

week13

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Model Diagnostics

Model Assumptions

Checking Assumptions

use data simulated from three models

1 Fitted versus Residuals Plot

```
sim_1 = function(sample_size = 500) {  
  x = runif(n = sample_size) * 5  
  y = 3 + 5 * x + rnorm(n = sample_size, mean = 0, sd = 1)  
  data.frame(x, y)  
}  
  
sim_2 = function(sample_size = 500) {  
  x = runif(n = sample_size) * 5  
  y = 3 + 5 * x + rnorm(n = sample_size, mean = 0, sd = x)  
  data.frame(x, y)  
}  
  
sim_3 = function(sample_size = 500) {  
  x = runif(n = sample_size) * 5  
  y = 3 + 5 * x ^ 2 + rnorm(n = sample_size, mean = 0, sd = 5)  
  data.frame(x, y)  
}
```

Fitted versus Residuals Plot

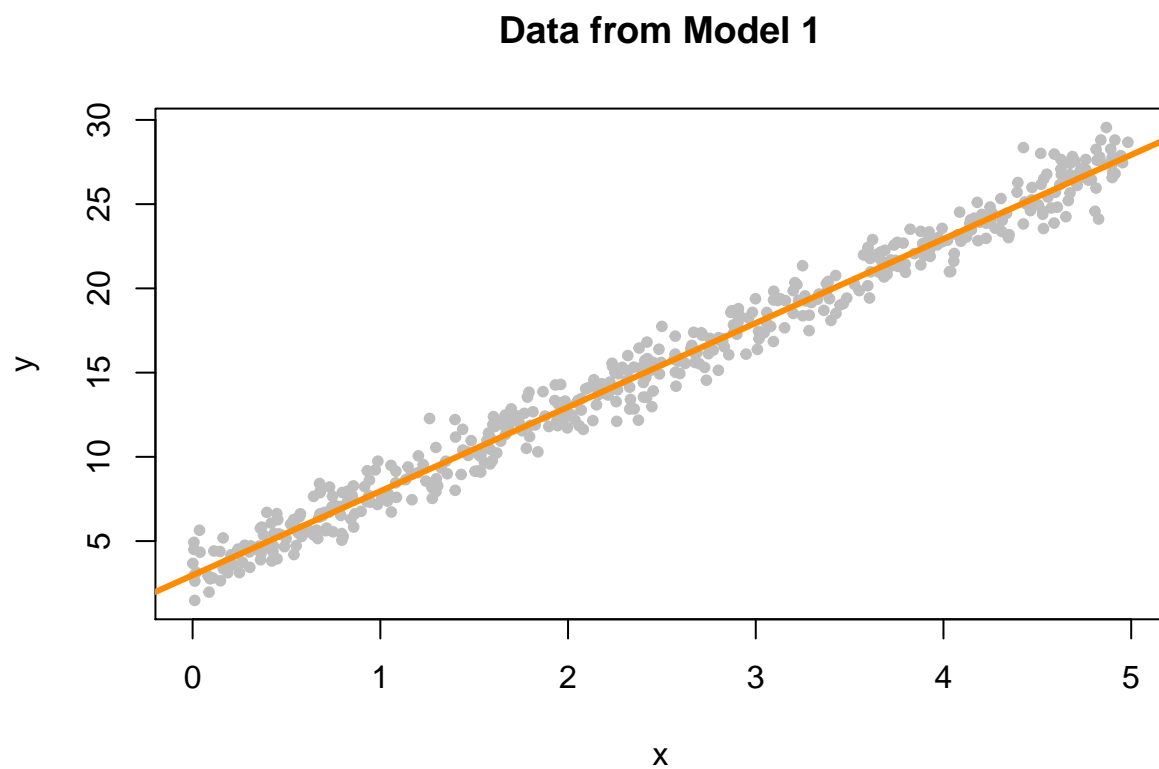
useful for checking both the linearity and constant variance assumptions

```
set.seed(42)  
sim_data_1 = sim_1()  
head(sim_data_1)
```

```
##           x           y  
## 1 4.574030 24.773995  
## 2 4.685377 26.475936  
## 3 1.430698  8.954993  
## 4 4.152238 23.951210  
## 5 3.208728 20.341344  
## 6 2.595480 14.943525
```

fit the model and add the fitted line to a scatterplot

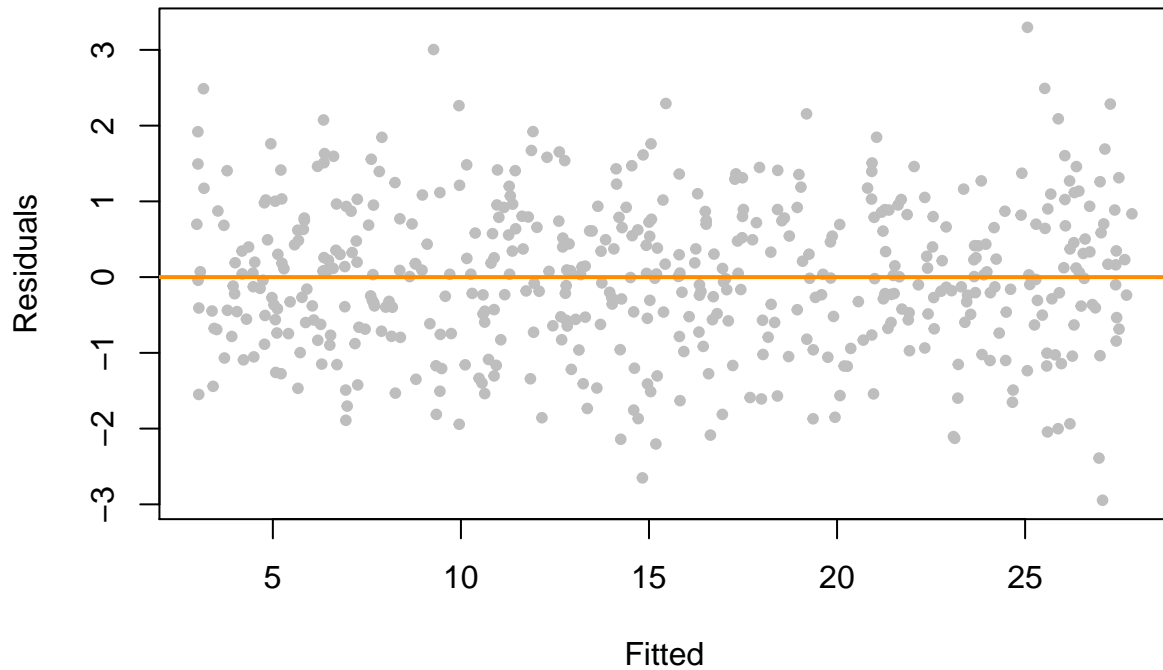
```
plot(y ~ x,  
     data = sim_data_1,  
     col = "grey",  
     pch = 20,  
     main = "Data from Model 1")  
fit_1 = lm(y ~ x,  
           data = sim_data_1)  
abline(fit_1,  
       col = "darkorange",  
       lwd = 3)
```



fitted versus residuals plot

```
plot(fitted(fit_1),  
     resid(fit_1),  
     col = "grey",  
     pch = 20,  
     xlab = "Fitted",  
     ylab = "Residuals",  
     main = "Data from Model 1")  
abline(h = 0,  
       col = "darkorange",  
       lwd = 2)
```

