3.7 Nonlinear Fits (Linear Regression with Higher Order Terms)

Linear regression is actually NOT linear when it comes to allowing nonlinear relationships between $x$ and $y$. (The term “linear” refers to the parameters of the model, i.e., the regression coefficients.) This is good news, because linear regression can fit any nonlinear data. But it’s also bad news, because the ability to fit nonlinear data also allows for overfitting. In developing regression models of data it is important to assure that the model is not overfitting the data, because such a model will have poor predictive capability. Toward the end of this book we will see how to assess the predictive capability of a regression model. Here, let’s first confirm that linear regression can overfit (memorize) data.

```r
set.seed(12)  # Set a seed to ensure reproducible results.
x <- seq(0, 0.9, 0.1)  # Pick 10 x's between 0 and 1.
y <- x + rnorm(10, 0, 0.3)  # x and y are "truly" linear, plus error.
plot(x,y)  # Look at the data.

lm.1 <- lm(y ~ x)  # Fit the simplest regression model
lines(x, lm.1$fitted.values)

lm.2 <- lm(y ~ x + I(x^2))  # Fit a regression model including the quadratic term.
lines(x, lm.2$fitted.values, col = 2)  # The I() is necessary. Don't ask why!

lm.3 <- lm(y ~ x + I(x^2) + I(x^3))  # Add a cubic term.
lines(x, lm.3$fitted.values, col = 3)  # Note that the fit is getting more curvy.

lm.4 <- lm(y ~ x + I(x^2) + I(x^3) + I(x^4) + I(x^5) + I(x^6) + I(x^7) + I(x^8) + I(x^9))
# Fit a 9th order polynomial.
lines(x, lm.4$fitted.values, col = 4)
summary(lm.4)$r.squared  # Examine the R-squared.

[1] 1

legend('bottomright', c('Linear', 'Quadratic', 'Cubic', '9th Order'),
       text.col = c(1, 2, 3, 4), bty = 'n')
```

# Note that the last model will have no predictive power since it overfits the data.
3.8 Model Comparison

Example: Hail Data

Note that the closer $R^2$ is to 1, the “better” the fit and the closer it is to 0, the worse. Higher $R^2$ does not necessarily mean better predictions.

dat <- read.table("hail_dat.txt", header = T)

x_1 <- dat[, 1]  # Divergence.
x_2 <- dat[, 2]  # Rotate.
y <- dat[, 3]  # Hail size. Size is in 100th-of-an-inch.

# Renaming the columns in dat:
colnames(dat) <- c("x_1", "x_2", "y")

lm.1 <- lm(y ~ x_1)  # Predicting size from divergence (simple regression).
summary(lm.1)

Call:

lm(formula = y ~ x_1)

Residuals:

Min 1Q Median 3Q Max
-126.1 -50.9 -19.8 44.8 262.6

Coefficients:

Estimate Std. Error t value Pr(>|t|)
(Intercept) 33.673 13.361 2.52 0.012 *
x_1 3.417 0.334 10.23 <2e-16 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 76 on 280 degrees of freedom
Multiple R-squared: 0.272, Adjusted R-squared: 0.269
F-statistic: 105 on 1 and 280 DF, p-value: <2e-16

lm.2 <- lm(y ~ x_2) # Predicting size from rotation (simple regression).
summary(lm.2)

Call:
lm(formula = y ~ x_2)

Residuals:
 Min 1Q Median 3Q Max
-180.9 -55.1 -11.6 36.6 268.4

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) 37.268 12.508 2.98 0.0031 **
x_2 7.858 0.735 10.70 <2e-16 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 75 on 280 degrees of freedom
Multiple R-squared: 0.29, Adjusted R-squared: 0.288
F-statistic: 114 on 1 and 280 DF, p-value: <2e-16

lm.3 <- lm(y ~ x_1 + x_2) # Predicting size from both (multiple regression).
summary(lm.3)

Call:
lm(formula = y ~ x_1 + x_2)

Residuals:
 Min 1Q Median 3Q Max
-157.4 -52.0 -12.2 35.5 261.8

Coefficients:
Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.179 13.684 -0.09 0.93
x_1 2.117 0.375 5.56 0.00000000401 ***
x_2 5.268 0.835 6.31 0.00000000011 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 71.2 on 279 degrees of freedom
Multiple R-squared: 0.363, Adjusted R-squared: 0.358
F-statistic: 79.5 on 2 and 279 DF, p-value: <2e-16

lm.4 <- lm(y ~ x_1 + x_2 + x_1:x_2)  # Multiple regression with interaction.
summary(lm.4)

