Experimental Statistics for Engineers I

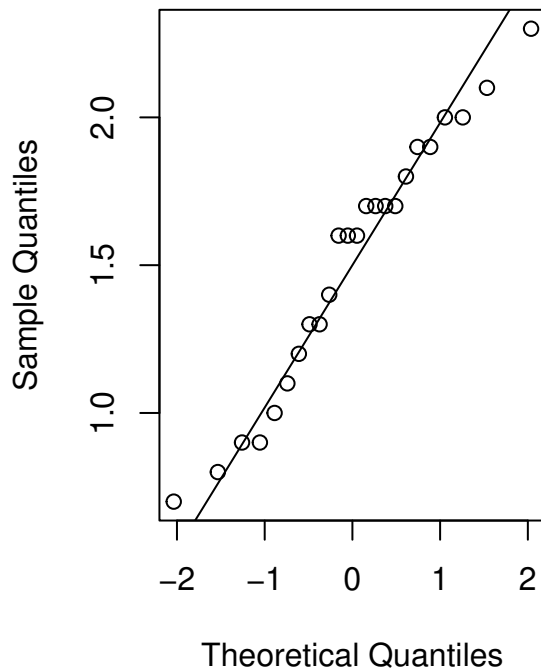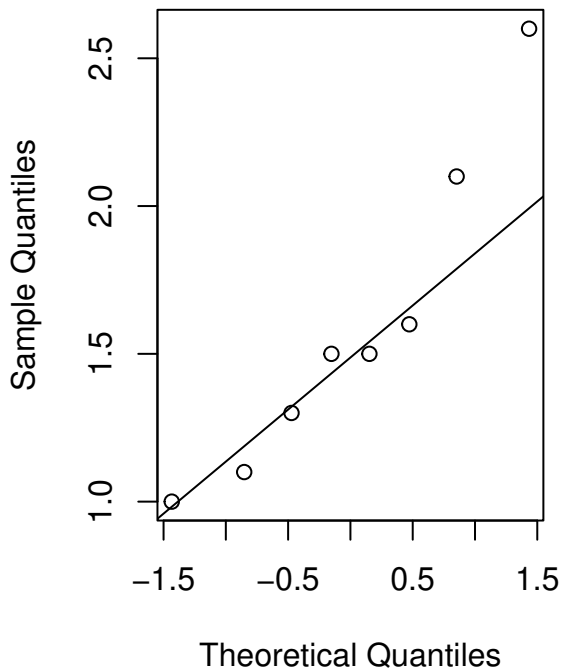Kamala Dadashova

Problem 1:

a) Construct normal probability plots to verify the plausibility of both samples having been selected from normal population distributions.

```
ex23 <- read.csv("ex9-23.csv")
attach(ex23)
par(mfrow=c(1,2))
H<- Extensibility..[1:24]
P<- Extensibility..[25:32]
# check for normality
qqnorm(H)
qqline(H)
qqnorm(P)
qqline(P)
```


We observe that both plots shows sufficient linearity. Thus, it is plausible to say that both samples have been selected from normal population distributions.

b) Construct a comparative boxplot. Does it suggest that there is a difference between true average extensibility for high-quality fabric specimens and that for poor-quality specimens?

```
boxplot(Extensibility..[1:24], Extensibility..[25:32],horizontal=TRUE,
        names=c("High- quality","Poor-quality"),xlab="extensibility",main="Comparative Box Plot for Hig
```

