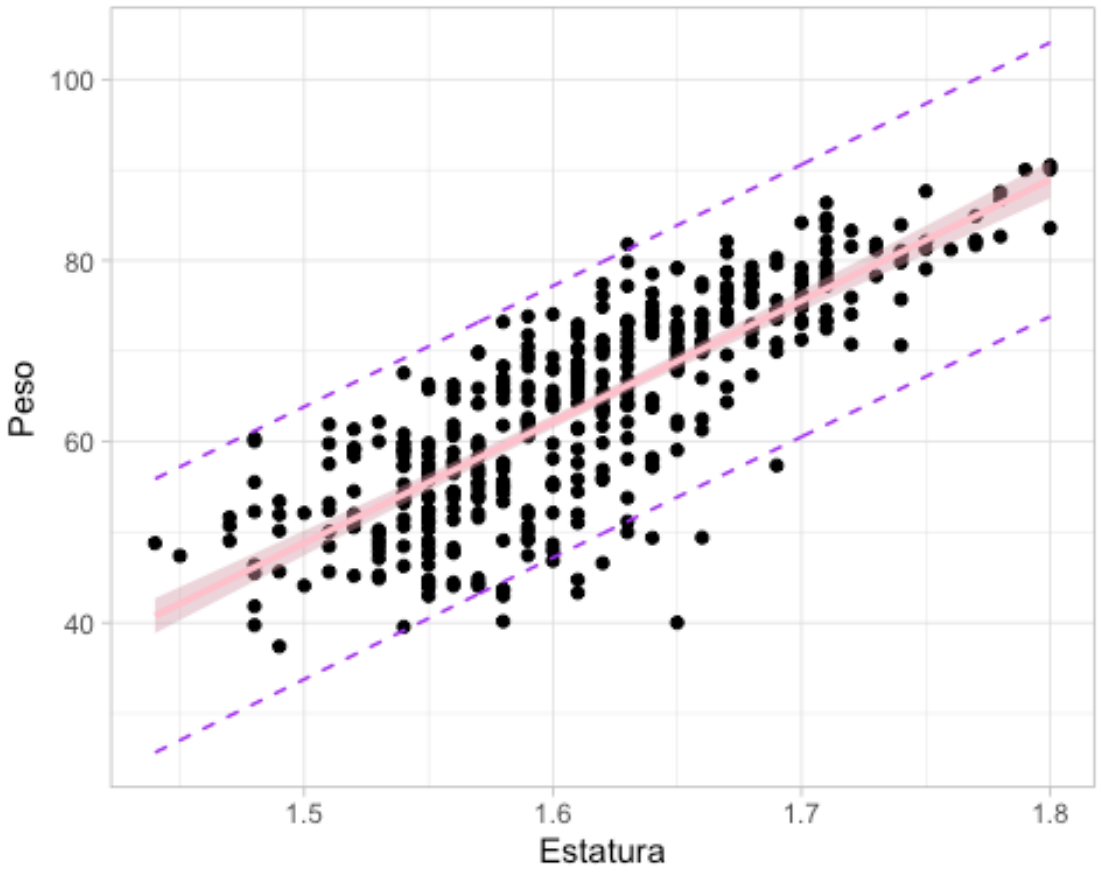
```
##
##  studentized Breusch-Pagan test
##
## data:  Modelo3
## BP = 59.211, df = 3, p-value = 8.667e-13
```

```
gqtest(Modelo3)
```

```
##
##  Goldfeld-Quandt test
##
## data:  Modelo3
## GQ = 3.2684, df1 = 216, df2 = 216, p-value < 2.2e-16
## alternative hypothesis: variance increases from segment 1 to 2
```

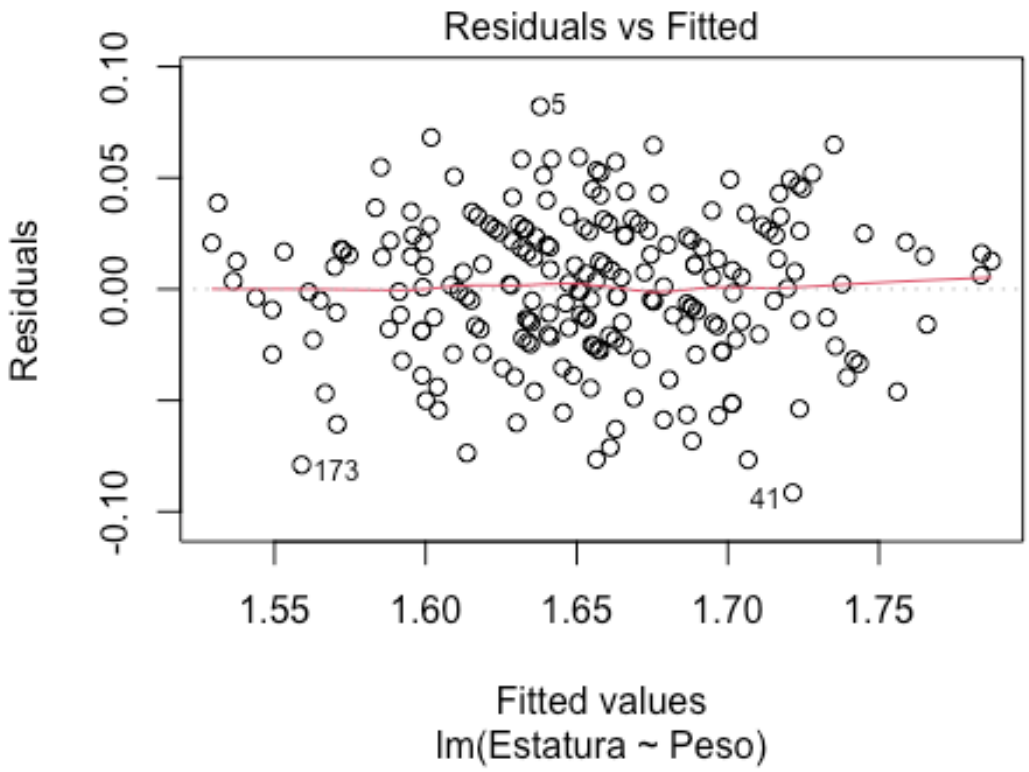
H_0: Los errores no están autocorrelacionados. H_1: Los errores están autocorrelacionados.

