Tutorial 7 R

Adam Shen

March 4, 2019

Question 8.2.23, Page 334

Automatic identification of the boundaries of significant structures within a medical image is an area of ongoing research. The paper "Automatic Segmentation of Medical Images Using Image Registration: Diagnostic and Simulation Applications" (J. of Medical Engr. and Tech., 2005: 53-63) discussed a new technique for such identification. A measure of the accuracy of the automatic region is the average linear displacement (ALD). The paper gave the following ALD observations for a sample of 49 kidneys (units of pixel dimensions).

Load the Data

```
ald <- c(1.38, 0.44, 1.09, 0.75, 0.66, 1.28, 0.51,
         0.39, 0.70, 0.46, 0.54, 0.83, 0.58, 0.64,
         1.30, 0.57, 0.43, 0.62, 1.00, 1.05, 0.82,
         1.10, 0.65, 0.99, 0.56, 0.56, 0.64, 0.45,
         0.82, 1.06, 0.41, 0.58, 0.66, 0.54, 0.83,
         0.59, 0.51, 1.04, 0.85, 0.45, 0.52, 0.58,
         1.11, 0.34, 1.25, 0.38, 1.44, 1.28, 0.51)
```
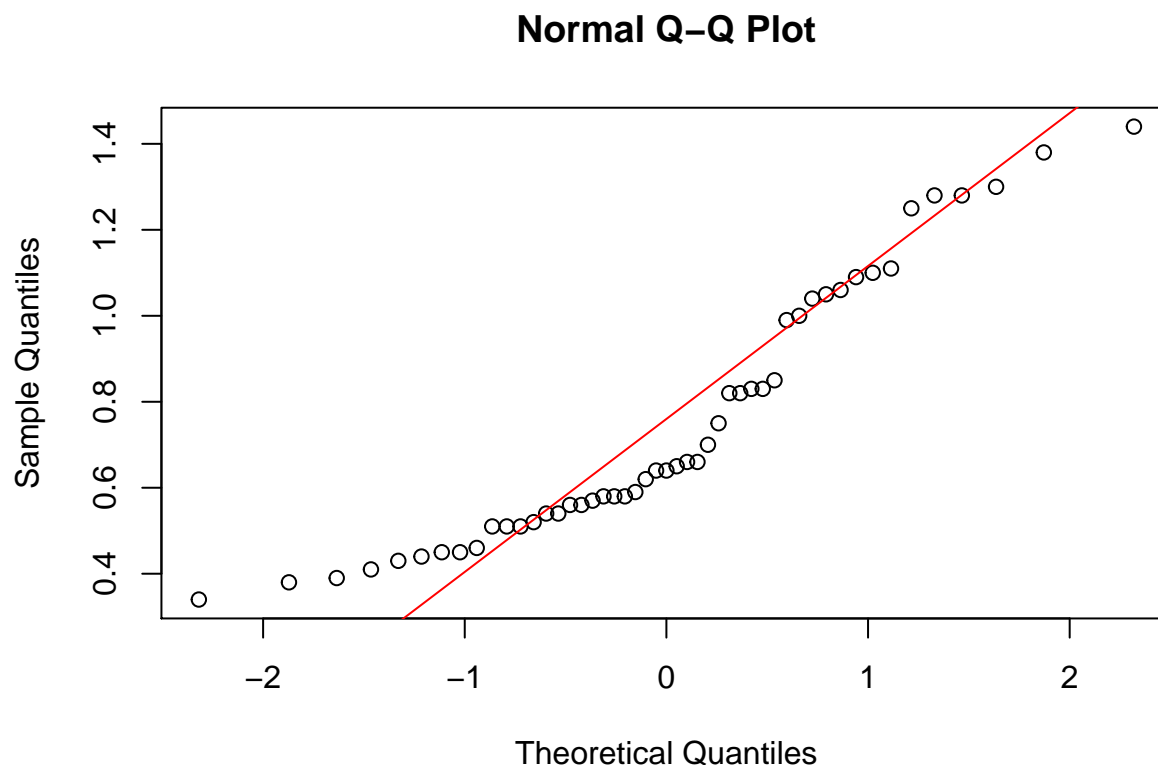
Summarize and Describe Data

```r
boxplot(ald, horizontal=TRUE, xlab="ALD", main="Boxplot of ALD")
```

