

Ch-02 R Codes

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Textbook: Montgomery, D. C. (2012). *Design and analysis of experiments*, 8th Edition. John Wiley & Sons.

Online handouts: https://github.com/PingYangChen/ANOVA_Course_R_Code

Chapter 2

Data Description and Visualization

The Tension Bond Strength Data is collected from the Portland Cement Formulation Experiment. For small dataset, one can directly create a dataframe in R,

```
df1 <- data.frame(  
  j = 1:10,  
  ModifiedMortar = c(  
    16.85, 16.4, 17.21, 16.35, 16.52,  
    17.04, 16.96, 17.15, 16.59, 16.57  
  ),  
  UnmodifiedMortar = c(  
    16.62, 16.75, 17.37, 17.12, 16.98,  
    16.87, 17.34, 17.02, 17.08, 17.27  
  )  
)
```

or create an csv file to store the data and then read it in R.

	A	B	C
1	j	ModifiedMortar	UnmodifiedMortar
2	1	16.85	16.62
3	2	16.4	16.75
4	3	17.21	17.37
5	4	16.35	17.12
6	5	16.52	16.98
7	6	17.04	16.87
8	7	16.96	17.34
9	8	17.15	17.02
10	9	16.59	17.08
11	10	16.57	17.27

Figure 1: Tension Bond Strength Data

```
df1 <- read.csv(file.path("data", "2_TensionBondStrength.csv"))
```

Descriptive statistics are essential when observing a dataset. In R, basic functions `mean()`, `median()`, `min()`, `max()`, `quantile()` and etc computes the central tendency of an univariate variable. There are also

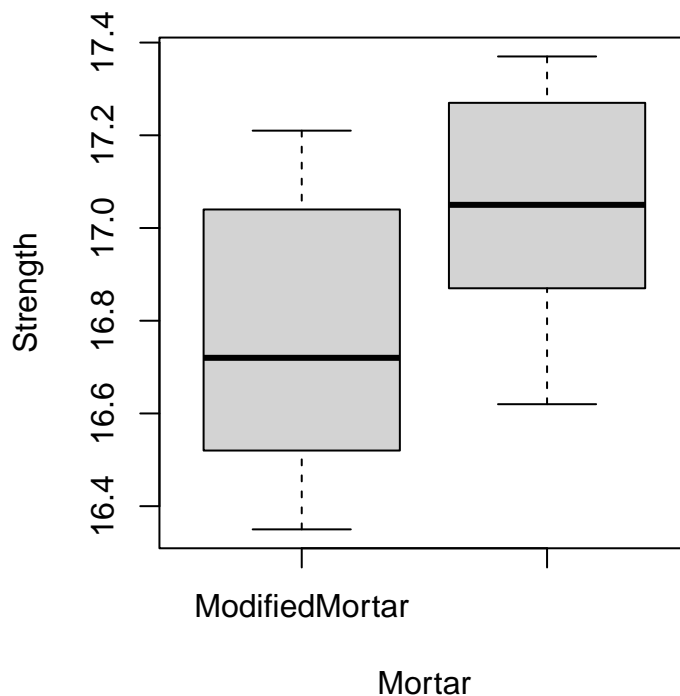
functions for computing the variation of an univariate variable, such as `var()`, `sd()`, `IQR()` and `range()`. The `summary()` function combines several of these statistics into one function call.

```
summary(df1)
```

```
##           j           ModifiedMortar  UnmodifiedMortar
##  Min.    : 1.00    Min.    :16.35    Min.    :16.62
## 1st Qu.: 3.25    1st Qu.:16.53    1st Qu.:16.90
## Median : 5.50    Median :16.72    Median :17.05
## Mean   : 5.50    Mean   :16.76    Mean   :17.04
## 3rd Qu.: 7.75    3rd Qu.:17.02    3rd Qu.:17.23
## Max.   :10.00    Max.   :17.21    Max.   :17.37
```

The quick and direct approach to examine the existence of the difference between the response of two treatments (groups, levels of a factor) is to use graphs. The most common way is to draw two boxplots for the response values of each treatment.

```
# Transform the dataset from wide layout to long layout
library(reshape2)
df1_L <- stack(df1, select = c("ModifiedMortar", "UnmodifiedMortar"))
colnames(df1_L) <- c("Strength", "Mortar")
# Draw the grouped boxplot
boxplot(Strength ~ Mortar, data = df1_L)
```



R Function of t-tests

```
t.test(x, y = NULL,
       alternative = c("two.sided", "less", "greater"),
       mu = 0, paired = FALSE, var.equal = FALSE,
       conf.level = 0.95, ...)
```

Syntax for different types of the t-test.