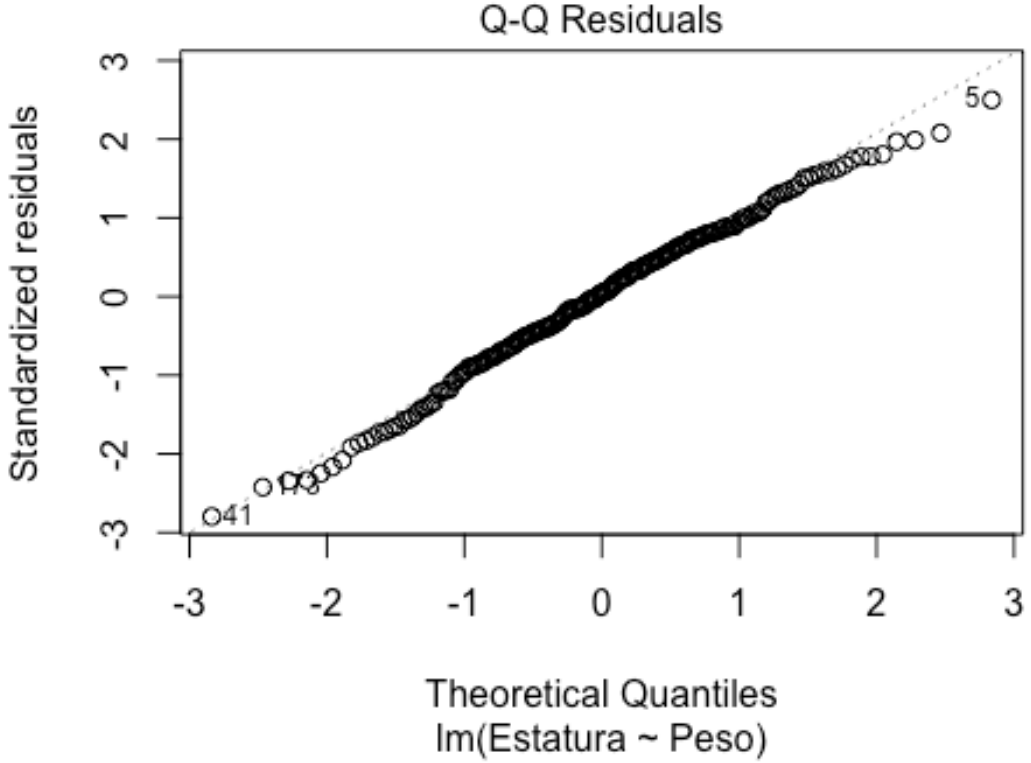
```
# Confidence and Prediction Intervals
Ip <- predict(object = modelo, newdata = M, interval = "prediction", level =
0.97)

# Combine the predicted intervals with the original data
M <- cbind(M, Ip)

# Load ggplot2 library for plotting
library(ggplot2)

# Plotting the data, regression line, and confidence intervals
ggplot(M, aes(x = Estatura, y = Peso)) +
  geom_point() +
  geom_line(aes(y = lwr), color = "purple", linetype = "dashed") +
  geom_line(aes(y = upr), color = "purple", linetype = "dashed") +
  geom_smooth(method = "lm", formula = y ~ x, se = TRUE, level = 0.97, col =
"pink", fill = "pink3") +
  theme_light()
```

