Análisis de Normalidad

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El análisis de normalidad define si una distribución de frecuencias relativas de una variable cuantitativa en una población se aproxima a una Distribución Normal con la misma media y desviación estándar que la variable.

Métodos Gráficos

Para estas demostraciones se creará una distribución aleatoria:

```
set.seed(12345)
x <- rnorm(n = 200, mean = 15, sd = 5)
x
```

```
##   [1] 17.927644 18.547330 14.453483 12.732514 18.029437  5.910220 18.150493
##   [8] 13.619079 13.579201 10.403390 14.418761 24.086560 16.853139 17.601082
##  [15] 11.247340 19.084499 10.568212 13.342112 20.603563 16.493618 18.898110
##  [22] 22.278925 11.778358  7.234313  7.011452 24.025488 12.591763 18.101899
##  [29] 18.060617 14.188445 19.059366 25.984168 25.245952 23.162228 16.271356
##  [36] 17.455941 13.379567  6.689749 23.838669 15.129005 20.642554  3.098210
##  [43]  9.698672 19.685703 19.272259 22.303647  7.934506 17.837016 17.915938
##  [50]  8.466006 12.298070 24.738463 15.267951 16.758314 11.645117 16.389768
##  [57] 18.455856 19.118977 25.725325  3.265280 15.747960  8.287343 17.766515
##  [64] 22.949814 12.065602  5.838113 19.440697 22.967442 17.584273  8.521642
##  [71] 15.273078 11.076753  9.753236 26.652560 22.013527 19.713004 19.131291
##  [78] 10.942298 17.381241 20.106292 18.226915 20.215718 13.478154 27.385555
##  [85] 19.856103 24.335496 18.360212 13.460233 17.682619 19.124350 10.180493
##  [92] 10.724587 24.434735 13.040903 10.096835 18.436661 12.474782 25.788599
##  [99] 12.001012 11.527267 16.119627  9.218883 17.112093  8.376224 15.705422
## [106] 12.319760 13.441970 22.780548 12.759834 16.605618  8.849139  8.379707
## [113] 21.306211 21.596159 14.596231 12.474551 14.739232 18.144303 25.900012
## [120] 14.654913 22.724318 21.607260 16.610758 22.654776 12.893802  9.205895
## [127]  5.773159 20.786626  4.382251  9.019842 23.210960 19.418274 17.624379
## [134]  9.076705 28.278941  9.760431  9.944387 18.344608 15.645886 12.887116
## [141]  9.298679  8.531424 12.026506  7.495930 15.079278 17.700848  7.263540
## [148] 19.248265 19.480066 15.693455  6.903358 17.741990 15.976411 10.967510
## [155] 14.456879 13.745267 23.496733 13.278506 15.338860 11.747151 12.561807
## [162] 16.515756 13.790130 12.591332 10.040986 13.596754 18.165087  8.800908
## [169] 23.821570 14.881601 15.999602 21.735964 15.180367 19.122906  6.486641
## [176] 17.404751 27.417750 17.006825 16.075886  5.921438 10.441303 14.754777
## [183] 12.973063 20.651909 19.077324 15.382088 22.268737 16.870605 14.145480
## [190] 12.488936 17.717611 12.474070 18.933979 16.504747 21.551120 18.992169
## [197] 19.254302 12.782160 12.766126 15.066525
```

Histograma de frencuencias

```
h <- hist(x, main = "Histograma de datos con distribución normal", xlab = "Datos
↪  aleatorios", ylab = "Frecuencia", probability = TRUE)
x2 <- seq(min(x), max(x), length = 50)
normal <- dnorm(x2, mean = mean(x), sd = sd(x))
lines(x2, normal, col = 2, lwd = 2)
lines(density(x), col = 4, lwd = 2)
```