Comparative Box Plot for High Quality and Poor Quality Fabric
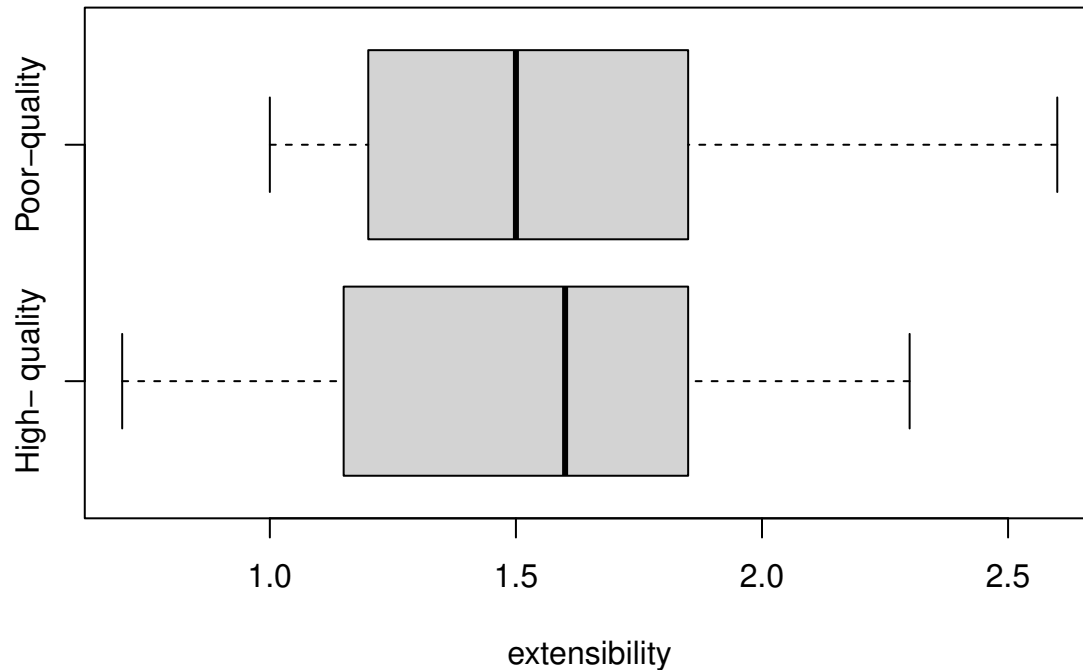
extensibility

The comparative boxplot does not give a difference between average extensibility for the two types of fabrics.

c) The sample mean and standard deviation for the highquality sample are 1.508 and .444, respectively, and those for the poor-quality sample are 1.588 and .530. Use the two-sample t test to decide whether true average extensibility differs for the two types of fabric.

We state our null and alternative hypothesis as follow $H_0 : \mu_1 - \mu_2 = 0$ $H_a : \mu_1 - \mu_2 \neq 0$

We are given $\bar{x}_1 = 1.508$, $\bar{x}_2 = 1.588$, $s_1 = 0.444$, $s_2 = 0.530$. Note that two samples are independent with $n_1 = 24$ and $n_2 = 8$. We also do not know the variances of the underlying distributions of the samples. Note also that we have 32 samples together which indicates that both are less than 40.

```
n1 <- 24
n2 <- 8
s1 <- 0.444
s2 <-0.530
delta <- 1.508-1.5888 #sample mean difference
delta
```

```
## [1] -0.0808
```

```
a1<-s1^2/n1
a2<-s2^2/n2
sd<-sqrt(a1+a2)
sd
```

```
## [1] 0.2081502
```

2

```
df<-(a1+a2)^2/((a1^2/(n1-1))+(a2^2/(n2-1)))
df
```

```
## [1] 10.48354
```

```
t=delta/sd #test statistics
t
```

```
## [1] -0.3881813
```

```
alpha=0.05
#p-test
p.value <- pt(t,df)+pt(-t,df,lower.tail=F)
p.value
```

```
## [1] 0.7056482
```

```
#rejection area
t.alpha <- c(qt(0.025,df),qt(0.975,df))
t.alpha
```

```
## [1] -2.214287  2.214287
```

```
#confidence interval
ci <-delta+t.alpha*sd
ci
```

```
## [1] -0.5417042  0.3801042
```

```
detach(ex23)
```

Since ($p = 0.7056482 > \alpha = 0.005$), rejection area $(-\infty, -2.214287) \cup (2.214287, \infty)$ does not include t statistics -0.3881813, and confidence interval$[-0.5417042, 0.3801042]$ does include mean difference which is zero, we accept H_0. Thus, there is insufficient evidence to claim that the true average extensibility differs for the two types of fabrics.