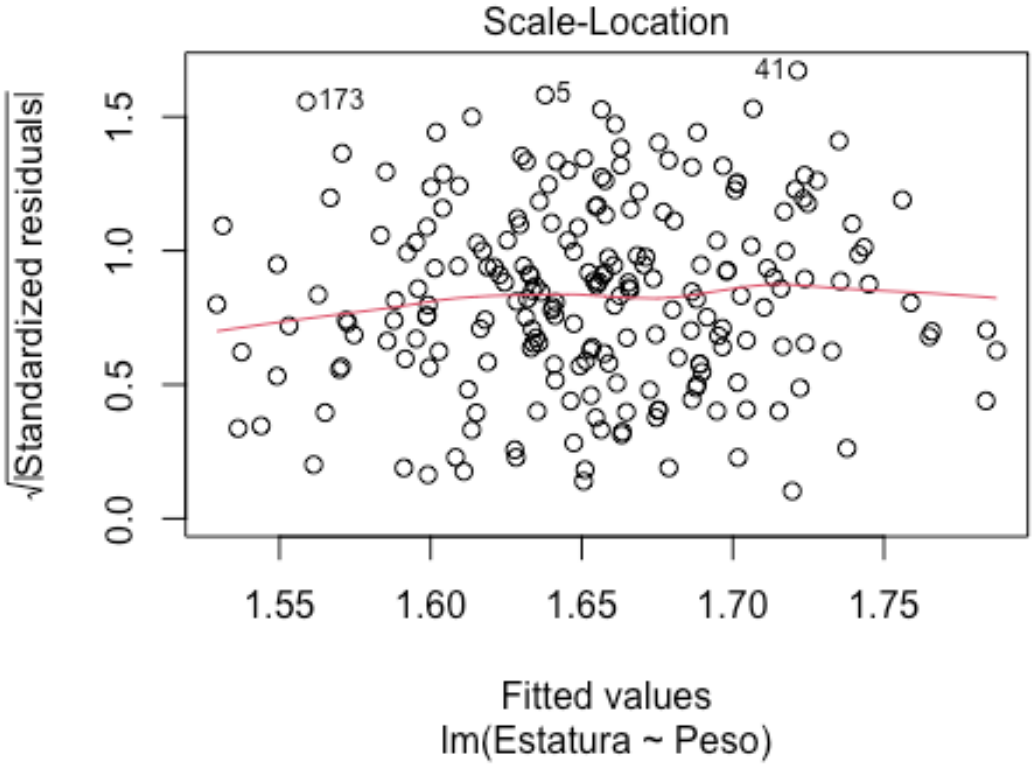


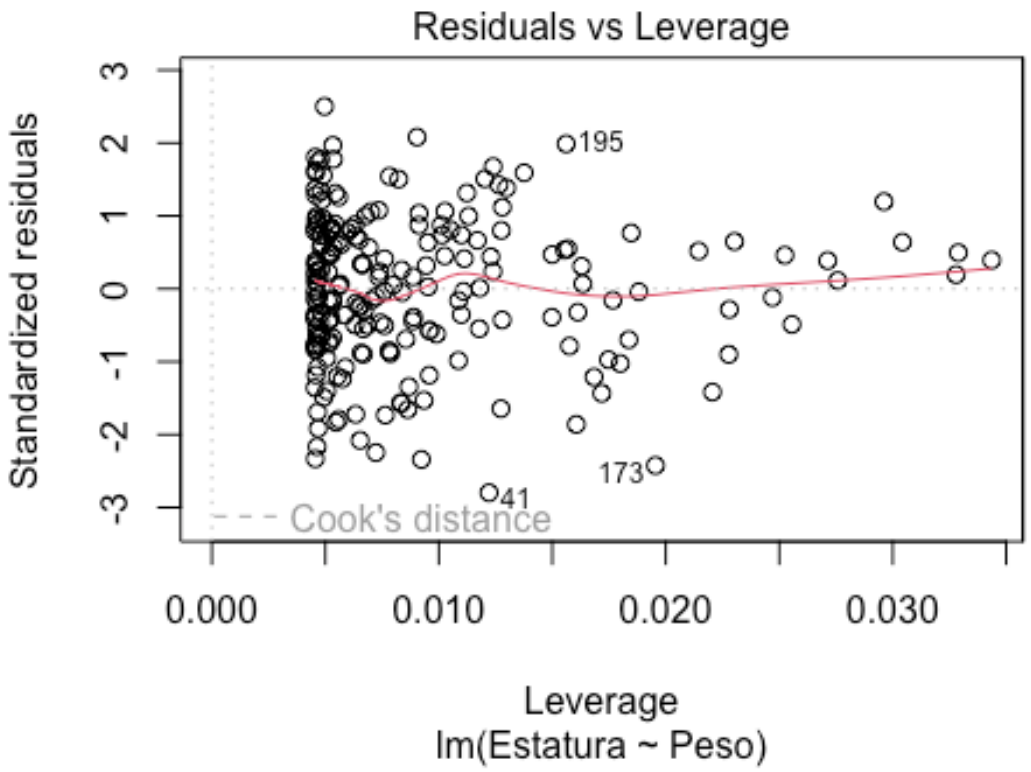
Utiliza el comando: plot(modelo). Observa las gráficas obtenidas y contesta:

```
plot(Modelo1H)
```

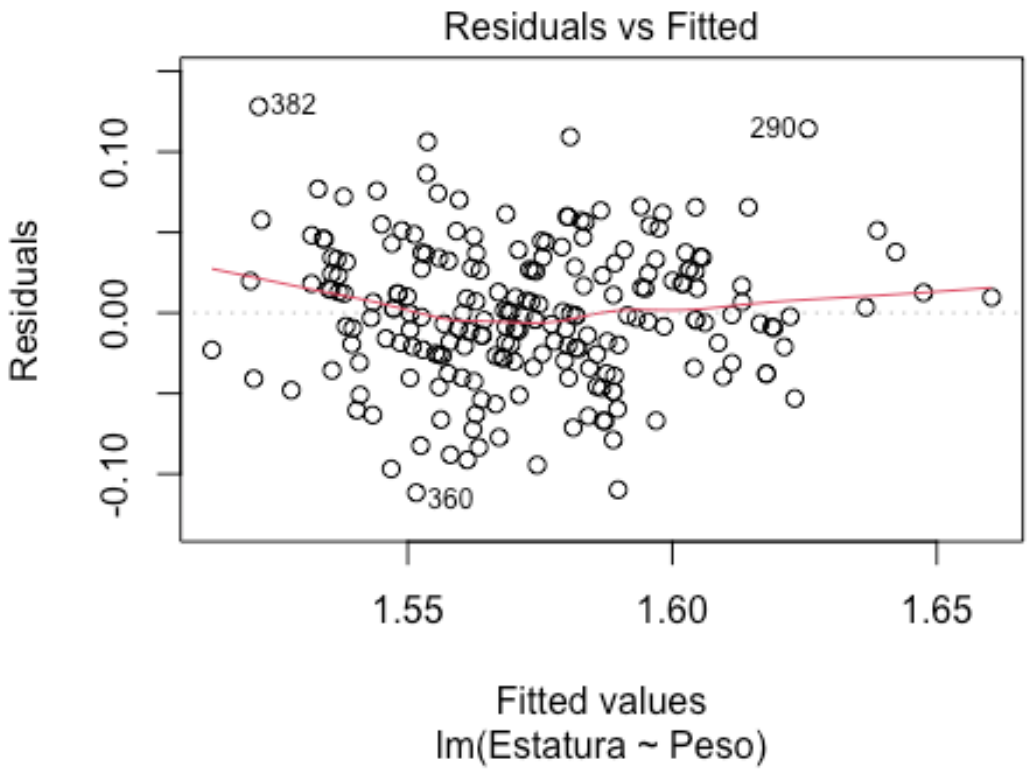

Residuals vs Fitted
Residuals
0.10
0.05
0.00
-0.10
5
173
41
1.55
1.60
1.65
1.70
1.75
Fitted values
lm(Estatura ~ Peso)

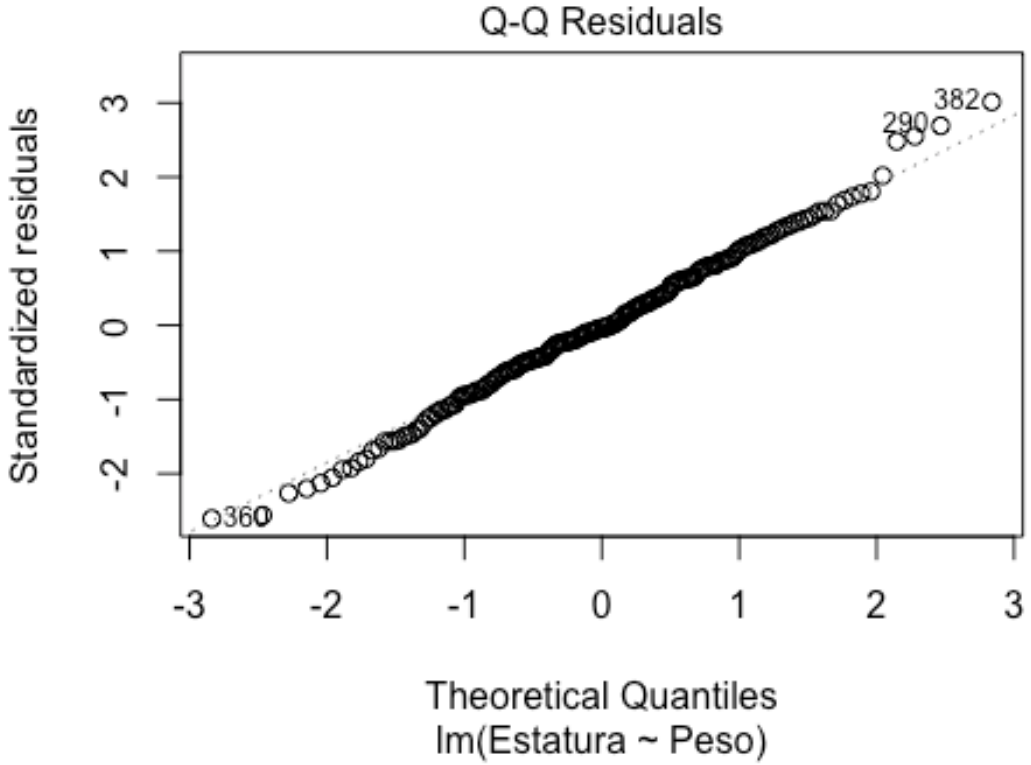

Q-Q Residuals
Standardized residuals
-3
-2
-1
0
1
2
3
41
5
Theoretical Quantiles
lm(Estatura ~ Peso)