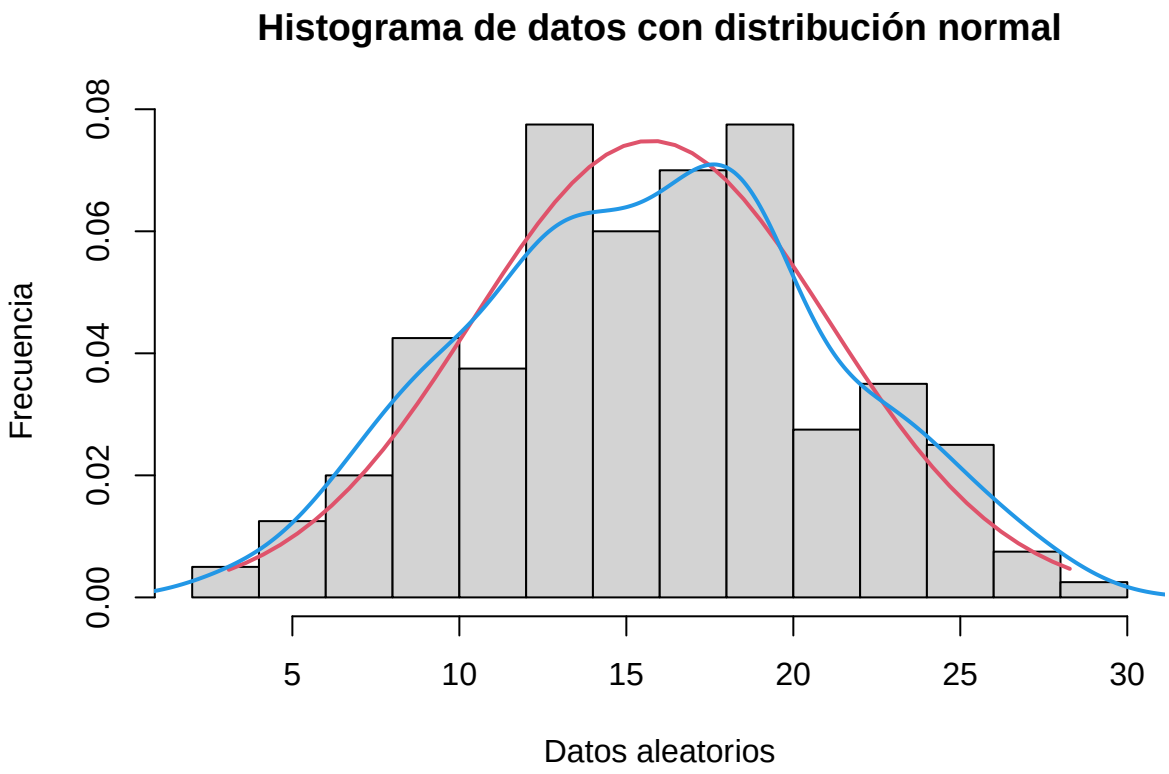


Gráfico de cuantiles teóricos (Gráfico Q-Q)

```
qqnorm(x, main = "Gráfico Q-Q Normal", xlab = "Cuantiles Teóricos", ylab = "Cuantiles de
↪  muestra", pch = 20, col = "blue")
qqline(x)
```

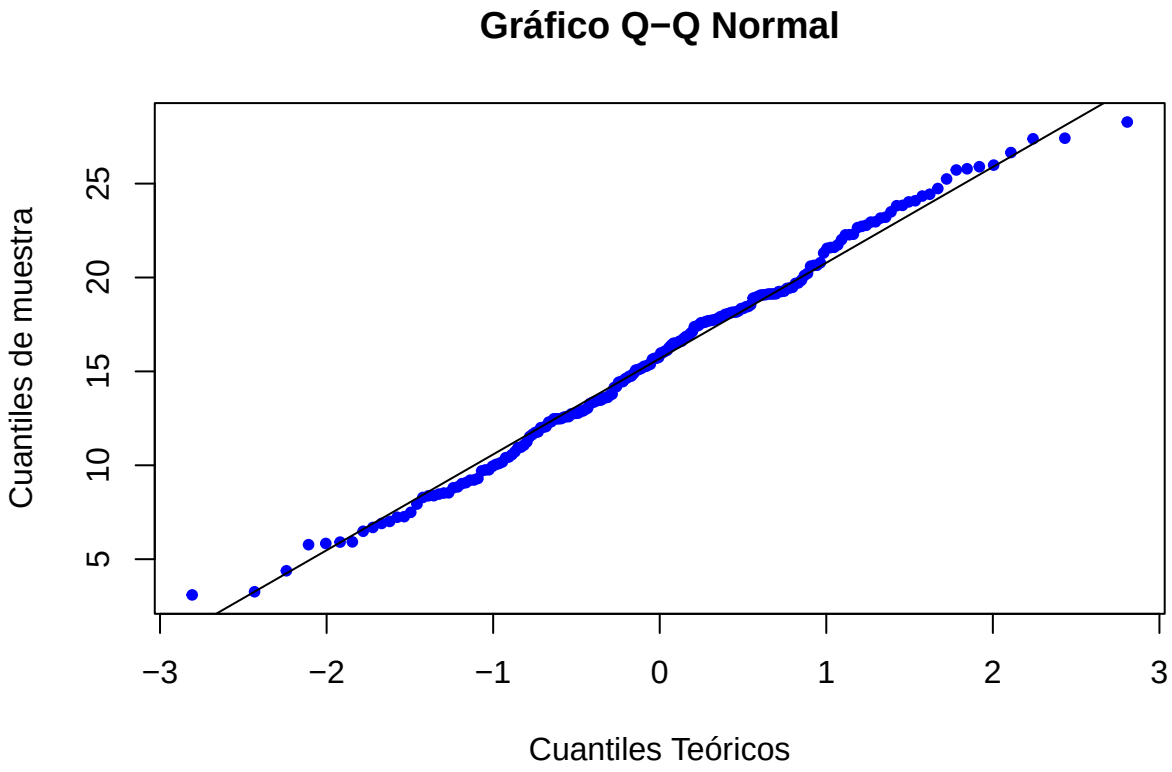
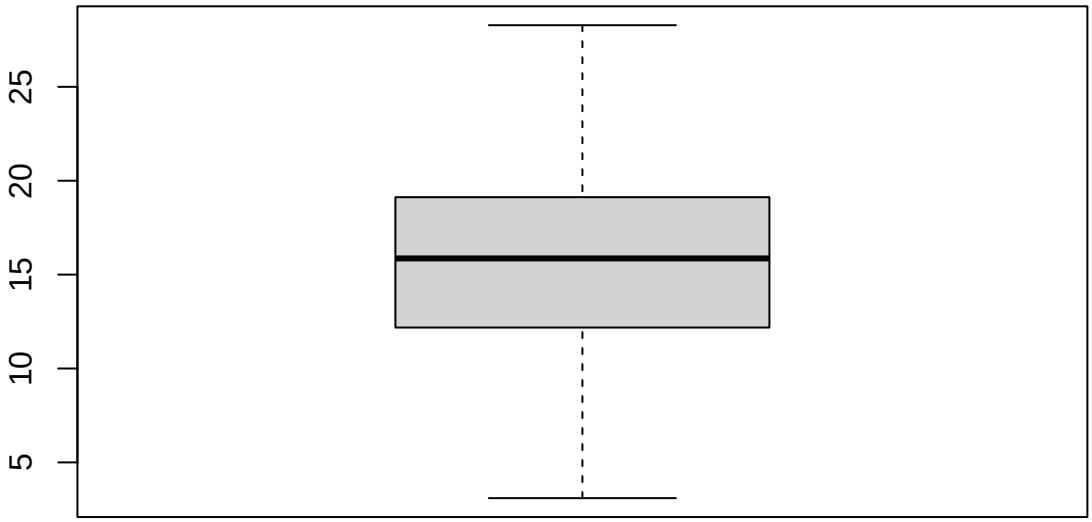