Data from Model 1

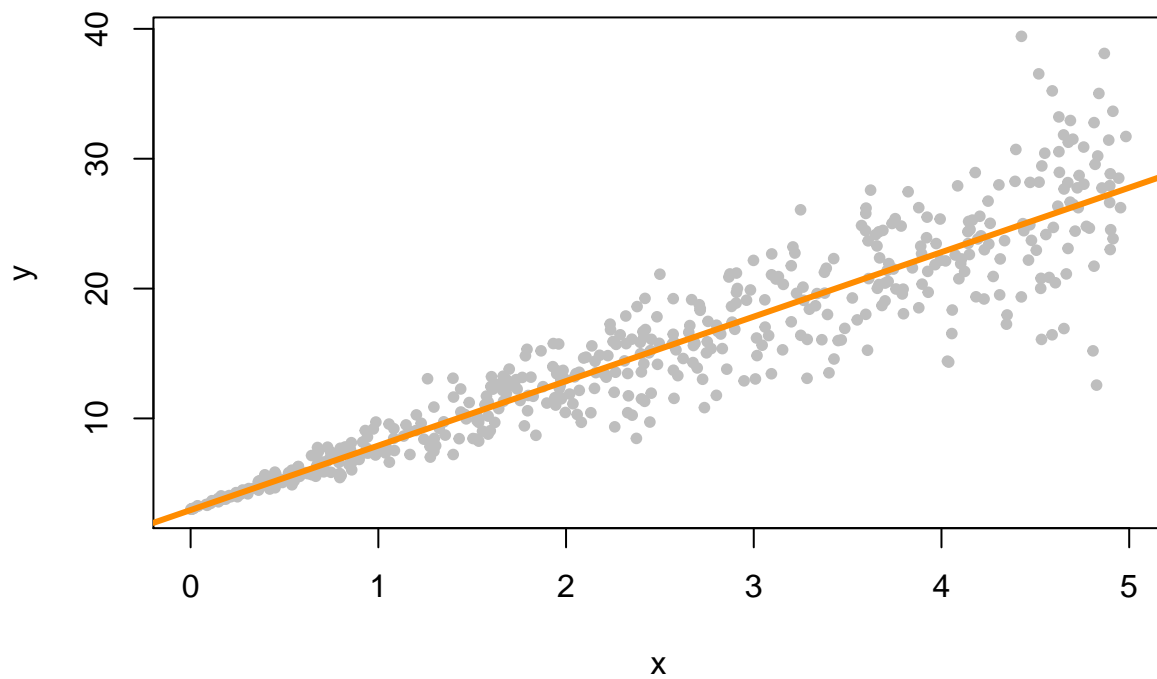


Model 2 non-constant variance

(the variance is larger for larger values of the predictor variable x)

```
set.seed(42)
sim_data_2 = sim_2()
fit_2 = lm(y ~ x, data = sim_data_2)
plot(y ~ x, data = sim_data_2, col = "grey", pch = 20,
     main = "Data from Model 2")
abline(fit_2, col = "darkorange", lwd = 3)
```

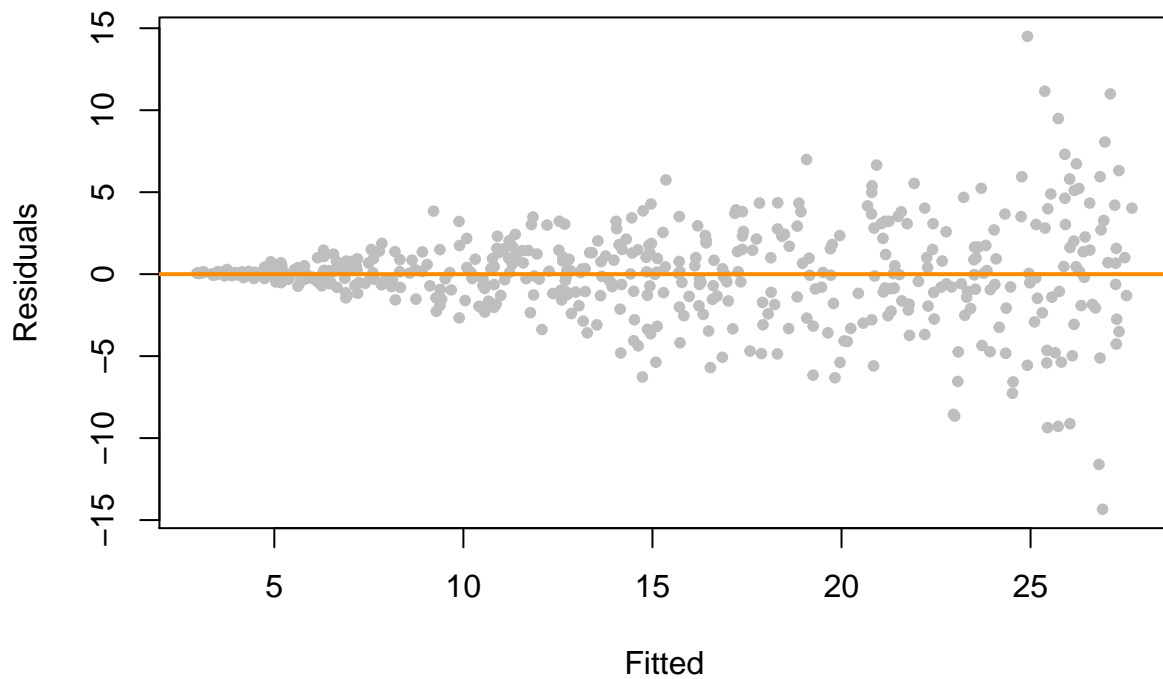
Data from Model 2



fitted versus residuals plot

```
plot(fitted(fit_2),  
     resid(fit_2),  
     col = "grey",  
     pch = 20,  
     xlab = "Fitted",  
     ylab = "Residuals",  
     main = "Data from Model 2")  
abline(h = 0,  
       col = "darkorange",  
       lwd = 2)
```