Call:
lm(formula = y ~ x_1 + x_2 + x_1:x_2)

Residuals:
        Min          1Q      Median          3Q         Max
-157.1    -50.8      -14.2       36.6     264.0

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  71.6091    34.7693   2.063  0.0407 *
x_1          0.1989     0.9217    0.220  0.8289
x_2          1.0612     2.0269    0.526  0.6016
x_1:x_2      0.1030     0.0453    2.273  0.0242 *

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 70.7 on 278 degrees of freedom
Multiple R-squared: 0.375, Adjusted R-squared: 0.368
F-statistic: 55.5 on 3 and 278 DF, p-value: <2e-16

lm.5 <- lm(y ~ x_1 + x_2 + I(x_1^2) + I(x_2^2))  # Multiple quadratic regression.
summary(lm.5)

Call:
lm(formula = y ~ x_1 + x_2 + I(x_1^2) + I(x_2^2))

Residuals:
        Min          1Q      Median          3Q         Max
-180.8    -48.6      -16.1       38.1     266.0

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  88.4961    38.1671   2.322  0.0212 *
x_1          0.4789     1.6626    0.290  0.7743
x_2         -1.9992     3.3297   -0.600  0.5492
I(x_1^2)    -0.0175     0.0186   -0.940  0.3488
I(x_2^2)    -0.2053     0.0918   -2.244  0.0265 *

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 70.5 on 277 degrees of freedom
Multiple R-squared: 0.38, Adjusted R-squared: 0.371
F-statistic: 42.4 on 4 and 277 DF, p-value: <2e-16

lm.6 <- lm(y ~ x_1 + x_2 + I(x_1^2) + I(x_2^2) + x_1:x_2)
summary(lm.6)
Call:
\texttt{lm(formula = y \sim x_1 + x_2 + I(x_1^2) + I(x_2^2) + x_1:x_2)}

Residuals:
\begin{tabular}{cccc}
Min & 1Q & Median & 3Q & Max \\
-179.7 & -48.9 & -16.1 & 38.0 & 265.7 \\
\end{tabular}

Coefficients:
\begin{tabular}{cccccc}
Estimate & Std. Error & t value & Pr(>|t|) \\
(Intercept) & 89.0739 & 38.4006 & 2.32 & 0.021 * \\
x_1 & 0.4974 & 1.6695 & 0.30 & 0.766 \\
x_2 & -2.0870 & 3.3794 & -0.62 & 0.537 \\
I(x_1^2) & 0.0145 & 0.0264 & 0.55 & 0.584 \\
I(x_2^2) & 0.1921 & 0.1228 & 1.56 & 0.119 \\
x_1:x_2 & 0.0137 & 0.0843 & 0.16 & 0.872 \\
\end{tabular}

---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 70.6 on 276 degrees of freedom
Multiple R-squared: 0.38, Adjusted R-squared: 0.369
F-statistic: 33.8 on 5 and 276 DF, p-value: <2e-16

# Here is a way of drawing the fit even if it's nonlinear.
# Suppose we pick a relatively simple quadratic model from above:
diverg <- dat[, 1]
rotate <- dat[, 2]
size <- dat[, 3]

lm.g <- \texttt{lm(size \sim rotate + I(rotate^2) )}

Call:
\texttt{lm(formula = size \sim rotate + I(rotate^2))}

Coefficients:
\begin{tabular}{ccc}
(Intercept) & rotate & I(rotate^2) \\
116.352 & -2.268 & 0.283 \\
\end{tabular}

x <- \texttt{seq(min(rotate), max(rotate), .01)}
y.fit <- \texttt{lm.g$coeff[1] + lm.g$coeff[2] * x + lm.g$coeff[3] * x ^ 2}
plot(rotate, size, \texttt{cex = 0.5})
points(x, y.fit, \texttt{col = "red", type="l"})