Diagrama de Caja

```
boxplot(x)
```



Métodos Analíticos

Asimetría

Existen tres tipos de asimetría

Para el analisis del mismo vamos a definir los siguientes rangos:

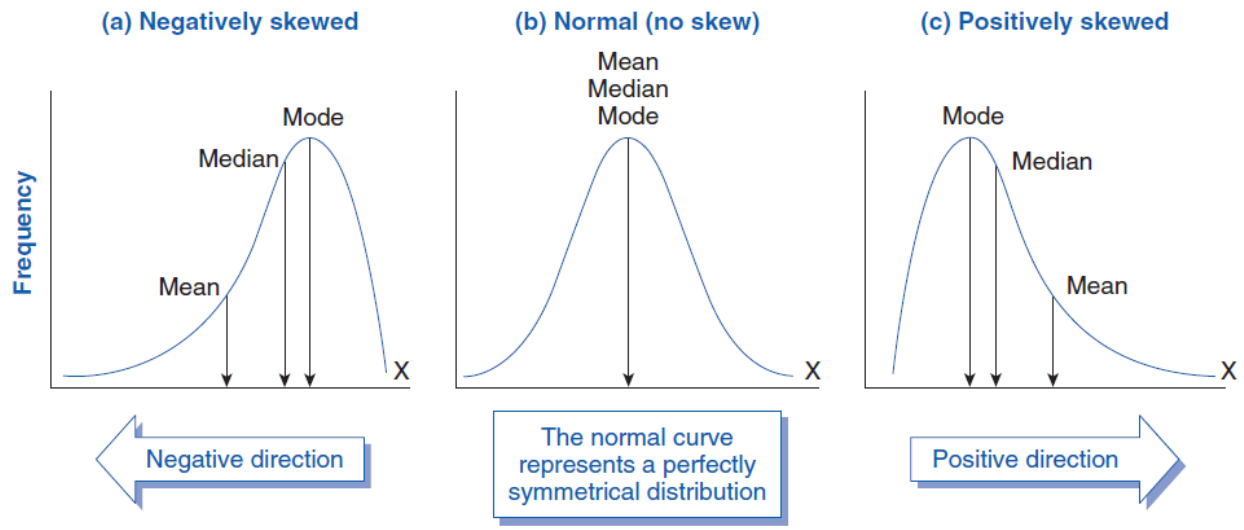


Figure 1: Comparativa de Normalidad

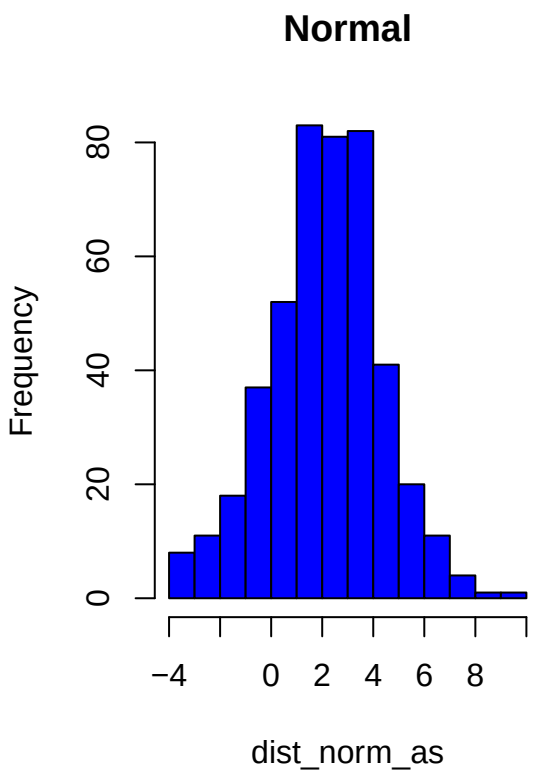
- El valor se encuentra entre -0.5 y 0.5. La distribución es aproximadamente sesgada.
- El valor se encuentra entre -1 a -5 o 1 a 5. La distribución es ligeramente sesgada.
- El valor es menor que -1 o mayor a 1. La distribución es moderadamente sesgada pero aceptable.
- Si el valor supera -2 o 2. La distribución no es normal