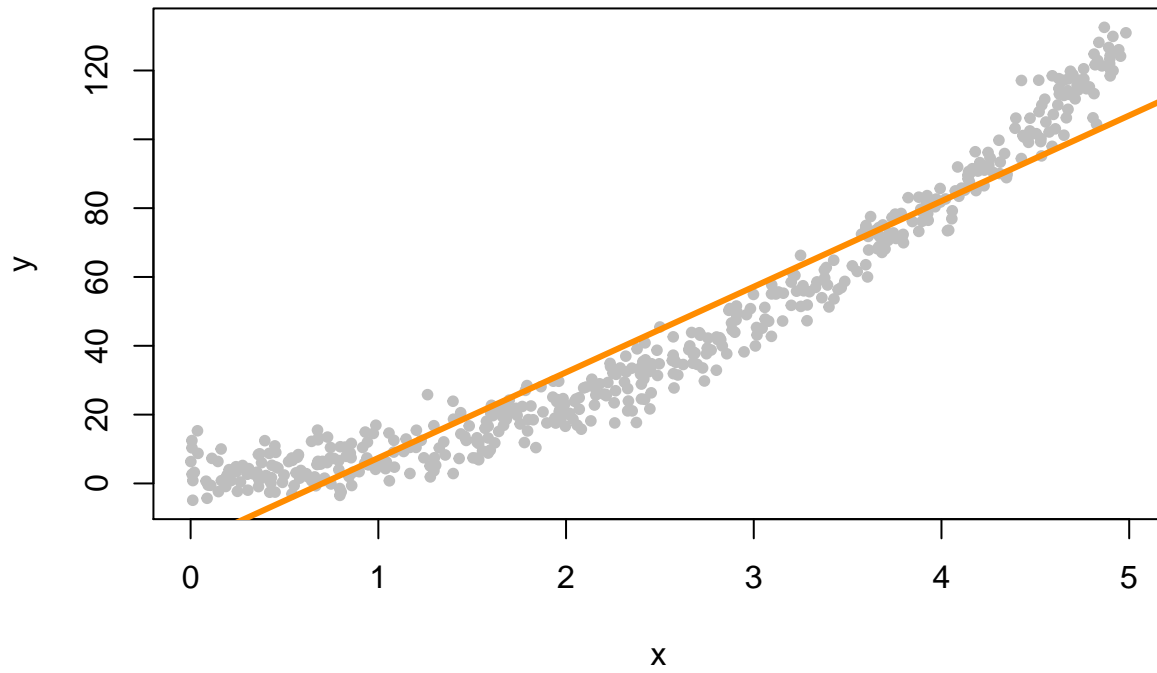
Data from Model 2



Model 3 Y is not a linear combination of the predictors. $Y \sim X^2$

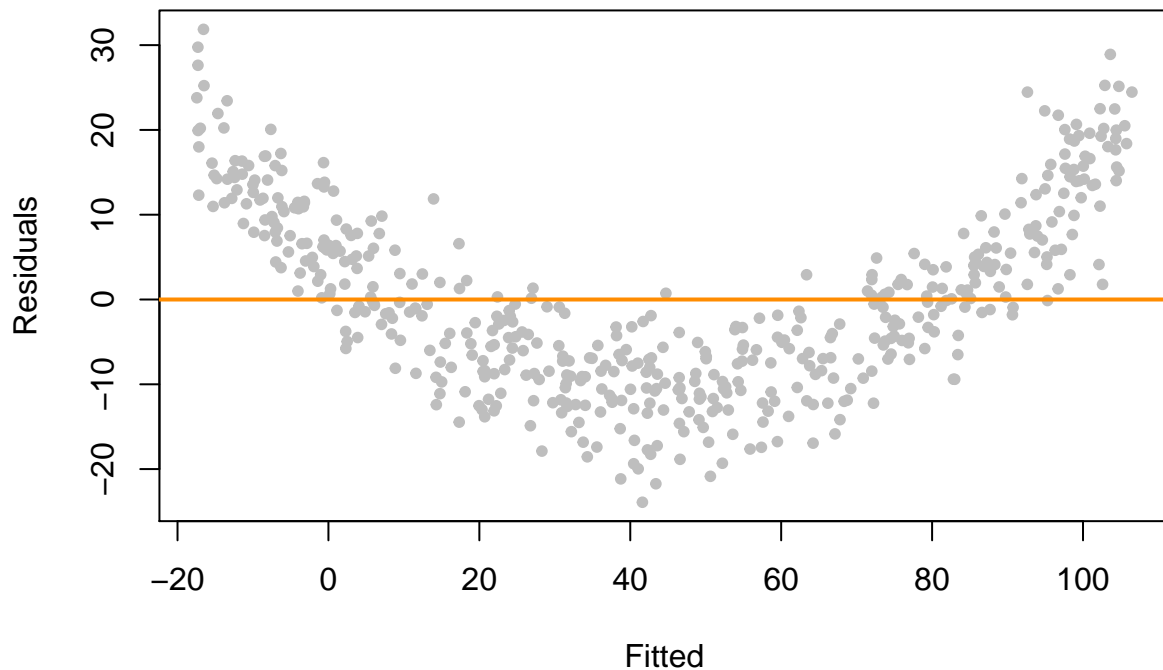
```
set.seed(42)
sim_data_3 = sim_3()
fit_3 = lm(y ~ x,
           data = sim_data_3)
plot(y ~ x,
     data = sim_data_3,
     col = "grey",
     pch = 20,
     main = "Data from Model 3")
abline(fit_3,
       col = "darkorange",
       lwd = 3)
```

Data from Model 3



```
plot(fitted(fit_3),  
     resid(fit_3),  
     col = "grey",  
     pch = 20,  
     xlab = "Fitted",  
     ylab = "Residuals",  
     main = "Data from Model 3")  
abline(h = 0,  
       col = "darkorange",  
       lwd = 2)
```

Data from Model 3



2 Breusch-Pagan Test

```
#install.packages("lmtest")  
library(lmtest)
```

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

```
##
```

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

```
## The following objects are masked from 'package:base':
```

```
##
```

```
## as.Date, as.Date.numeric
```

```
bptest(fit_1)
```

```
##
```

```
## studentized Breusch-Pagan test
```

```
##
```

```
## data: fit_1
```

```
## BP = 1.0234, df = 1, p-value = 0.3117
```

```
bptest(fit_2)
```

```
##  
## studentized Breusch-Pagan test  
##  
## data: fit_2  
## BP = 76.693, df = 1, p-value < 2.2e-16
```

```
bptest(fit_3)
```