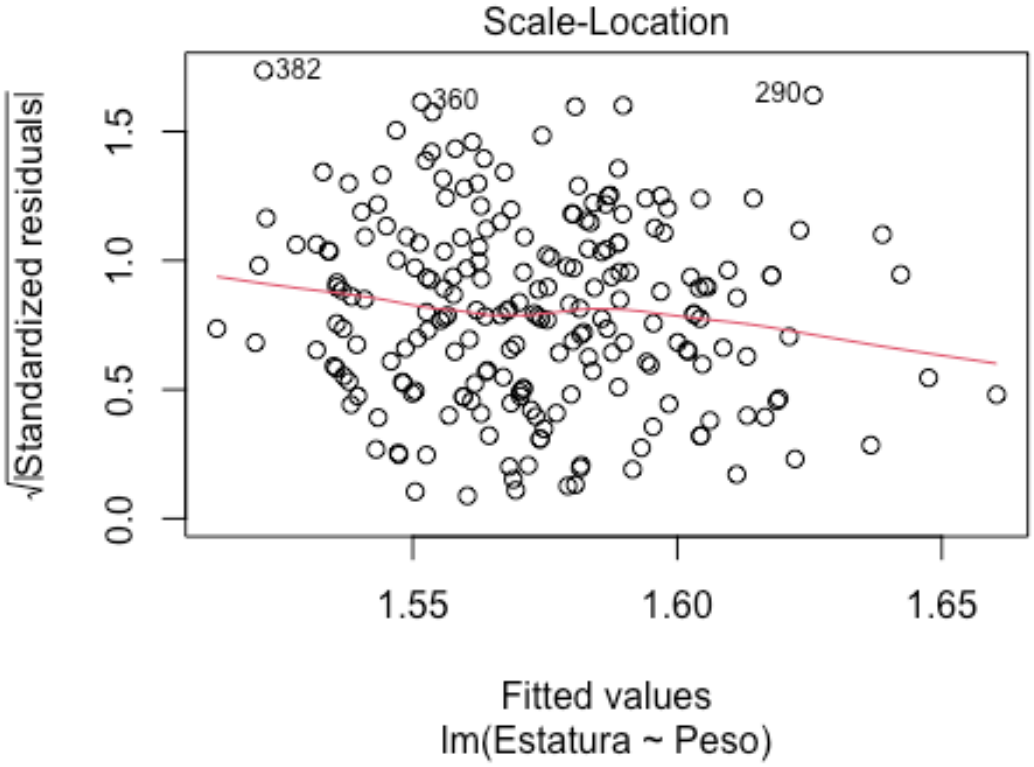

Scale-Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
173
5
41
1.55
1.60
1.65
1.70
1.75
Fitted values
lm(Estatura ~ Peso)