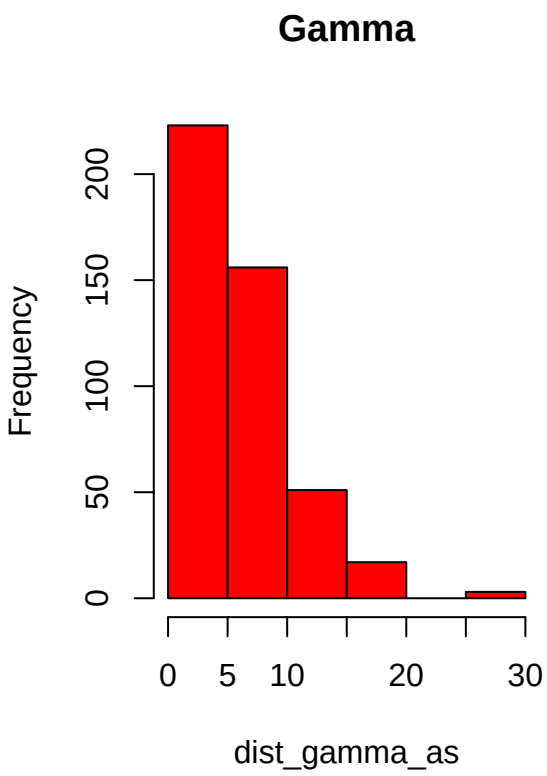
```
dist_norm_as <- rnorm(n = 450, mean = 2, sd = 2.3)
dist_gamma_as <- rgamma(n = 450, shape = 2, scale = 3)
```

```
# Configurar la disposición de los gráficos
par(mfrow = c(1, 2))

# Dibujar el primer histograma
hist(dist_norm_as, main = "Normal", col = "blue")

# Dibujar el segundo histograma
hist(dist_gamma_as, main = "Gamma", col = "red")
```






```
library(moments)

print(skewness(dist_norm_as))
```

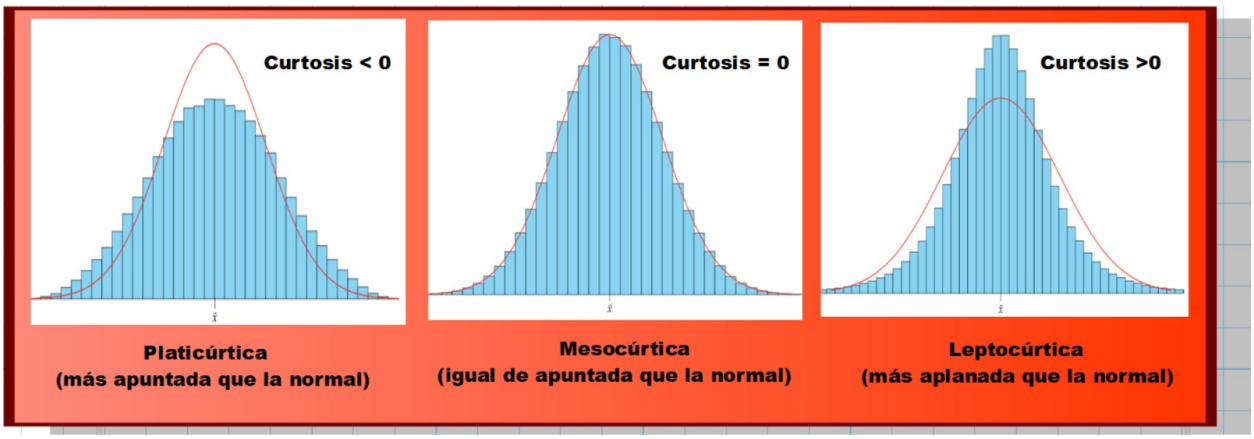
```
## [1] -0.08919541
```

```
print(skewness(dist_gamma_as))
```

```
## [1] 1.392248
```

Curtosis

Permite medir el grado de apuntamiento o achatamiento de la distribución de frecuencia, respecto a la curva de la distribución normal que tiene coeficiente igual a 0.



```r
print(kurtosis(dist_norm_as))
```

```
## [1] 3.27443
```

```r
print(kurtosis(dist_gamma_as))
```

```
## [1] 5.905284
```

Contraste de hipótesis

```r
library("nortest")
```

En todas las pruebas a realizar se considera como hipótesis nula que los datos sí proceden de una distribución normal y como hipótesis alternativa que no lo hacen. El *p-value* de estos test indica la probabilidad de obtener una distribución como la observada si los datos proceden realmente de una población con una distribución normal.