Type of t-test	x	y	var.equal	paired
One-sample	Numeric	NULL	—	—
Two-sample (equal variance)	Numeric	Numeric	TRUE	FALSE
Two-sample (unequal variance)	Numeric	Numeric	FALSE	FALSE
Paired	Numeric	Numeric	—	TRUE

One-sample t-test

Suppose the goal is to determine whether the strength of the cement made by the modified Mortar formula is greater than 16.5 or not. Let μ be the population mean of the strength of the cement using modified Mortar formula. The hypothesis is

$$H_0 : \mu = 16.5 \text{ vs. } H_1 : \mu > 16.5$$

Under significance level $\alpha = 0.05$, we perform the one-sample t-test as the following code.

```
t.test(df1$ModifiedMortar, y = NULL,
       alternative = "greater",
       mu = 16.5)

##
##  One Sample t-test
##
## data:  df1$ModifiedMortar
## t = 2.6382, df = 9, p-value = 0.0135
## alternative hypothesis: true mean is greater than 16.5
## 95 percent confidence interval:
##  16.58056      Inf
## sample estimates:
## mean of x
##  16.764
```

The test shows that the p-value is 0.02699 which is less than α , and therefore we reject H_0 . That is, the mean of the population of the strength of the modified Mortar formula is greater than 16.5.

Two-sample t-test for Equal Variance

Let μ_1 be the population mean of the strength of the cement using modified Mortar formula, and μ_2 be the population mean of the strength of the cement using original Mortar formula. The experimenter is investigating on the difference of the strengths between the two Mortar formula, the modified one and the original one. The hypothesis is

$$H_0 : \mu_1 = \mu_2 \text{ vs. } H_1 : \mu_1 \neq \mu_2$$

First, we need to identify the proper type of the two-sample t-test by examining the equality of variances of the two set of the data.

```
cat(sprintf(
  "The std.dev. of the strength data of the modified Mortar is %.4f\n",
  "The std.dev. of the strength data of the original Mortar is %.4f",
  sd(df1$ModifiedMortar), sd(df1$UnmodifiedMortar)
))
```

```
## The std.dev. of the strength data of the modified Mortar is 0.3164
## The std.dev. of the strength data of the original Mortar is 0.2479
```

The standard deviations of these groups seems to be different. We can further check for the equality of variance using F-test. If independent random samples of size n_1 and n_2 are taken from populations 1 and 2, respectively, to test for the equality of variance of two Normal populations, the test statistic for

$$H_{V0} : \sigma_1^2 = \sigma_2^2 \text{ vs. } H_{V1} : \sigma_1^2 \neq \sigma_2^2$$

is the ratio of the sample variances

$$F_0 = \frac{S_1^2}{S_2^2}$$

Under H_{V0} , F_0 follows the F distribution with $n_1 - 1$ numerator degrees of freedom and $n_2 - 1$ denominator degrees of freedom. Given the significance level α , We reject H_{V0} if $F_0 > F_{\alpha/2, n_1-1, n_2-1}$ or if $F_0 < F_{1-\alpha/2, n_1-1, n_2-1}$. In R, we use the function `var.test`.

```
var.test(df1$ModifiedMortar, df1$UnmodifiedMortar,
  alternative = "two.sided")
```

```
##
## F test to compare two variances
##
## data: df1$ModifiedMortar and df1$UnmodifiedMortar
## F = 1.6293, num df = 9, denom df = 9, p-value = 0.4785
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  0.4046845 6.5593806
## sample estimates:
## ratio of variances
##      1.629257
```

The F-test shows a large p-value, 0.4785, and hence, we do not reject H_{V0} . That is, there is no evidence to conclude the variances of the two populations, strength of modified and original Mortar, are different.