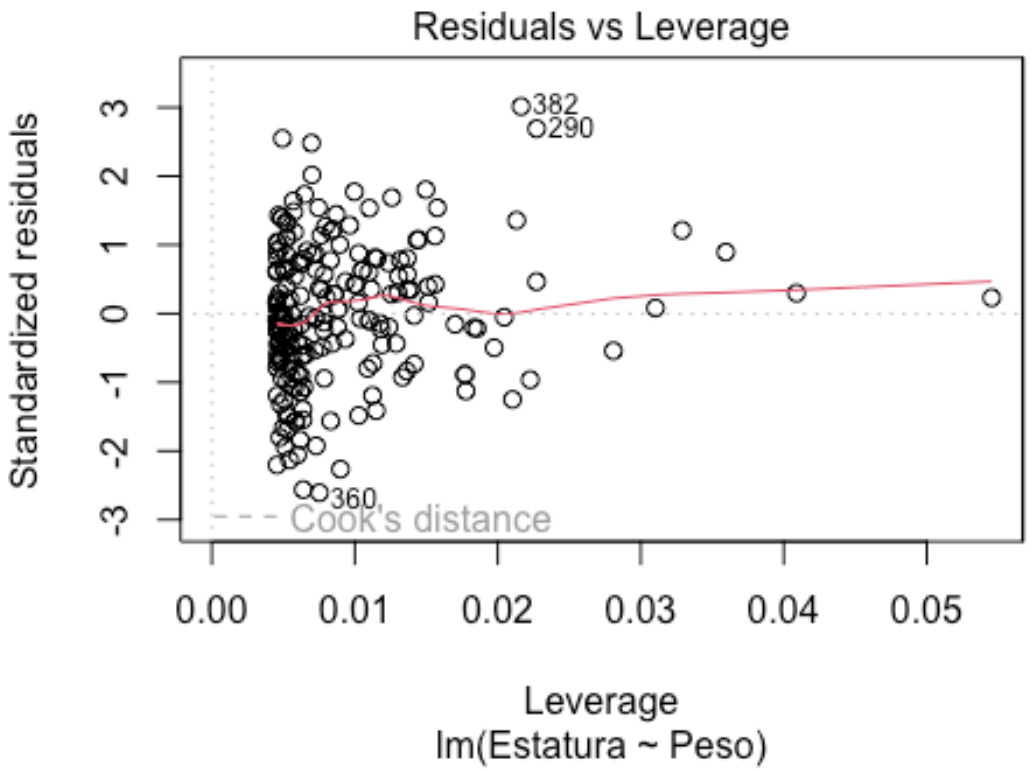



```
plot(Modelo1M)
```

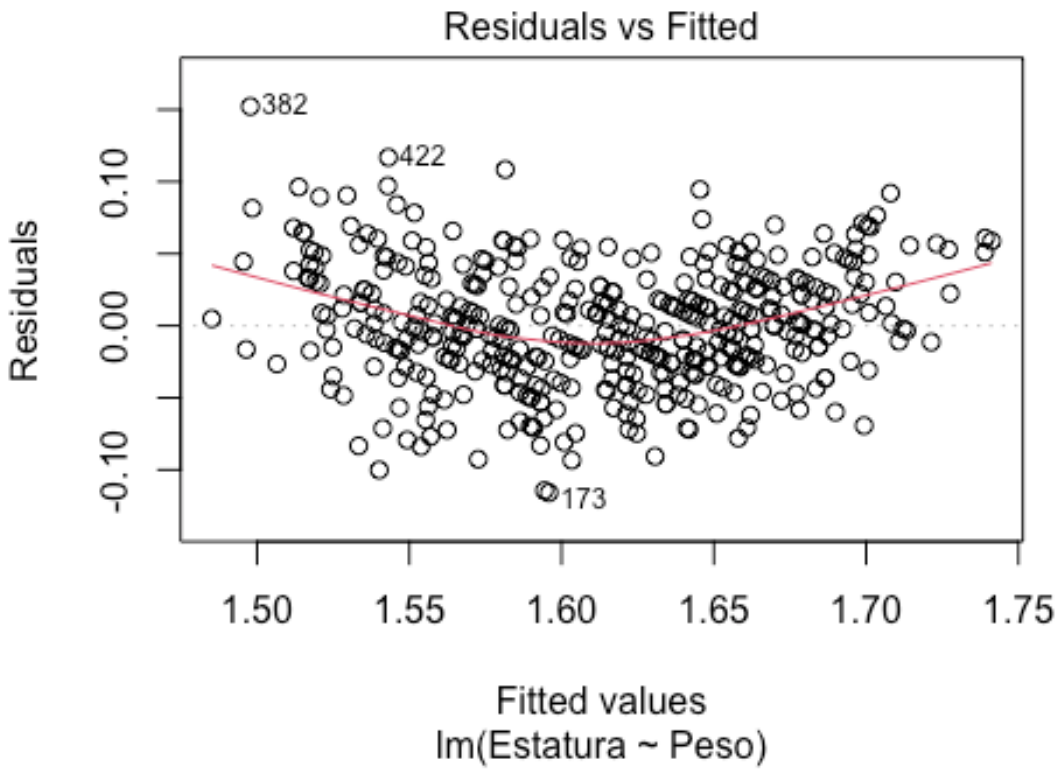

Residuals vs Fitted
382
290
360
0.10
0.00
-0.10
Residuals
1.55
1.60
1.65
Fitted values
lm(Estatura ~ Peso)

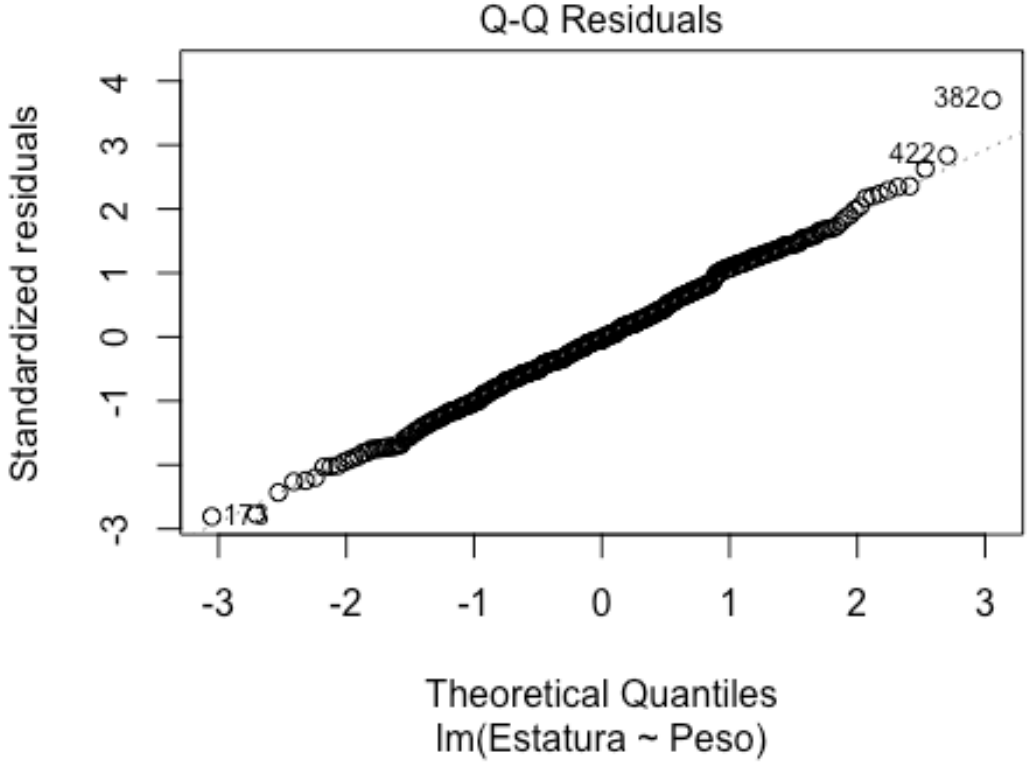

Q-Q Residuals
Standardized residuals
-2
-1
0
1
2
3
382
290
360
-3
-2
-1
0
1
2
3
Theoretical Quantiles
lm(Estatura ~ Peso)

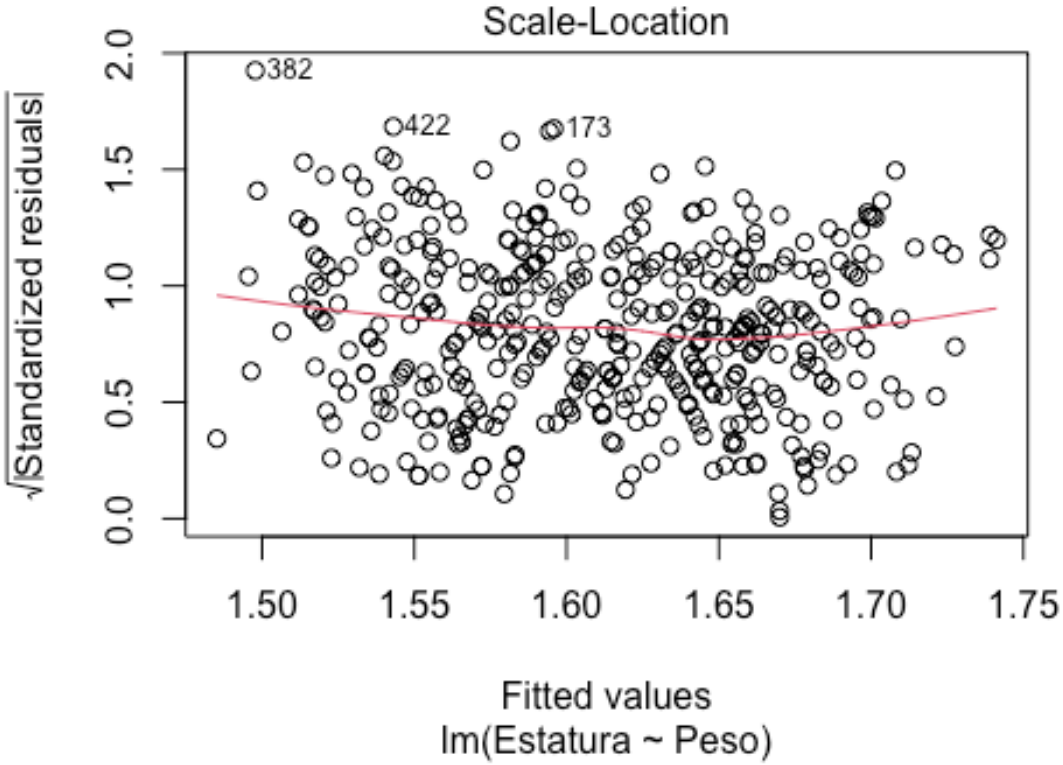

Scale-Location
382
360
290
√|Standardized residuals|
0.0
0.5
1.0
1.5
1.55
1.60
1.65
Fitted values
lm(Estatura ~ Peso)