El nivel de significancia es 0.05

Prueba de Shapiro-Wilk

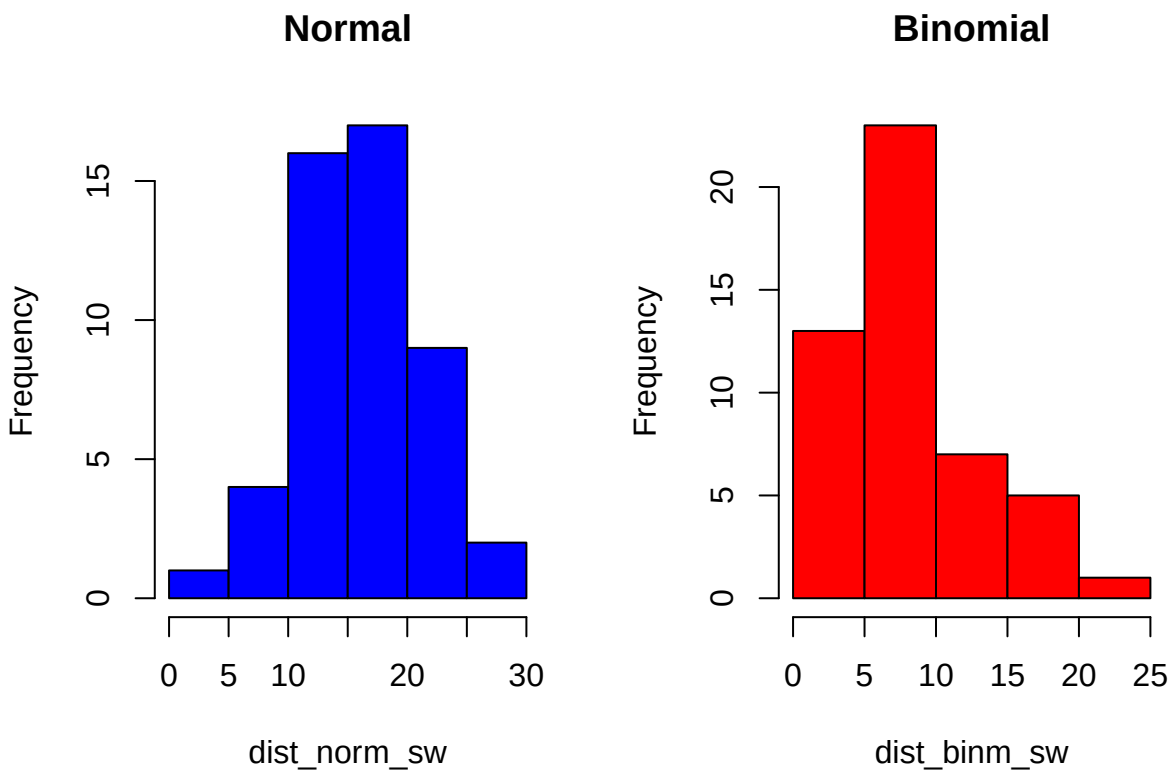
La muestra debe ser menor a 50 datos.

```r
dist_norm_sw <- rnorm(n = 49, mean = 15, sd = 5)
dist_binm_sw <- rnbinom(n = 49, size = 5, prob = 0.35)
```

```r
# Configurar la disposición de los gráficos
par(mfrow = c(1, 2))

# Dibujar el primer histograma
hist(dist_norm_sw, main = "Normal", col = "blue")

# Dibujar el segundo histograma
hist(dist_binm_sw, main = "Binomial", col = "red")
```




```
print(shapiro.test(x = dist_norm_sw))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  dist_norm_sw
## W = 0.99103, p-value = 0.9695
```

```
print(shapiro.test(x = dist_binm_sw))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  dist_binm_sw
## W = 0.94026, p-value = 0.01513
```