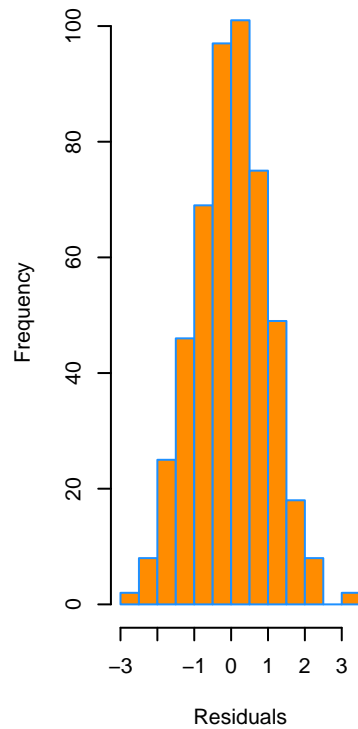
```
##  
## studentized Breusch-Pagan test  
##  
## data: fit_3  
## BP = 0.33466, df = 1, p-value = 0.5629
```

3 Histograms

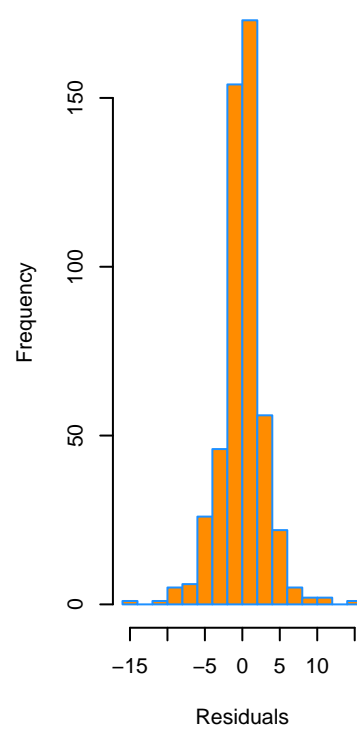
make a histogram of the residuals

```
par(mfrow = c(1, 3))  
  
hist(resid(fit_1),  
     xlab = "Residuals",  
     main = "Histogram of Residuals, fit_1",  
     col = "darkorange",  
     border = "dodgerblue",  
     breaks = 20)  
  
hist(resid(fit_2),  
     xlab = "Residuals",  
     main = "Histogram of Residuals, fit_2",  
     col = "darkorange",  
     border = "dodgerblue",  
     breaks = 20)  
  
hist(resid(fit_3),  
     xlab = "Residuals",  
     main = "Histogram of Residuals, fit_3",  
     col = "darkorange",  
     border = "dodgerblue",  
     breaks = 20)
```

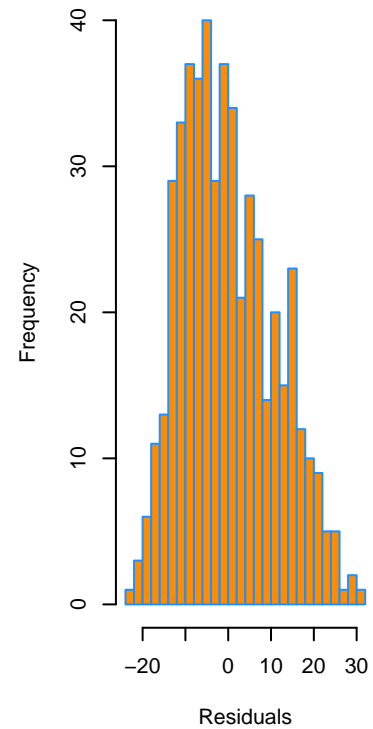

Histogram of Residuals, fit_1



Histogram of Residuals, fit_2



Histogram of Residuals, fit_3



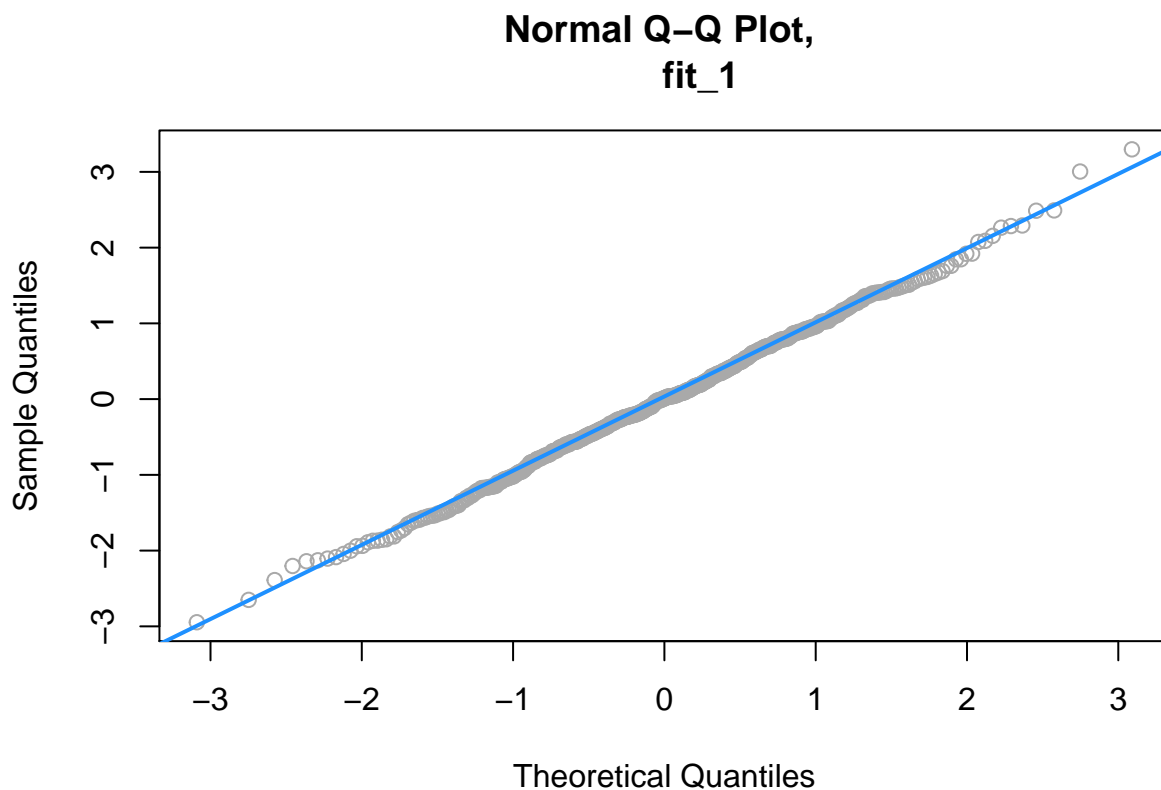
4 Q-Q Plots

quantile-quantile plot

qqnorm() function plots the points qqline() function adds the necessary line

```
qqnorm(resid(fit_1),
       main = "Normal Q-Q Plot,
              fit_1",
       col = "darkgrey")

qqline(resid(fit_1),
       col = "dodgerblue",
       lwd = 2)
```