# Alternatively, a fancier way is presented below:
x <- \texttt{matrix(seq(min(rotate), max(rotate), .01), byrow = T)}
colnames(x) <- \texttt{"rotate"}  # Necessary for predict().
plot(rotate, size, \texttt{cex = 0.5})
lines(x, predict(lm.g, \texttt{newdata = data.frame(x)} , \texttt{col = 2})

# Plotting a surface that goes through the cloud of points in 3d.
# Suppose we decided that the best model is the most complex model, above:
lm.e <- lm(size ~ diverg + rotate + I(diverg^2) + I(rotate^2) + I(diverg * rotate))

x <- seq(min(rotate), max(rotate), length = 100)  # x and y simply define a
y <- seq(min(diverg), max(diverg), length = 100)  # grid in the x-y plane.

f <- function(x, y) {
}
y.fit <- outer(x, y, f)  # y contains the "height" values of the surface,
                          # over the x-y grid; that's what outer() does. Look it up.

library(lattice)  # Loading the library that contains the function cloud().
# Making a 3d plot of the points of the plane.
cloud(y.fit, type = "p", screen = list(z = 10, x = -70, y = 0))

# Note that in spite of the nonlinearity of the regression function
# itself, i.e. with quadratic and an interaction terms, the surface is
# mostly planar in the range of our data (i.e., x and y).
Here is a discussion of all of the above results based on the $R^2$ values: It seems like

1. Rotate is a better predictor of size than diverge.

2. The two of them together make for an even better model.

3. Quadratic terms for each, make the model even better, but not by much

4. $R^2$ goes from 0.3629 to 0.3800.

5. An interaction term, without quadratic terms, gives a model that is comparable to what we got from a quadratic model with no interaction.

6. Quadratic and interaction terms, together, “seem” to give the best model.

Note that $R^2$ increases as the complexity of the model increases (adding more terms). The main question (which can be addressed only qualitatively at this point) is this: is the gain in $R^2$ big enough
to warrant the new term, knowing that a new term can lead to over-fitting. In this example, the gain from $R^2 = 0.3629$ to $R^2 = 0.3800$ is probably NOT worth the risk of overfitting. So, we should keep the simpler model. That’s called the principle of “Occam’s Razor,” which posits that one should go with simpler things.

```
anova(lm.6)
```

Analysis of Variance Table

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>x_1</td>
<td>1</td>
<td>603829</td>
<td>603829</td>
<td>121.05</td>
<td>&lt; 2e-16 ***</td>
</tr>
<tr>
<td>x_2</td>
<td>1</td>
<td>202064</td>
<td>202064</td>
<td>40.51</td>
<td>0.000000000081 ***</td>
</tr>
<tr>
<td>I(x_1^2)</td>
<td>1</td>
<td>13086</td>
<td>13086</td>
<td>2.62</td>
<td>0.106</td>
</tr>
<tr>
<td>I(x_2^2)</td>
<td>1</td>
<td>24838</td>
<td>24838</td>
<td>4.98</td>
<td>0.026 *</td>
</tr>
<tr>
<td>x_1:x_2</td>
<td>1</td>
<td>131</td>
<td>131</td>
<td>0.03</td>
<td>0.872</td>
</tr>
<tr>
<td>Residuals</td>
<td>276</td>
<td>1376791</td>
<td>4988</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

---

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

In the anova() output, each term in the regression equation is accompanied by an SS term. They are obtained from a sequential analysis of variance. These SS terms will change depending on the order of the terms in the regression equation.

It’s important to realize that all of these SS terms are measures of variability. Specifically, SST is the numerator of the sample variance of the y‘s, $SS_{explained}$ is the numerator of the sample variance of the predictions, and $SS_{unexplained}$ (SSE) is converted to variance when it is divided by $n-(k+1)$, where $k$ is the number of parameters in the regression model. You can confirm these:

```
y_hat <- predict(lm.6)  # From 9.3.
n <- nrow(dat)
(n - 1) * var(y_hat)    # 843948 = 603829 + 202064 + 13086 + 24838 + 131 = SS_explained

[1] 843948
```

**Prediction on New Data**

The best way to do prediction on new data is to just attach the new data to the bottom of the old data. Suppose the new data consists of the following 2 case:

- $x_1 = 33$, $x_2 = 9$
- $x_1 = 36$, $x_2 = 14$

Then we can do the following:

```
n <- nrow(dat)  # number of cases in dat.
new_1 = c(33, 8, NA)  # y = NA because we don’t know y for new data.
new_2 = c(35, 14, NA)
new.dat = rbind(dat, new_1, new_2)  # Using row-bind to attach new data to old data.

# In the next line, we redevelop lm.4, but on the first n cases:
lm.7 <- lm(y ~ x_1 + x_2 + x_1:x_2, dat = new.dat[1:n,])  # NOTE: dat=new.dat[1:n,].
summary(lm.7)  # Same as lm.4.
```
Call:
\( \text{lm(formula = y ~ x_1 + x_2 + x_1:x_2, data = new.dat[1:n,])} \)

Residuals:

<table>
<thead>
<tr>
<th></th>
<th>Min</th>
<th>1Q</th>
<th>Median</th>
<th>3Q</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>-157.1</td>
<td>-50.8</td>
<td>-14.2</td>
<td>36.6</td>
<td>264.0</td>
</tr>
</tbody>
</table>

Coefficients:

|          | Estimate | Std. Error | t value | Pr(> |t|) |
|----------|----------|------------|---------|------|-----|
| (Intercept) | 71.6091  | 34.7693    | 2.06    | 0.040 * |
| x_1       | 0.1989   | 0.9217     | 0.22    | 0.829 |
| x_2       | 1.0612   | 2.0269     | 0.52    | 0.601 |
| x_1:x_2   | 0.1030   | 0.0453     | 2.27    | 0.024 * |

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 70.7 on 278 degrees of freedom
Multiple R-squared: 0.375, Adjusted R-squared: 0.368
F-statistic: 55.5 on 3 and 278 DF,  p-value: <2e-16

colnames\(\text{new.dat}\) <- c("x_1", "x_2", "x_1:x_2")
predict\(\text{lm.7, newdata <- new.dat[(n+1):(n+2),]}\)  # Predict the last 2 cases.

\[ 283 \quad 284 \]
\[ 113.8 \quad 143.9 \]

3.9 Collinearity

Another distressing issue that arises in multiple regression is collinearity, i.e., a linear association between the predictors themselves. One reason collinearity is disturbing is that it renders the regression coefficients uninterpretable; i.e., a given beta can no longer be interpreted as the average rate of change of \(y\) with respect to a unit change in \(x\) with everything else held fixed. Insisting on that kind of interpretation, in the presence of collinearity, can lead to wrong (or even absurd) conclusions. Collinearity also makes the predictions more uncertain, but here we will focus on the effect of collinearity on the regression coefficients.

# To that end, we'll write an R function, which is nothing but some lines
# of code intended to be used over and over again.
make.fit <- function(r) {
    # The function first makes data on x_1, x_2, and y, with collinearity
    # (i.e., correlation between x_1 and x_2) equal to r.
    # The input of the function is r (i.e., correlation between x_1 and x_2.
    # NOT between y and anything).
    # The function then fits that data using y, and returns some stats about
    # the estimated regression coefficients.
    library(MASS)  # This library contains \mvrnorm(); see below.
    set.seed(1)   # Ensures reproducible outputs.
    n <- 100
    # The R function \mvrnorm() below takes a sample from a multivariate normal,
    # which is a higher-dimensional analog of the normal distribution.
dat <- mvnorm(n, rep(0, 2); matrix(c(1, r, r, 1), 2, 2))
x_1 <- dat[, 1]
x_2 <- dat[, 2]
y <- 1 + 2 * x_1 + 3 * x_2 + rnorm(n, 0, 2)  # Generate y, and add noise.
dat <- data.frame(x_1, x_2, y)  # Here is the whole data.
plot(dat)
lm1 <- lm(y ~ x_1 + x_2)  # Fit a plane through the data.
# return(lm1) returns the whole R object lm1.
# return(summary(lm1)) returns only the summary results.
return(summary(lm1)$coeff)  # Returns only the regression coefficients.
}

# Examining data and the regression coefficients for different amounts of
# collinearity.
make.fit(0)  # No collinearity.

| Estimate | Std. Error | t value | Pr(>|t|) |
|----------|------------|---------|---------|
| (Intercept) | 1.051       | 0.2104  | 4.994   | 2.609e-06|
| x_1       | 2.107       | 0.2190  | 9.623   | 8.760e-16|
| x_2       | 3.042       | 0.2335  | 13.028  | 4.968e-23|

make.fit(0.7)  # Some collinearity.