Prueba de Anderson-Darling

El número de muestras tiene que ser mayor a 7

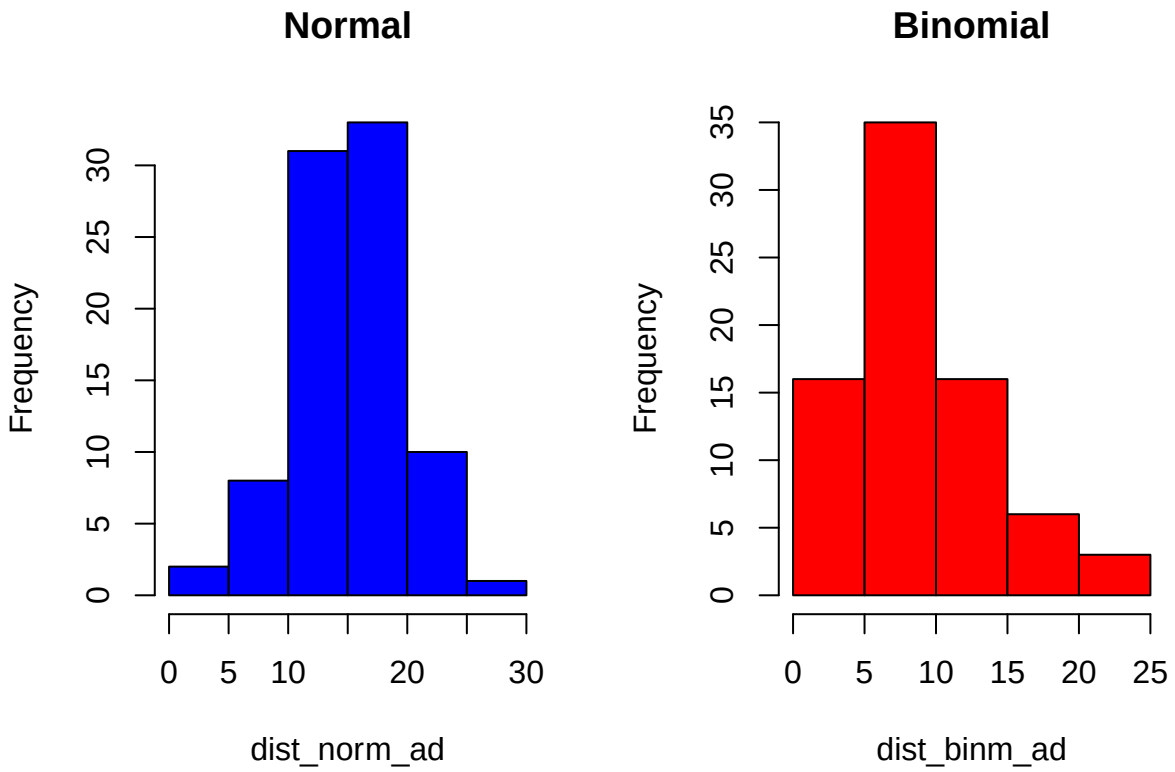
```
dist_norm_ad <- rnorm(n = 85, mean = 15, sd = 5)
dist_binm_ad <- rnbinom(n = 76, size = 5, prob = 0.35)
```

```
# Configurar la disposición de los gráficos
par(mfrow = c(1, 2))

# Dibujar el primer histograma
hist(dist_norm_ad, main = "Normal", col = "blue")

# Dibujar el segundo histograma
```

```r
hist(dist_binm_ad, main = "Binomial", col = "red")
```




```r
print(ad.test(x = dist_norm_ad))
```

```
##
##  Anderson-Darling normality test
##
## data:  dist_norm_ad
## A = 0.22851, p-value = 0.8053
```

```r
print(ad.test(x = dist_binm_ad))
```

```
##
##  Anderson-Darling normality test
##
## data:  dist_binm_ad
## A = 1.329, p-value = 0.001768
```

Prueba de Cramer-von Mises

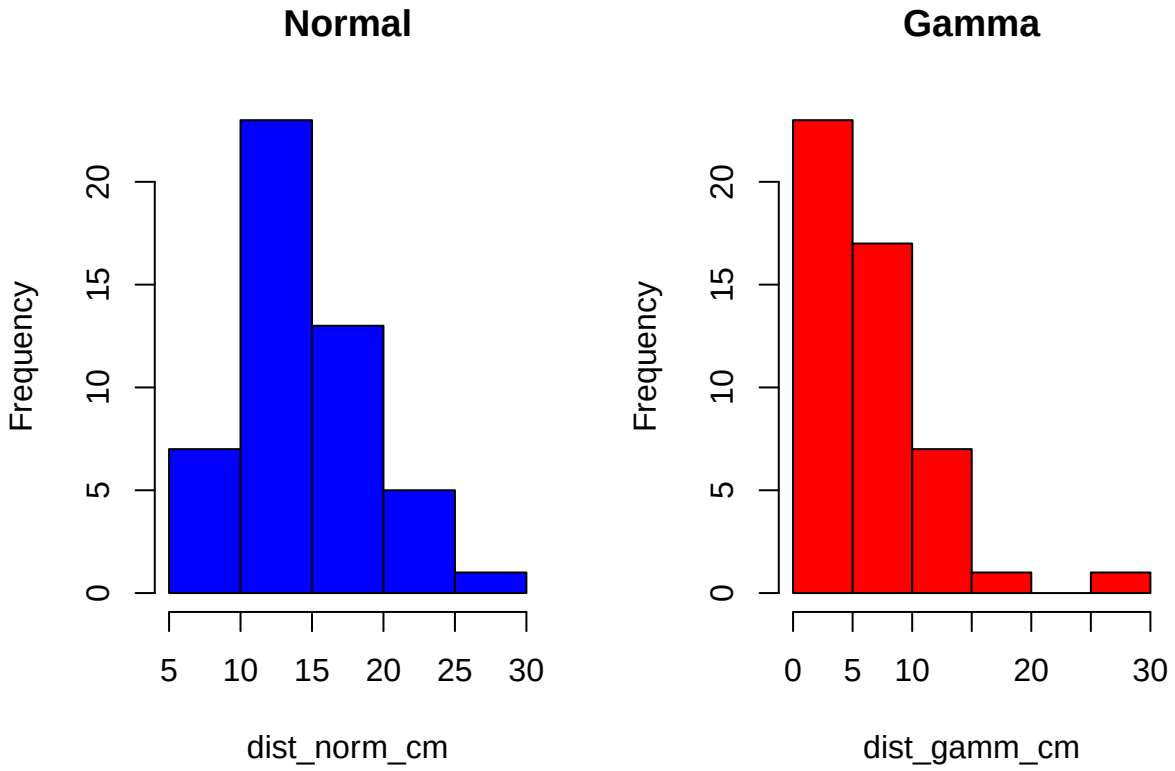
Útil para muestras pequeñas

```r
dist_norm_cm <- rnorm(n = 49, mean = 15, sd = 5)
dist_gamm_cm <- rgamma(n = 49, shape = 2, scale = 3)
```

```r
# Configurar la disposición de los gráficos
par(mfrow = c(1, 2))

# Dibujar el primer histograma
hist(dist_norm_cm, main = "Normal", col = "blue")
```

```r
# Dibujar el segundo histograma
hist(dist_gamm_cm, main = "Gamma", col = "red")
```




```r
print(cvm.test(x = dist_norm_cm))
```

```
##
##  Cramer-von Mises normality test
##
## data:  dist_norm_cm
## W = 0.078312, p-value = 0.2128
```

```r
print(cvm.test(x = dist_gamm_cm))
```

```
##
##  Cramer-von Mises normality test
##
## data:  dist_gamm_cm
## W = 0.23438, p-value = 0.001879
```