Q-Q plots

```
qq_plot = function(e) {

  n = length(e)
  normal_quantiles = qnorm(((1:n - 0.5) / n))
  # normal_quantiles = qnorm(((1:n) / (n + 1)))

  # plot theoretical versus observed quantiles
  plot(normal_quantiles, sort(e),
        xlab = c("Theoretical Quantiles"),
        ylab = c("Sample Quantiles"),
        col = "darkgrey")
  title("Normal Q-Q Plot")

  # calculate line through the first and third quartiles
  slope      = (quantile(e, 0.75) - quantile(e, 0.25)) / (qnorm(0.75) - qnorm(0.25))
  intercept = quantile(e, 0.25) - slope * qnorm(0.25)

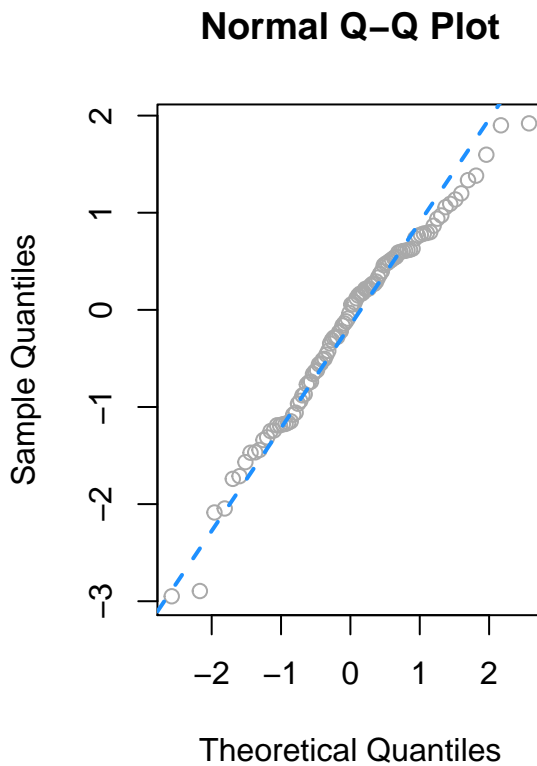
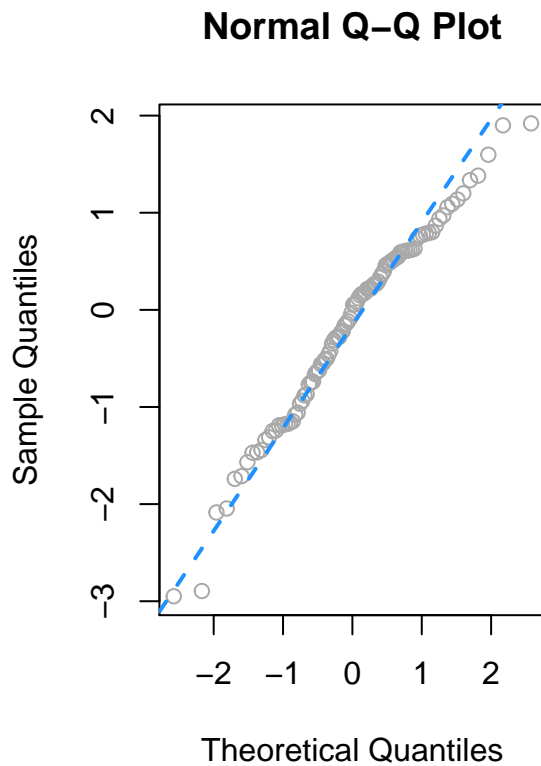
  # add to existing plot
  abline(intercept, slope, lty = 2, lwd = 2, col = "dodgerblue")
}
```

qqnorm() and qqline()

```

set.seed(420)
x = rnorm(100, mean = 0 , sd = 1)
par(mfrow = c(1, 2))
qqnorm(x, col = "darkgrey")
qqline(x, lty = 2, lwd = 2, col = "dodgerblue")
qq_plot(x)

```



equivalent

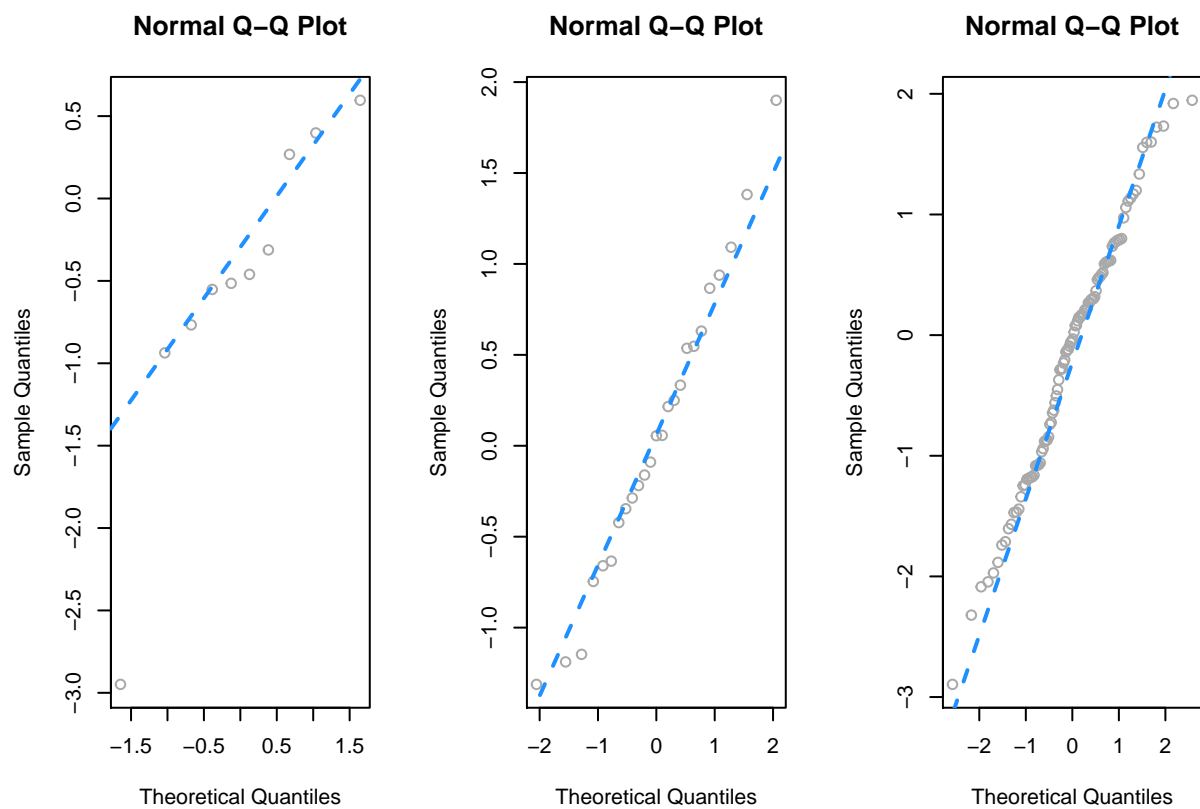
perform a number of simulations “close to the line”