| Estimate | Std. Error | t value | Pr(>|t|) |
|----------|------------|---------|---------|
| (Intercept) | 1.051       | 0.2104  | 4.994   | 2.609e-06|
| x_1       | 2.161       | 0.3096  | 6.979   | 3.684e-10|
| x_2       | 2.885       | 0.3099  | 9.310   | 4.141e-15|

make.fit(0.9)  # Extreme collinearity.

| Estimate | Std. Error | t value | Pr(>|t|) |
|----------|------------|---------|---------|
| (Intercept) | 1.051       | 0.2104  | 4.994   | 0.0000026091|
| x_1       | 2.261       | 0.5039  | 4.486   | 0.0000199246|
| x_2       | 2.783       | 0.5042  | 5.519   | 0.000002837|

make.fit(0.999)

| Estimate | Std. Error | t value | Pr(>|t|) |
|----------|------------|---------|---------|
| (Intercept) | 1.051       | 0.2104  | 4.9941  | 0.000002609|
| x_1       | 4.412       | 4.8973  | 0.9009  | 0.369846805|
| x_2       | 0.630       | 4.8976  | 0.1286  | 0.897910878|
When collinearity is extreme, not only are the standard errors huge, but the estimated regression coefficients themselves (β) are way off. As collinearity increases, the regression coefficients become more uncertain, and so we are unable to interpret them, like we would if there were no collinearity. The regression equation is still OK to use for predictions. But, of course, the predictions will be less certain as well. Note that in practice we don’t control/adjust the data or the collinearity; all we see are the scatterplots, and based on the scatterplots between the predictors, we decide how much collinearity there is. For example, for the hail data:

```r
plot(dat)
```
In the scatterplots, the one for $x_1$ versus $x_2$ (or vice versa) suggests some collinearity; it is not extreme, but it is present. As such, we have to be cautious in interpreting the regression coefficients. But the regression model is still okay for making predictions (as long as it does not overfit, of course).

3.10 Plotting Curved Fits on a Scatterplot

We plotted polynomial fits, but the “curves” were just the result of connecting points with straight lines, and as a result, the “curves” did not look smooth. Here is a way to get a smoother looking fit on the scatterplot.

```r
# Suppose we pick a relatively simple quadratic model for the hail data:
dat <- read.table("hail.dat.txt", header = T)

x_1 <- dat[, 1] # Divergence.
x_2 <- dat[, 2] # Rotate.
y <- dat[, 3] # Hail size. Size is in 100th-of-an-inch.

lm.g <- lm(y ~ x_2 + I(x_2 ^ 2))

lm.g$coeff # Examine the regression coeff.

(Intercept) x_2 I(x_2^2)
 116.3519  -2.2682   0.2827

x <- seq(min(x_2), max(x_2), .01) # Generate a fake x.
y.fit <- lm.g$coeff[1] + lm.g$coeff[2] * x + lm.g$coeff[3] * x^2

plot(x_2, y, cex = 0.5)
points(x, y.fit, col = "red", type = "l")
```
# Alternatively, a fancier way is as follows.
x <- matrix(seq(min(x_2), max(x_2), .01), byrow = T)  # Generate a fake x.
colnames(x) <- "x_2"
plot(x_2, y)
lines(x, predict(lm.g, newdata = data.frame(x)), col=2)
4 Sampling Distributions of the Sample Mean and Median