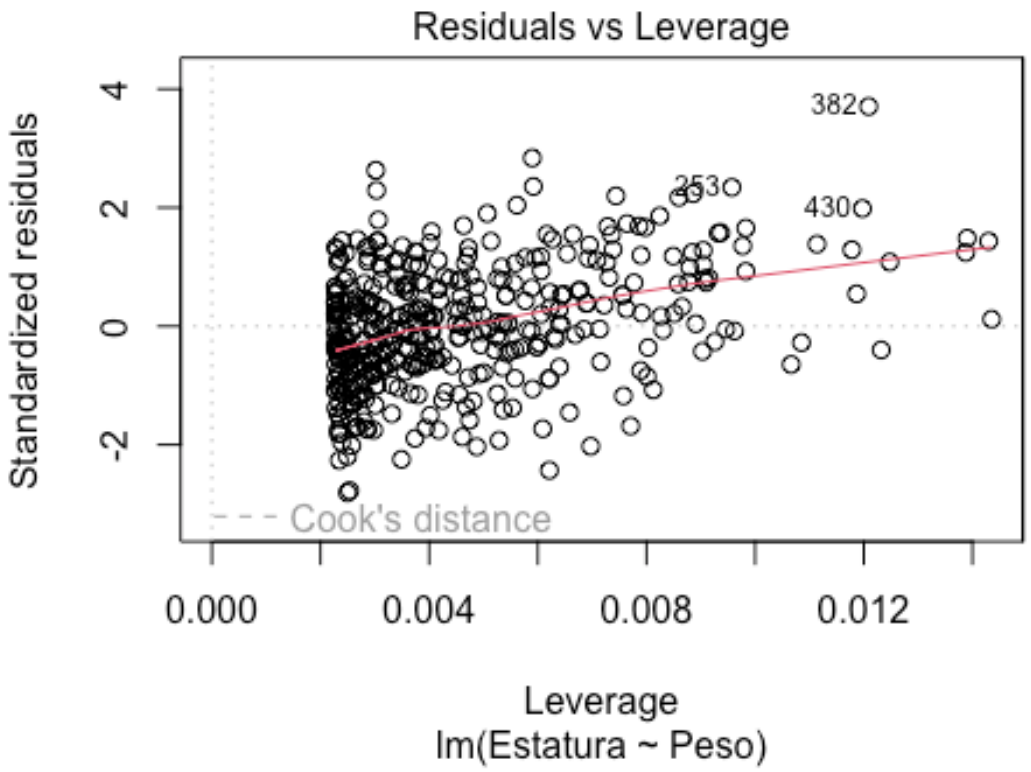



```r
plot(Modelo2)
```

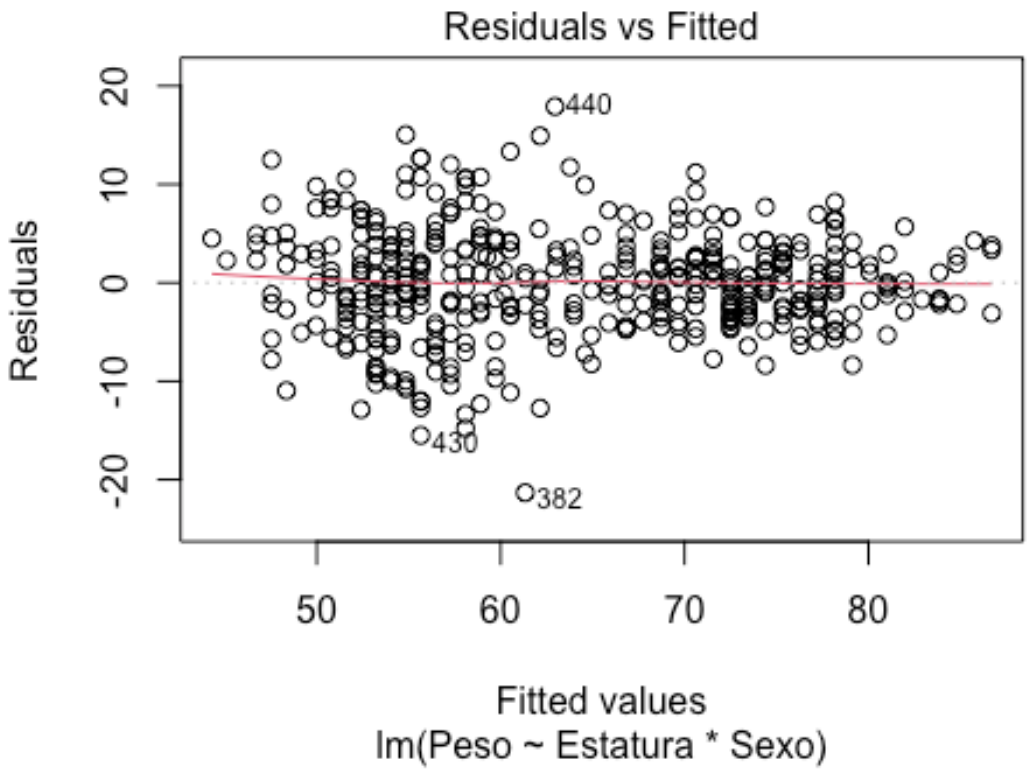

Residuals vs Fitted
382
422
173
Residuals
0.10
0.00
-0.10
1.50
1.55
1.60
1.65
1.70
1.75
Fitted values
lm(Estatura ~ Peso)