Then, we know that we are using two-sample t-test under equal variance setting. For significance level $\alpha = 0.05$, we set `var.equal = TRUE` and perform the two-sample t-test as the following code.

```
t.test(df1$ModifiedMortar, df1$UnmodifiedMortar,
       alternative = "two.sided",
       paired = FALSE, var.equal = TRUE)
```

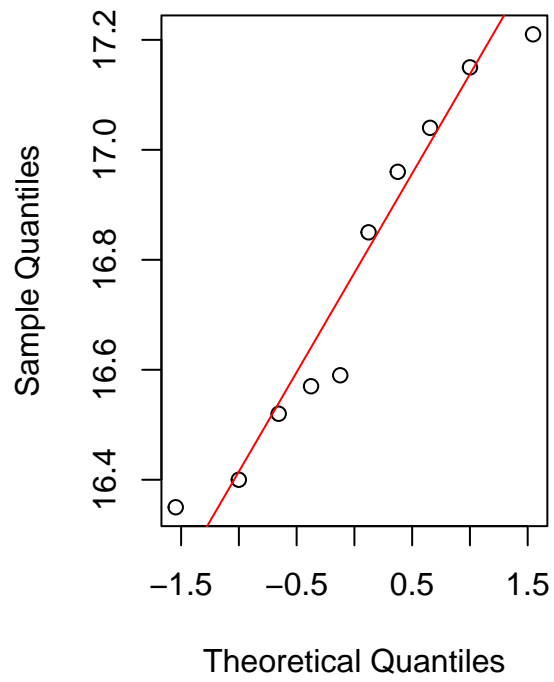
```
##
## Two Sample t-test
##
## data: df1$ModifiedMortar and df1$UnmodifiedMortar
## t = -2.1869, df = 18, p-value = 0.0422
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.54507339 -0.01092661
## sample estimates:
## mean of x mean of y
## 16.764 17.042
```

The test shows that the p-value is 0.0422 which is less than α , and therefore we reject H_0 . That is, the means of the population of the strength of the modified and original Mortar formula are different. The estimated mean strength difference is $\bar{X}_1 - \bar{X}_2 = 16.764 - 17.042 = -0.278$ (`mean(df1$ModifiedMortar) - mena(df1$UnmodifiedMortar)`).

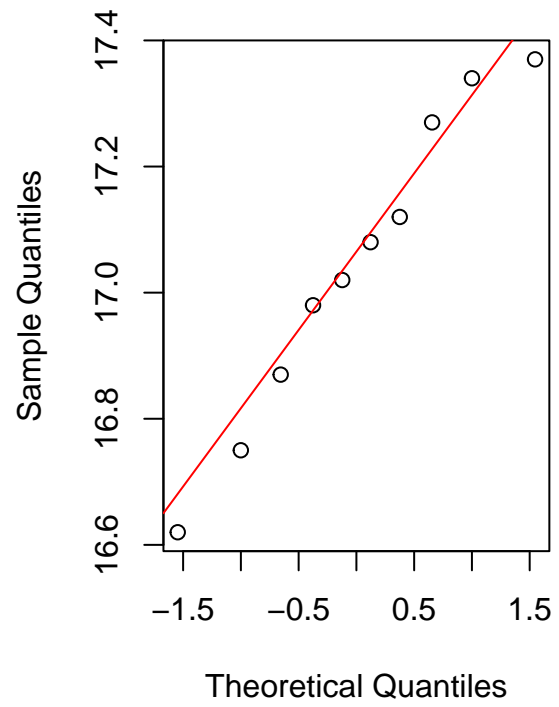
According to the QQ plots, Normality check for the data is passed because, for the observations in each treatment, most of the data points on the QQ plots are closed to the straight line. The equality of variance could be confirmed due to the slopes of the lines on two plots are similar.

```
par(mfrow=c(1,2))
qqnorm(df1$ModifiedMortar, main = "QQ Plot of Modified Mortar")
qqline(df1$ModifiedMortar, col = "red")
qqnorm(df1$UnmodifiedMortar, main = "QQ Plot of Unmodified Mortar")
qqline(df1$UnmodifiedMortar, col = "red")
```

QQ Plot of Modified Mortar



QQ Plot of Unmodified Mortar



Two-sample t-test for Unequal Variances

The dataset in this subsection is collected from an experiment of the use of a fluorescently labeled peptide that assists the identification of the nerves. The response variable is the normalized fluorescence two hours after the injection.