4.1 Sampling Distribution of the Mean

4.1.1 Normal Population

Instead of taking samples from a normal population, using `rnorm()`, we are going to take ONE huge sample from a normal population, using `rnorm()`, and then just treat it as our population. The main reason for this is mostly to set the stage for something called “bootstrapping,” which we will study later.

```r
N <- 1000000 # Let N be the population size.
pop <- rnorm(N, 1, 2) # Take a random sample and treat it as pop.
pop.mean <- mean(pop) # This is mu, the population mean.
pop.sd <- sd(pop) # This is sigma, the pop standard deviation.
pop.median <- median(pop) # Get the population median, for later.
c(pop.mean, pop.sd, pop.median) # Print them for comparison, below.
[1] 0.9958 2.0070 1.0022
hist(pop, breaks = 400) # This shows that the population is pretty normal.

# Experiment underlying the sampling distribution.
n.trial <- 10000 # Take 10000 samples of
sample.size <- 10 # size 10 (i.e., small) from the population.
sample.stat <- numeric(n.trial) # Create space to store the 10000 sample means.

for (i in 1:n.trial) {
  samp <- sample(pop, sample.size, replace = T) # Take a sample (with replacement).
  sample.stat[i] <- mean(samp) # Compute each sample's mean.
}
mean(sample.stat) # Compare mean of sample means
[1] 0.986

pop.mean # with the population mean.
[1] 0.9958

sd(sample.stat) # Compare the standard deviation of sample means
[1] 0.6304

pop.sd # with the pop standard deviation.
[1] 2.007

pop.sd / sqrt(sample.size) # But compare with (pop std dev)/sqrt(n)
[1] 0.6347
```
According to the Central Limit Theorem (CLT), the sampling distribution of the sample mean should be normal. To confirm:

```r
hist(sample.stat, breaks = 40)
qqnorm(sample.stat)  # Pretty normal.
```

As the sample size increases, the mean of the sample means gets pretty close to the population mean, and the standard deviation of the sample means gets pretty close to the \( \frac{sd(pop)}{\sqrt{n}} \). So, the CLT is confirmed.

4.1.2 Non-normal Population

```r
N <- 100000
pop <- rgamma(N, 1, 1)
```
pop.mean <- mean(pop)
pop.sd <- sd(pop)
pop.median <- median(pop)
c(pop.mean, pop.sd, pop.median)

[1] 0.9946 0.9948 0.6895

hist(pop, breaks = 400)  # The distribution of sample means looks non-normal.

n.trial <- 10000  # Take 10000 samples of
sample.size <- 10   # size 10 (i.e., small) from the population.
sample.stat <- numeric(n.trial)  # Space for storing the 10000 sample means.

for (i in 1:n.trial) {
    samp <- sample(pop, sample.size, replace = TRUE)  # Take a sample (with replacement).
    sample.stat[i] <- mean(samp)  # and compute each sample's mean.
}

mean(sample.stat)  # Compare mean of sample means with population mean.

[1] 0.9949

pop.mean

[1] 0.9946

sd(sample.stat)  # Compare the sd of sample means with population sd.

[1] 0.3199

pop.sd

[1] 0.9948

pop.sd / sqrt(sample.size)  # Compare with (pop.sd)/root(n).

[1] 0.3146

hist(sample.stat, breaks = 40)
qqnorm(sample.stat, cex = 0.5)
When the population is NOT normal, for small samples (10) the sampling distribution of the sample mean resists looking normal; but with larger samples (100), it is normal even though the population is not normal.

4.2 Sampling Distribution of Median

4.2.1 Non-normal Population

```r
N <- 100000
c <- rgamma(N, 1, 1)
pop.mean <- mean(c)
pop.sd <- sd(c)
pop.median <- median(c)
c(pop.mean, pop.sd, pop.median)
```
```r
# Generate a histogram of the population
hist(pop, breaks = 400)

n.trial <- 10000  # Take 10000 samples of
data.size <- 10  # size 10 (i.e., small) from the population.
sample.stat <- numeric(n.trial)  # Space for storing the 10000 sample medians.

for (i in 1:n.trial) {
  samp <- sample(pop, sample.size, replace = T)  # Take a sample (with replacement).
sample.stat[i] <- median(samp)  # Compute each sample's MEDIAN.
}

mean(sample.stat)  # Compare the MEAN of sample MEDIANs with pop MEDIAN.
[1] 0.7441

pop.median
[1] 0.6943

sd(sample.stat)  # Compare the sd of sample MEDIANs with population sd.
[1] 0.3086

pop.sd
[1] 0.9948

# Note that the formula sigma/root(n) applies only to the sample MEAN.

hist(sample.stat, breaks = 40)

qqnorm(sample.stat, cex = 0.5)
```

# Histogram of pop

![Histogram of pop](image)

# Histogram of sample.stat

![Histogram of sample.stat](image)
The sampling distribution doesn’t look too normal. But if the sample size is relatively large, the distribution of a bunch of sample medians, taken from even a non-normal population, is still normal. Most statistics (e.g., sample mean, sample median, sample standard deviation, ...) ultimately end up having a normal distribution, but some require a larger sample size.