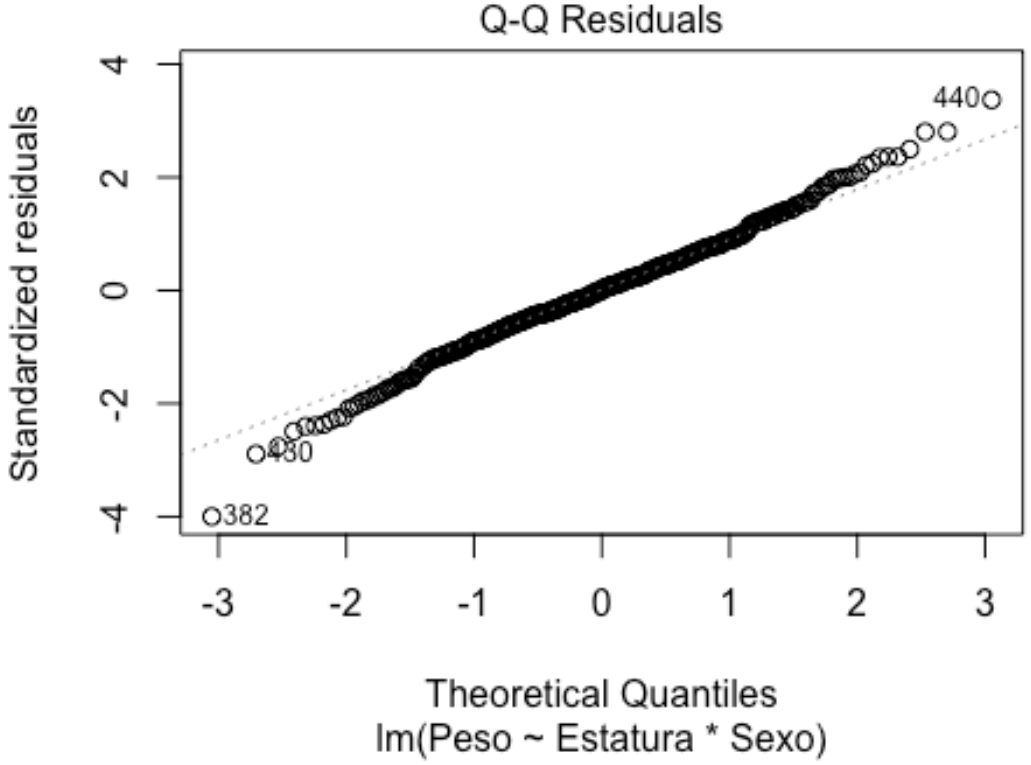

Q-Q Residuals
Standardized residuals
-3
-1
0
1
2
3
4
382
422
173
-3
-2
-1
0
1
2
3
Theoretical Quantiles
lm(Estatura ~ Peso)

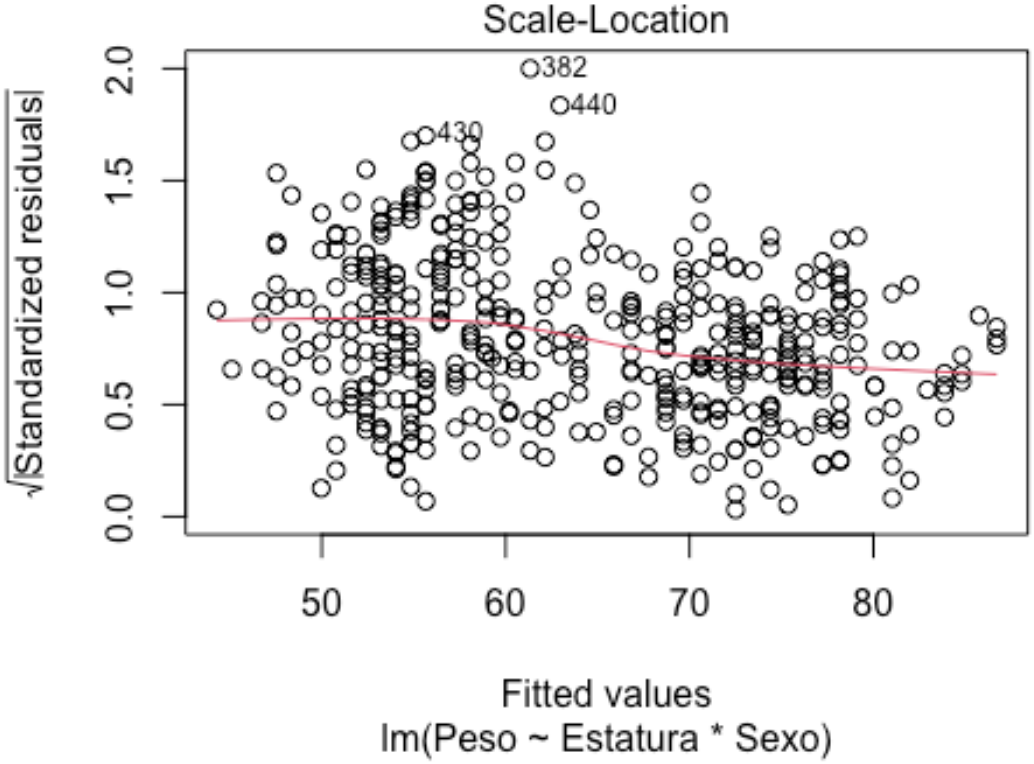

Scale-Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
2.0
382
422
173
1.50
1.55
1.60
1.65
1.70
1.75
Fitted values
lm(Estatura ~ Peso)

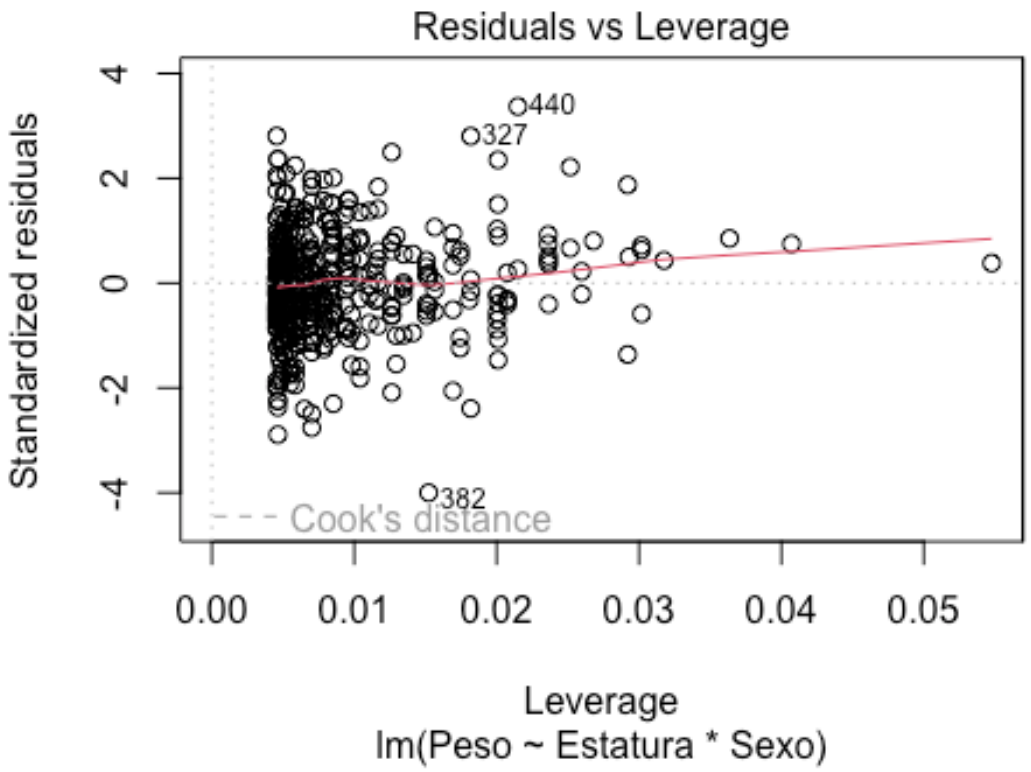



```
plot(Modelo3)
```


Residuals vs Fitted
Residuals
20
10
0
-10
-20
440
430
382
50
60
70
80
Fitted values
lm(Peso ~ Estatura * Sexo)