different sample sizes

```

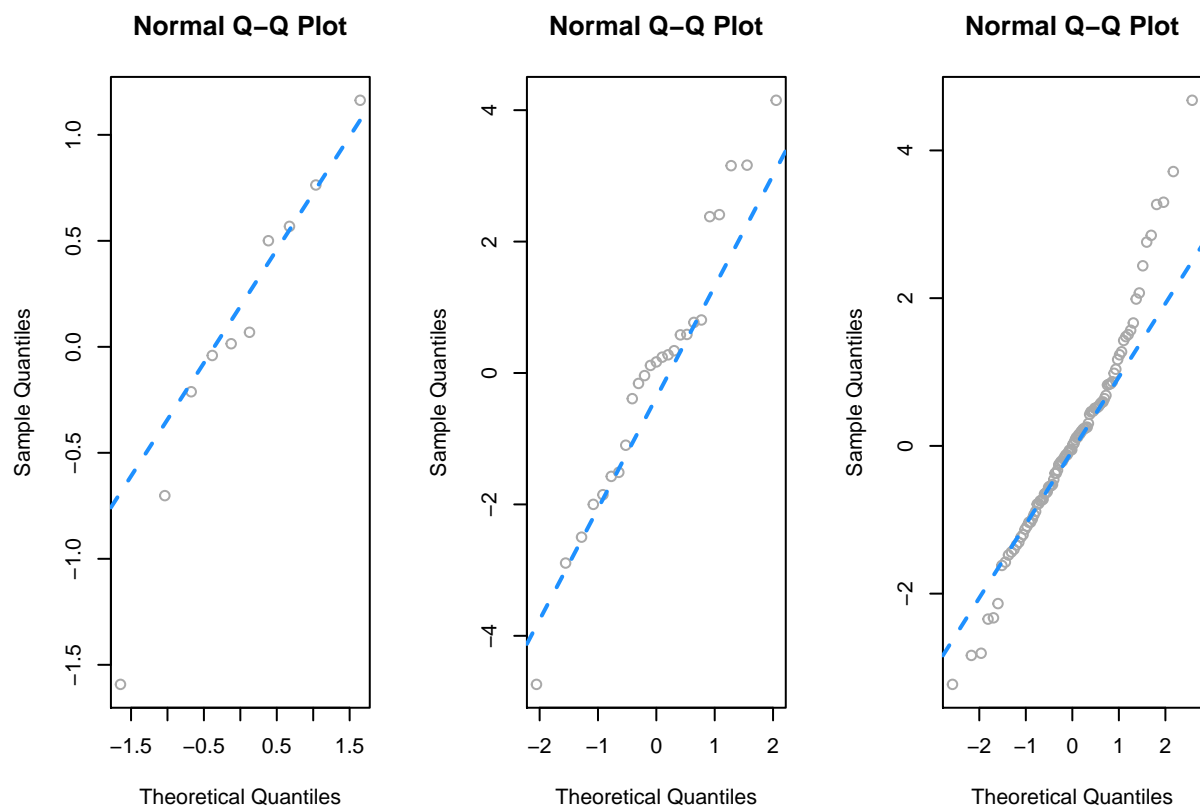
par(mfrow = c(1, 3))
set.seed(420)
qq_plot(rnorm(10))
qq_plot(rnorm(25))
qq_plot(rnorm(100))

```



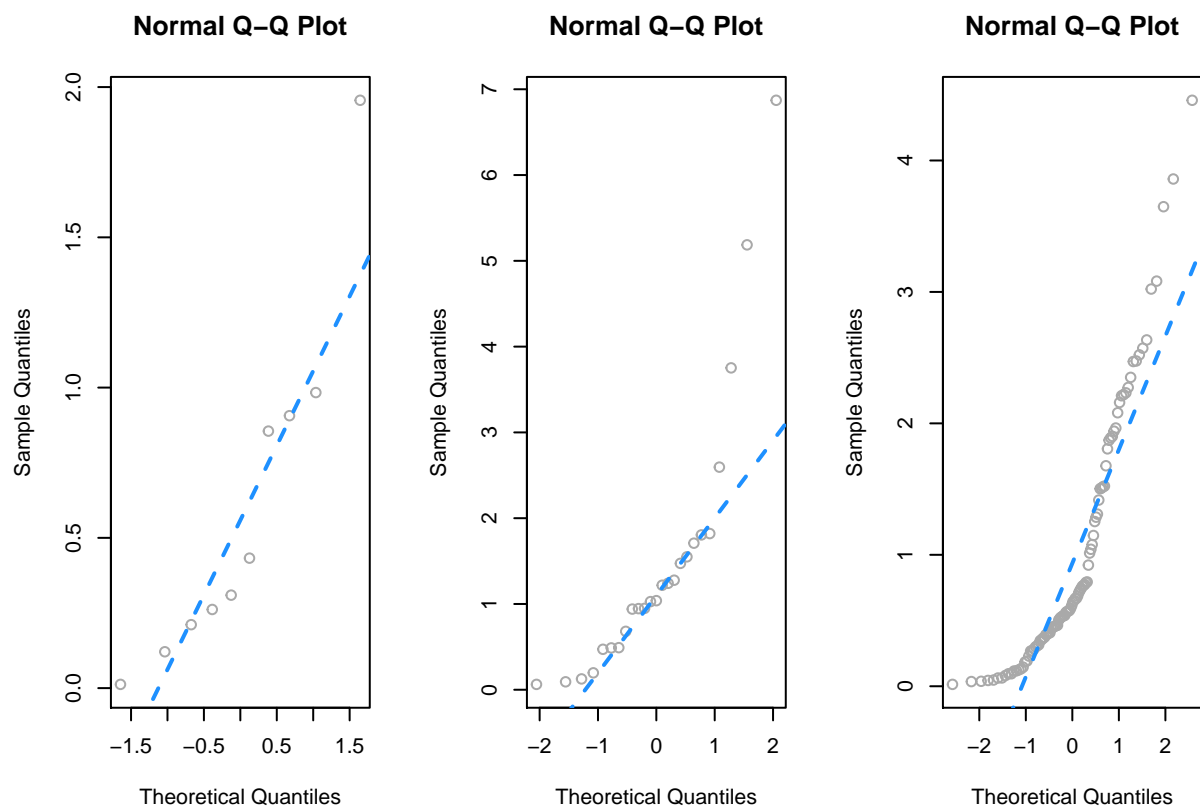
simulate data from a t distribution with a small degrees of freedom, for different sample sizes.

```
par(mfrow = c(1, 3))
set.seed(420)
qq_plot(rt(10, df = 4))
qq_plot(rt(25, df = 4))
qq_plot(rt(100, df = 4))
```