Prueba Lilliefors

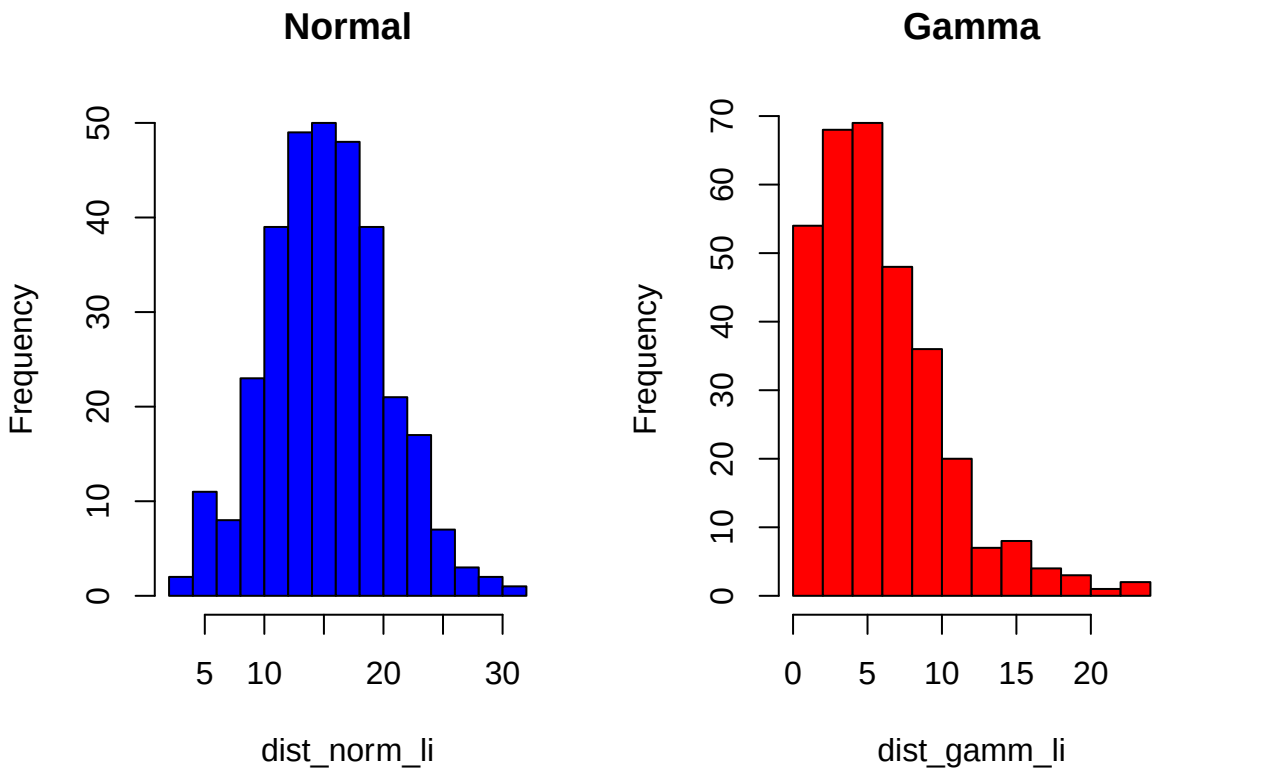
Número de observaciones mayor a 50

```r
dist_norm_li <- rnorm(n = 320, mean = 15, sd = 5)
dist_gamm_li <- rgamma(n = 320, shape = 2, scale = 3)
```

```r
# Configurar la disposición de los gráficos
par(mfrow = c(1, 2))
```

```r
# Dibujar el primer histograma
hist(dist_norm_li, main = "Normal", col = "blue")

# Dibujar el segundo histograma
hist(dist_gamm_li, main = "Gamma", col = "red")
```




```r
print(lillie.test(x = dist_norm_li))
```

```
##
##  Lilliefors (Kolmogorov-Smirnov) normality test
##
## data:  dist_norm_li
## D = 0.021506, p-value = 0.9744
```

```r
print(lillie.test(x = dist_gamm_li))
```

```
##
##  Lilliefors (Kolmogorov-Smirnov) normality test
##
## data:  dist_gamm_li
## D = 0.097141, p-value = 1.066e-07
```