Q-Q Residuals
Standardized residuals
4
2
0
-2
-4
440
430
382
-3
-2
-1
0
1
2
3
Theoretical Quantiles
lm(Peso ~ Estatura * Sexo)


Scale-Location
382
440
430
√|Standardized residuals|
0.0
0.5
1.0
1.5
2.0
50
60
70
80
Fitted values
lm(Peso ~ Estatura * Sexo)



¿Cuáles son las diferencias y similitudes de estos gráficos con respecto a los que ya habías analizado?

En cuanto a las escalas, estos gráficos amplifican las escalas para facilitar una mejor visualización de los errores.

Estos gráficos, ¿cambian en algo las conclusiones que ya habías obtenido?

No alteran mis conclusiones previas; sin embargo, puedo observar que, aunque se rechacen algunas hipótesis, las diferencias en los gráficos no son drásticamente significativas.

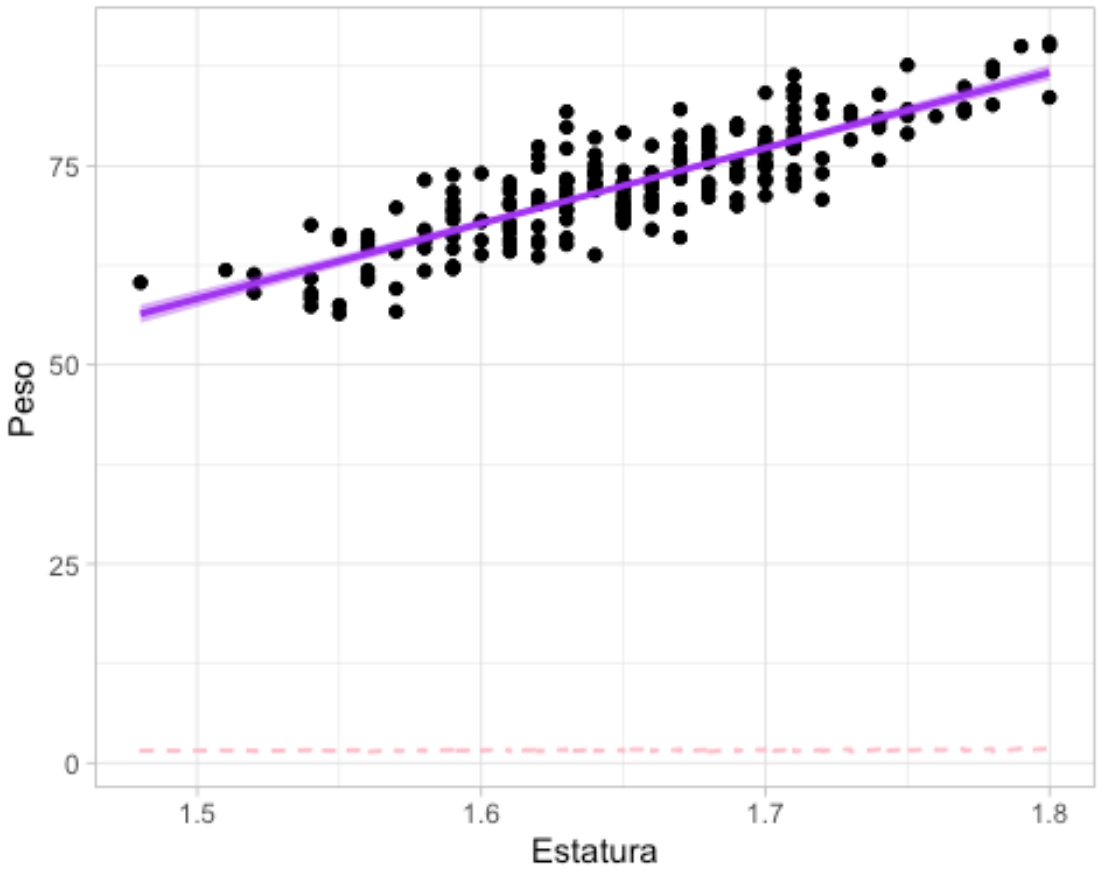
Emite una conclusión final sobre el mejor modelo de regresión lineal que conjunte lo que hiciste en las tres partes de esta actividad.

Aunque el modelo 2 tiene un buen desempeño, optaremos por el modelo 1 (Hombres y Mujeres), ya que el modelo para los hombres es el más consistente. Además, los modelos 1 de hombres y mujeres presentan homocedasticidad.

Intervalos de confianza

Con los datos de las estaturas y pesos de los hombres y las mujeres construye la gráfica de los intervalos de confianza y predicción para la estimación y predicción de Y para el mejor modelo seleccionado.

```
# Confidence and Prediction Intervals
Ip <- predict(object = Modelo1H, newdata = M, interval = "prediction", level
= 0.97)

# Combine the predicted intervals with the original data
M <- cbind(MH, Ip)

## Warning in data.frame(..., check.names = FALSE): row names were found from
a
## short variable and have been discarded

# Load ggplot2 library for plotting
library(ggplot2)

# Plotting the data, regression line, and confidence intervals
ggplot(M, aes(x = Estatura, y = Peso)) +
  geom_point() +
  geom_line(aes(y = lwr), color = "pink", linetype = "dashed") +
  geom_line(aes(y = upr), color = "pink", linetype = "dashed") +
  geom_smooth(method = "lm", formula = y ~ x, se = TRUE, level = 0.97, col =
"purple", fill = "purple") +
  theme_light()
```



Interpreta y comenta los resultados obtenidos

El modelo se ajusta ligeramente mejor porque la parte correspondiente a los hombres es más consistente; sin embargo, el inconveniente radica en los datos de las mujeres. Estos problemas podrían resolverse aplicando alguna transformación a los datos al desarrollar los modelos.