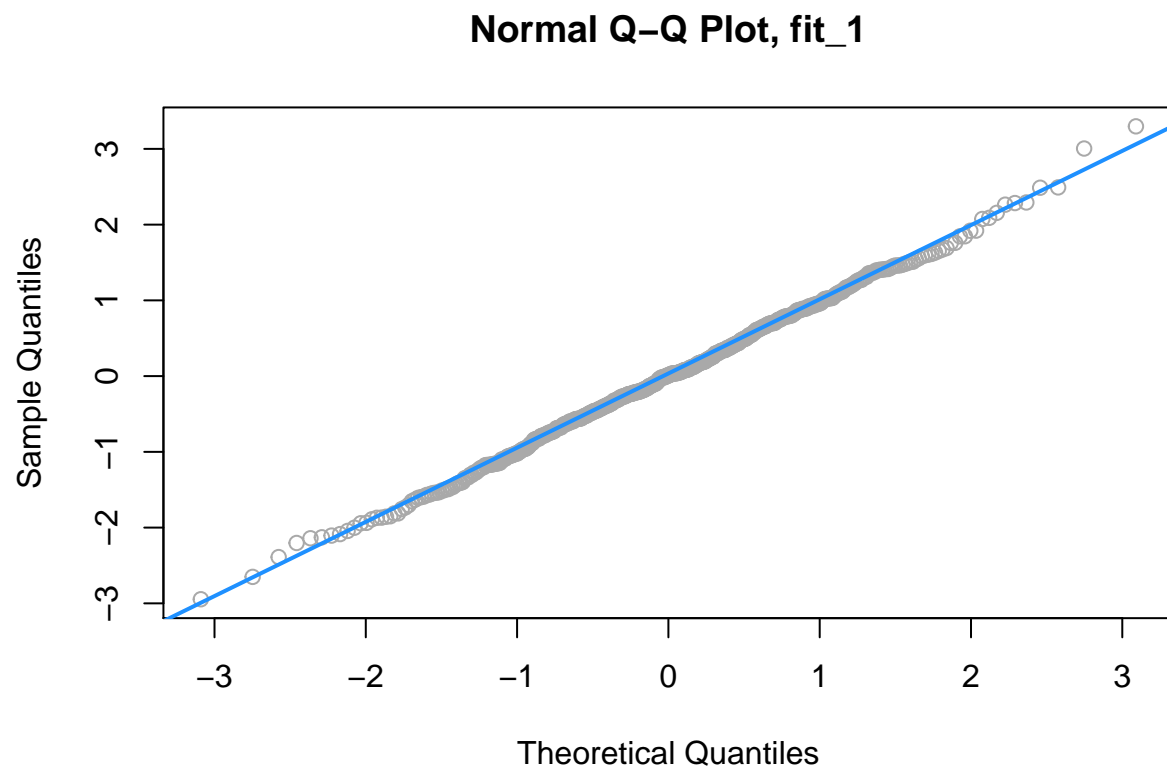
simulate data from an exponential distribution

```
par(mfrow = c(1, 3))
set.seed(420)
qq_plot(rexp(10))
qq_plot(rexp(25))
qq_plot(rexp(100))
```



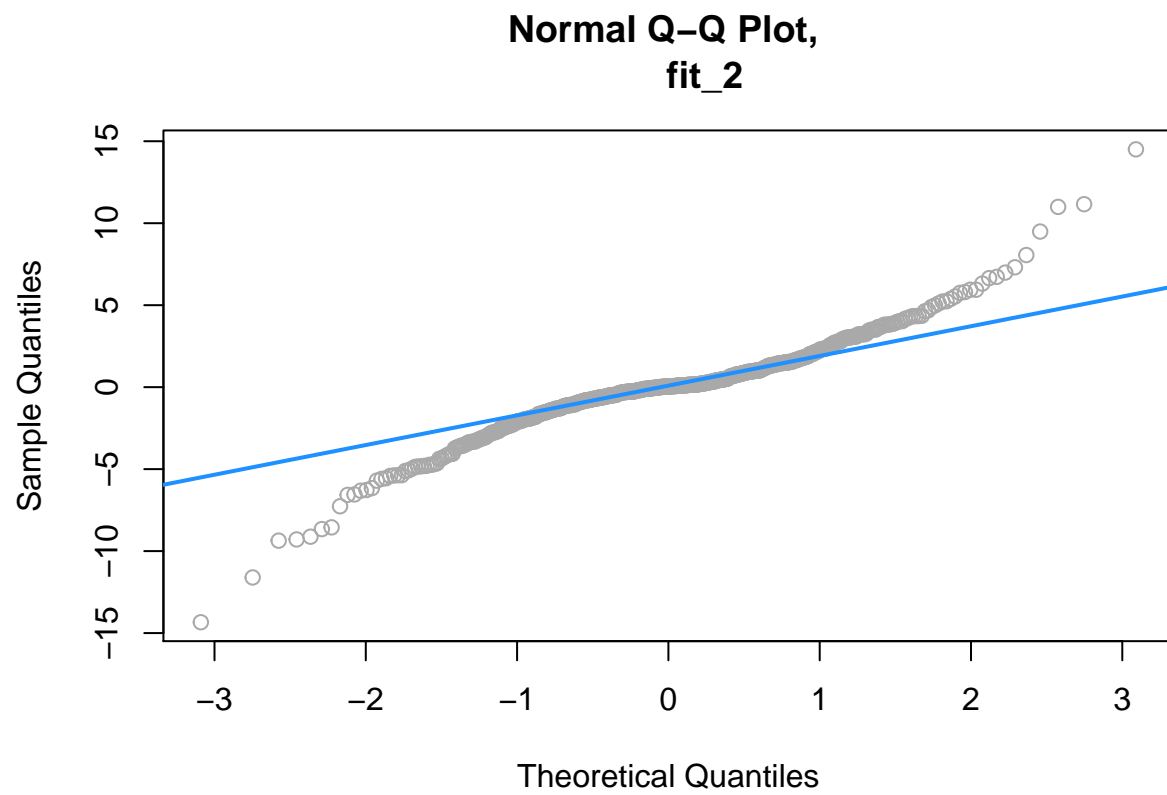
create a Q-Q plot for each to assess normality of errors

```
qqnorm(resid(fit_1), main = "Normal Q-Q Plot, fit_1", col = "darkgrey")
qqline(resid(fit_1), col = "dodgerblue", lwd = 2)
```