Boxplot of ALD

ALD
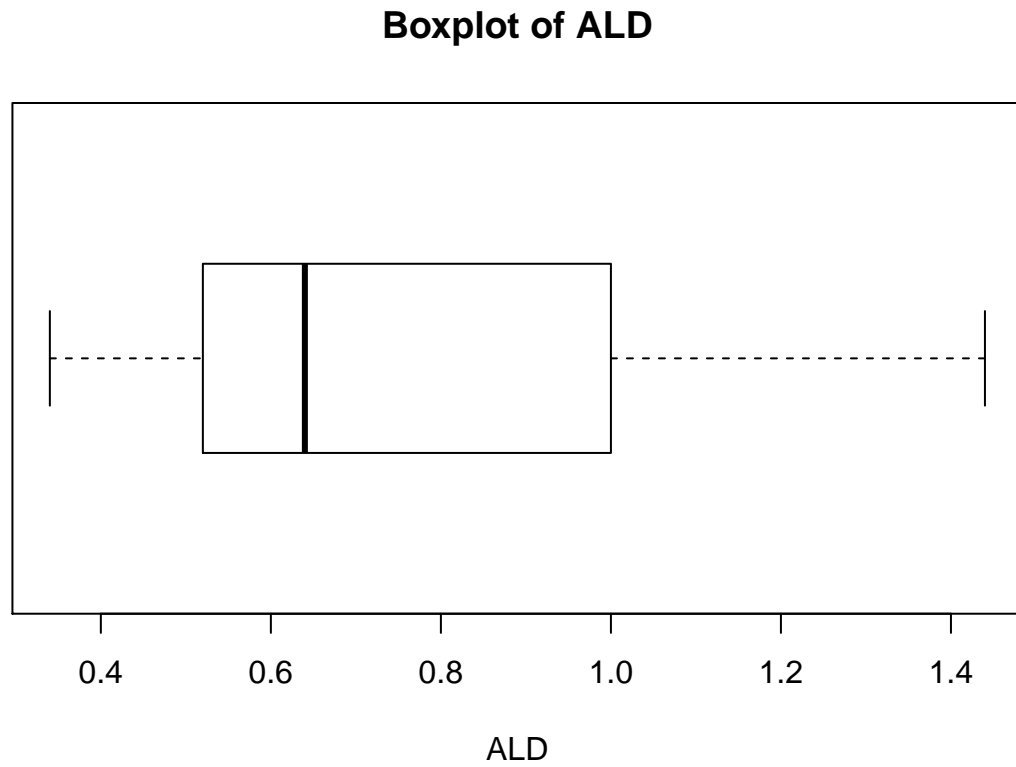
Plausible that data is normally distributed?

```
qqnorm(ald)
qqline(ald, col="red")
```

Normal Q–Q Plot

Must normality be assumed prior to calculating a CI for true average ALD or testing hypotheses about true average ALD? Explain.

Carry out the hypothesis test

The authors commented that in most cases the ALD is better than or of the order of 1.0. Does the data in fact provide strong evidence for concluding that true average ALD under these circumstances is less than 1.0? Carry out an appropriate test of hypotheses.

We want to test whether the true average ALD is less than 1.0. Therefore we have:

$$H_0 : \mu \geq 1.0 \quad H_A : \mu < 1.0$$

The test statistic is:

$$Z = \frac{\overline{X} - \mu}{S/\sqrt{n}} \overset{approx}{\sim} N(0,1)$$

```
(xbar <- mean(ald))
```

```
## [1] 0.7497959
```

```
(s <- sd(ald))
```

```
## [1] 0.3024655
```

```r
(n <- length(ald))
```

```
## [1] 49
```

```r
(z <- (xbar-1.0)/(s/sqrt(n)))
```

```
## [1] -5.790507
```

Since this is a lower tailed test, by the critical region method we reject the null hypothesis if $z < z_\alpha$, where α is the area to the left of z. α is not given so assume that $\alpha = 0.05$. Then $z_\alpha = z_{0.05} = -1.645$. Since $z < -1.645$, we reject the null hypothesis in favour of the alternative hypothesis. The p-value of this test can be found as the area to the left of z:

```r
pnorm(z)
```

```
## [1] 3.508712e-09
```

Remember that R by default uses areas to the left. In this case, area to the left of z is what we needed. By the p-value method, we reject the null hypothesis if $p < 0.05$. Since $p < 0.05$ we reject the null hypothesis in favour of the alternative hypothesis.

Calculate a 95% Upper Confidence Bound

```r
xbar - qnorm(0.05)*s/sqrt(n)
```

```
## [1] 0.820869
```

```r
# Alternatively: xbar + qnorm(0.95)*s/sqrt(n)
```

Therefore, a 95% upper confidence bound for μ is:

$$\mu < 0.821$$

This means that based on this sample, plausible values for the true mean are values less than 0.821. Notice that our null value $\mu_0 = 1.0$ does not lie in this interval. Coincidence? No! It turns out that there is a relationship between a $100(1 - \alpha)\%$ confidence interval (or confidence bound) and a hypothesis test carried out at the α level of significance. **This is mentioned in the proposition on page 354, which you are responsible for knowing!**

Since $\mu_0 = 1.0$ does not lie in this interval, we once again reject the null hypothesis in favour of the alternative hypothesis.