Prueba Pearson chi-square

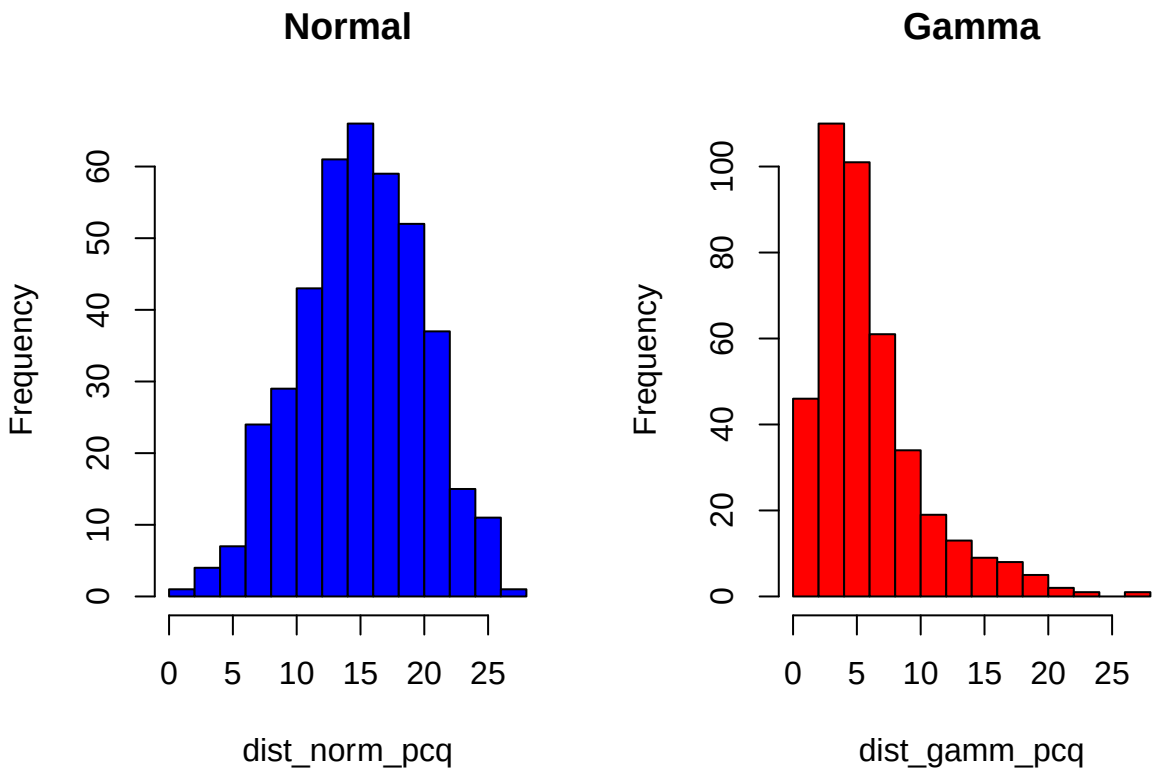
Basa en una distribución Chi Cuadrada

```r
dist_norm_pcq <- rnorm(n = 410, mean = 15, sd = 5)
dist_gamm_pcq <- rgamma(n = 410, shape = 2, scale = 3)
```

```r
# Configurar la disposición de los gráficos
par(mfrow = c(1, 2))

# Dibujar el primer histograma
hist(dist_norm_pcq, main = "Normal", col = "blue")

# Dibujar el segundo histograma
hist(dist_gamm_pcq, main = "Gamma", col = "red")
```




```r
print(pearson.test(x = dist_norm_pcq))
```

```
##
##  Pearson chi-square normality test
##
## data:  dist_norm_pcq
## P = 24.868, p-value = 0.2065
```

```r
print(pearson.test(x = dist_gamm_pcq))
```

```
##
##  Pearson chi-square normality test
##
## data:  dist_gamm_pcq
## P = 133.92, p-value < 2.2e-16
```