fit_1, perfect Q-Q plot, errors follow a normal distribution

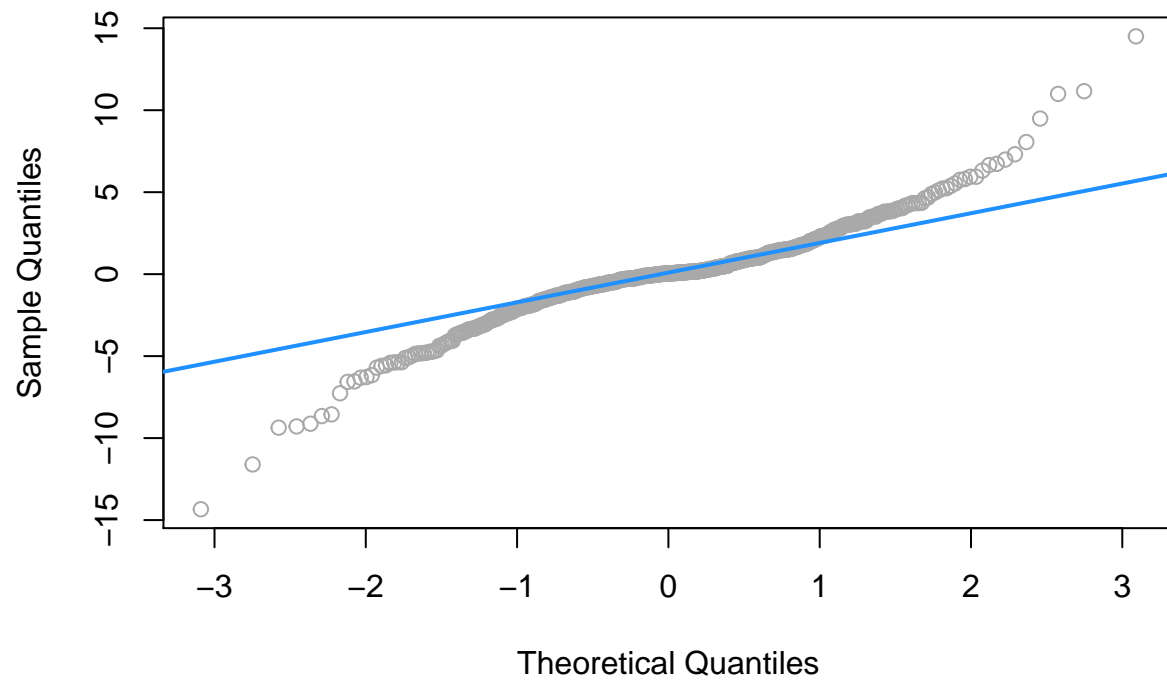
```
qqnorm(resid(fit_2),  
        main = "Normal Q-Q Plot,  
        fit_2",  
        col = "darkgrey")  
qqline(resid(fit_2),  
        col = "dodgerblue",  
        lwd = 2)
```



fit_2, suspect Q-Q plot

```
qqnorm(resid(fit_2), main = "Normal Q-Q Plot, fit_2", col = "darkgrey")  
qqline(resid(fit_2), col = "dodgerblue", lwd = 2)
```

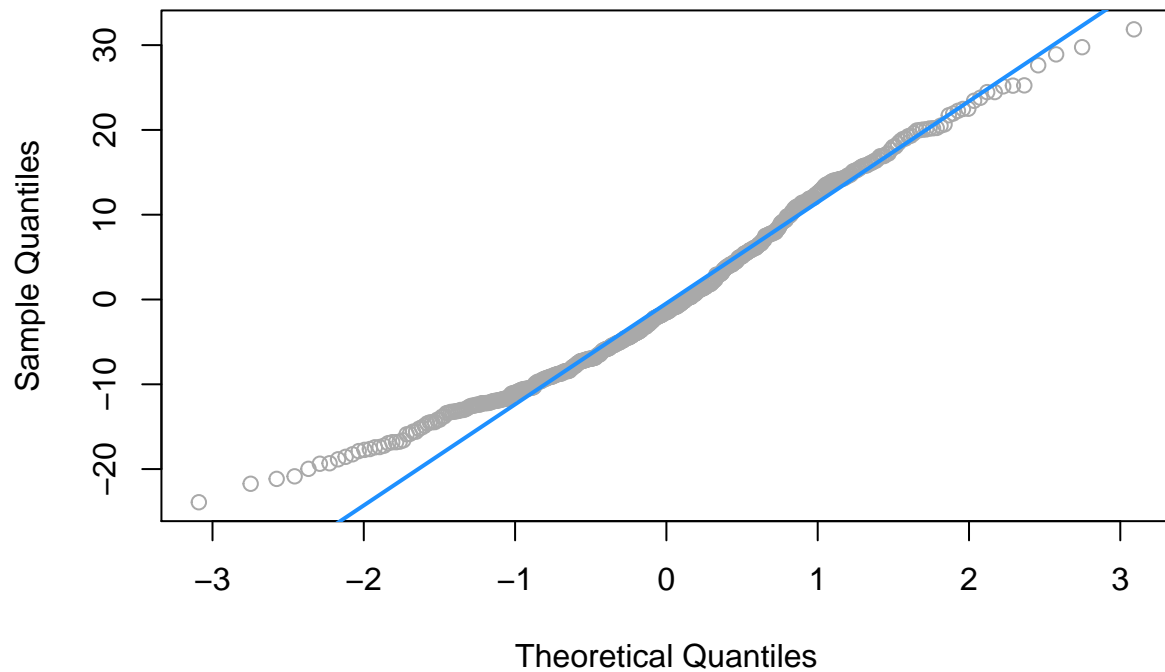

Normal Q-Q Plot, fit_2



fit_3, suspect Q-Q plot

```
qqnorm(resid(fit_3), main = "Normal Q-Q Plot, fit_3", col = "darkgrey")  
qqline(resid(fit_3), col = "dodgerblue", lwd = 2)
```

Normal Q-Q Plot, fit_3



5 Shapiro-Wilk Test

formal testing `shapiro.test()`

```
set.seed(42)
shapiro.test(rnorm(25))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  rnorm(25)
## W = 0.9499, p-value = 0.2495
```

```
## W = 0.71164, p-value = 1.05e-05
```

```
shapiro.test(rexp(25))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  rexp(25)
## W = 0.71164, p-value = 1.05e-05
```

```
##  $W = 0.99858$ ,  $p\text{-value} = 0.9622$ 
```

```
shapiro.test(resid(fit_3))
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: resid(fit_3)
```

```
##  $W = 0.97643$ ,  $p\text{-value} = 3.231e-07$ 
```

```
##  $W = 0.97643$ ,  $p\text{-value} = 3.231e-07$ 
```

Outliers

resid() for residual rstandard() for Standardized residual