	A	B	C
Observation	Nerve	Muscle	
1	6625	3900	
2	6000	3500	
3	5450	3450	
4	5200	3200	
5	5175	2980	
6	4900	2800	
7	4750	2500	
8	4500	2400	
9	3985	2200	
10	900	1200	
11	450	1150	
12	2800	1130	

Figure 2: Normalized Fluorescence After Two Hours

```
df2 <- data.frame(  
  Observation = 1:12,  
  Nerve = c(  
    6625, 6000, 5450, 5200, 5175, 4900,  
    4750, 4500, 3985, 900, 450, 2800  
  ),  
  Muscle = c(  
    3900, 3500, 3450, 3200, 2980, 2800,  
    2500, 2400, 2200, 1200, 1150, 1130  
  )  
)
```

```
df2 <- read.csv(file.path("data", "2_Fluorescence.csv"))
```

Let μ_1 be the population mean of fluorescence of the nerve, and μ_2 be the population mean of fluorescence of the muscle. To confirm the existence of the difference between the fluorescence of nerve and muscle, the hypothesis is

$$H_0 : \mu_1 = \mu_2 \text{ vs. } H_1 : \mu_1 \neq \mu_2$$

First, we examine the equality of variances of the two set of the data.

```
cat(sprintf(  
  "The std.dev. of the fluorescence of the nerve is %.4f  
  The std.dev. of the fluorescence of the muscle is %.4f",  
  sd(df2$Nerve), sd(df2$Muscle)  
)
```

```
## The std.dev. of the fluorescence of the nerve is 1917.9919  
## The std.dev. of the fluorescence of the muscle is 960.5061
```

The standard deviations are quite different. The inequality of the variance of the two populations is confirmed by the F-test:

$$H_{V0} : \sigma_1^2 = \sigma_2^2 \text{ vs. } H_{V1} : \sigma_1^2 \neq \sigma_2^2$$

where σ_1^2 represents the variance of the population of the fluorescence of the nerve and σ_2^2 represents that of the fluorescence of the muscle.

```
var.test(df2$Nerve, df2$Muscle,
         alternative = "two.sided")
```

```
##
## F test to compare two variances
##
## data: df2$Nerve and df2$Muscle
## F = 3.9874, num df = 11, denom df = 11, p-value = 0.03052
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  1.147892 13.851139
## sample estimates:
## ratio of variances
##           3.987432
```

The F-test reports the p-value being 0.03052 which is less than the significance level $\alpha = 0.05$. Therefore, H_{V0} is rejected and we confirm that the variances of the two populations, fluorescence of the nerve and the muscle, are different.

Then, the two-sample t-test for unequal variance is used. For significance level $\alpha = 0.05$, we set `var.equal = FALSE` and perform the two-sample t-test as the following code.

```
t.test(df2$Nerve, df2$Muscle,
       alternative = "two.sided",
       paired = FALSE, var.equal = FALSE)
```

```
##
## Welch Two Sample t-test
##
## data: df2$Nerve and df2$Muscle
## t = 2.7353, df = 16.191, p-value = 0.01456
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  382.3096 3005.1904
## sample estimates:
## mean of x mean of y
## 4227.917 2534.167
```

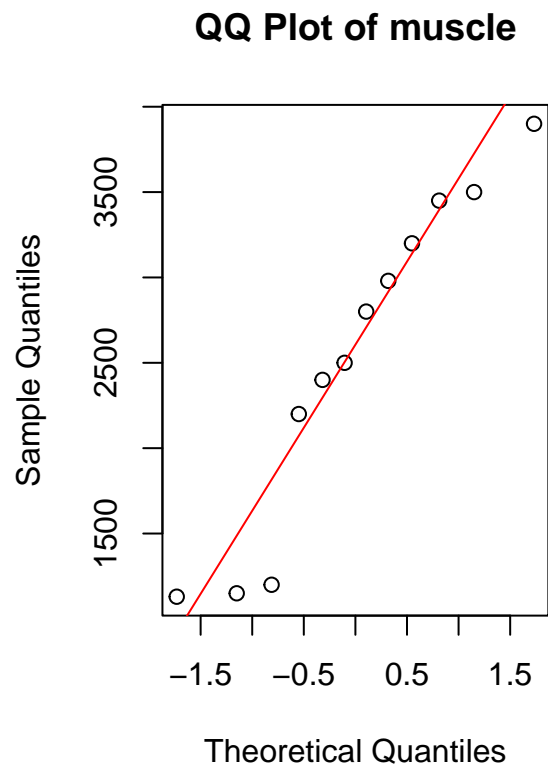
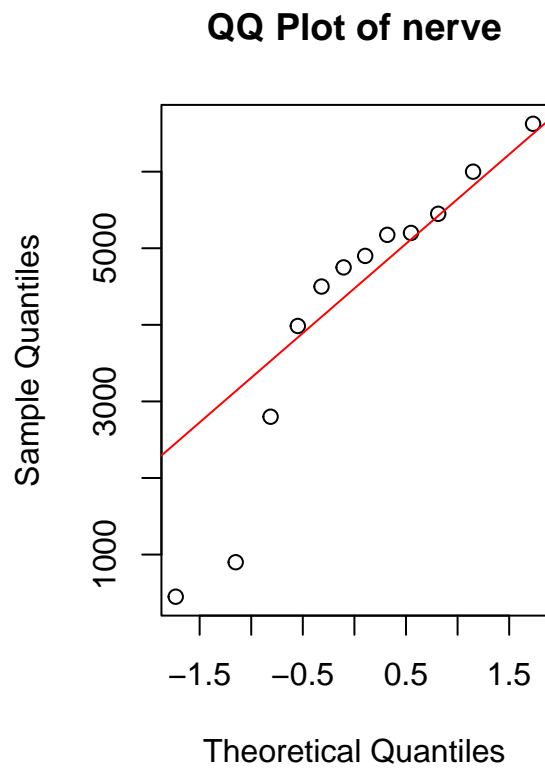
The test shows that the p-value is 0.01456 which is less than α , and therefore we reject H_0 . That is, the means of the population of the fluorescence of the nerve and the muscle are different. The estimated mean fluorescence difference is $\bar{X}_1 - \bar{X}_2 = 4227.9172534.167 = 1693.75$ (`mean(df2$Nerve) - mean(df2$Muscle)`).

According to the QQ plots, Normality check for the data is passed because, for the observations in each treatment, most of the data points on the QQ plots are closed to the straight line. By comparing the two QQ plots, we can also confirm the data in each treatment are of unequal variance by observing different slopes of the straight lines.


```

par(mfrow=c(1,2))
qqnorm(df2$Nerve, main = "QQ Plot of nerve")
qqline(df2$Nerve, col = "red")
qqnorm(df2$Muscle, main = "QQ Plot of muscle")
qqline(df2$Muscle, col = "red")

```



Paired t-test

Two tips are both available to be used on the hardness testing machine and they should produce similar hardness testing results. However, the experimenter now suspect that the measurements made by two tips on the testing machine seems to be different. The dataset in this subsection is the depth measurements of the depression of 10 metal specimens caused by two different tips of the hardness testing machine.

Specimen	Tip1	Tip2
1	7	6
2	3	3
3	3	5
4	4	3
5	8	8
6	3	2
7	2	4
8	9	9
9	5	4
10	4	5

Figure 3: Data for the Hardness Testing Experiment

```
df3 <- data.frame(  
  Specimen = 1:10,  
  Tip1 = c(7, 3, 3, 4, 8, 3, 2, 9, 5, 4),  
  Tip2 = c(6, 3, 5, 3, 8, 2, 4, 9, 4, 5)  
)
```

```
df3 <- read.csv(file.path("data", "2_Hardness.csv"))
```

The goal is to find out is there any difference between the test results made by the two tips. Let μ_1 be the population mean of hardness reading of tip 1, and μ_2 be the population mean of hardness reading of tip 2.

The 10 specimens are expected to be of different hardness due to uncontrolled variables during their manufacturing process. This lack of homogeneity between specimens will contribute to the variability of the hardness measurements and will tend to inflate the experimental error, thus making a true difference between tips harder to detect.

The paired t-test is used to determine whether the difference between two tips is zero or not. By testing on the nonzeroness of the difference, the effect on the hardness caused by the specimens can be neglected. Define $d_j = y_{1j} - y_{2j}$ where y_{ij} is the hardness measurement of the i th specimen and j th tip. The population mean of this difference is denoted by μ_d . The hypothesis of the paired t-test is

$$H_0 : \mu_d = 0 \text{ vs. } H_1 : \mu_d \neq 0$$

For significance level $\alpha = 0.05$, we set `paired = TRUE` and perform the paired t-test as the following code.

```
t.test(df3$Tip1, df3$Tip2,  
  alternative = "two.sided",  
  paired = TRUE)
```

```
##  
## Paired t-test  
##  
## data: df3$Tip1 and df3$Tip2
```

```
## t = -0.26414, df = 9, p-value = 0.7976
## alternative hypothesis: true mean difference is not equal to 0
## 95 percent confidence interval:
##  -0.9564389  0.7564389
## sample estimates:
## mean difference
##          -0.1
```

The test shows that the p-value is 0.7976 which is greater than α , and therefore we do not reject H_0 . That is, there is no evidence to confirm the non-zero mean of the population of the difference between measurements of two tips.

Normality check is needed. I skip the assumption checking process here due to redundancy.