Problem 2: J.Devore. Problem 26.

We use SAS output. Since $N = 20 < 40$, we use t statistics test. $H_0 : \mu_1 - \mu_2 = 0$, $H_a : \mu_1 - \mu_2 > 0$

```
t=3.6362
df=38
alpha=0.01
p.value <- pt(t,df,lower.tail=F)
p.value
```

```
## [1] 0.0004086498
```

Since p value is less than 0.01 so we reject null hypothesis. According to this result, we might commit type I error.

Problem 3:

  a) Does the data suggest that true average total body bone mineral content during postweaning exceeds that during lactation by more than 25 g? State and test the appropriate hypotheses using a significance level of .05. [Note: The appropriate normal probability plot shows some curvature but not enough to cast substantial doubt on a normality assumption.]
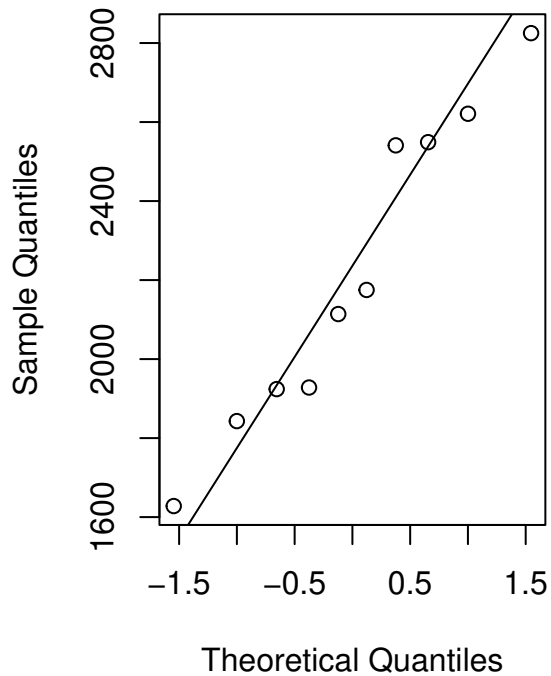
```
ex40 <- read.csv("ex9-40.csv")
attach(ex40)
par(mfrow=c(1,2))
```
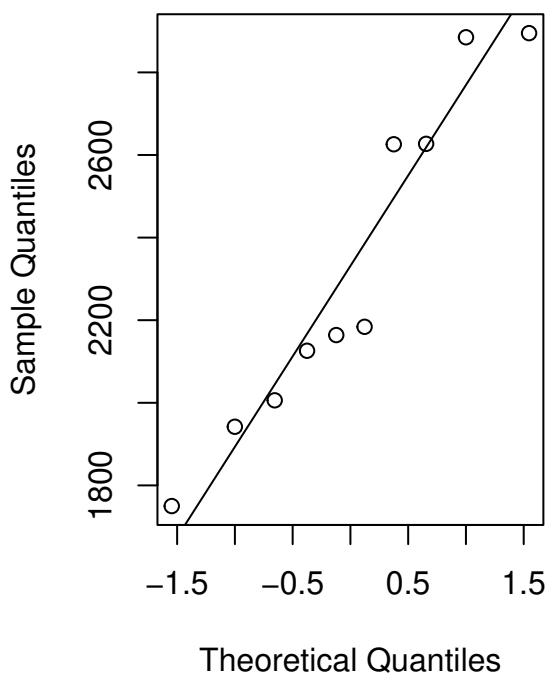
```
L<- TBBMC[1:10]
P<- TBBMC[11:20]
# check for normality
qqnorm(L)
qqline(L)
qqnorm(P)
qqline(P)
```

Normal Q–Q Plot

Normal Q–Q Plot

As we see from plot, data is almost normally distributed. Let us state $H_0 : \mu_1 - \mu_2 \geq 25$ and $H_a : \mu_1 - \mu_2 < 25$. Note that $n_1 = n_2 = n = 10$

```
delta <-TBBMC[1:10]-TBBMC[11:20]
x.bar <- mean(delta)    # calculate sample statistics
s<-sd(delta)
s
```

```
## [1] 103.845
```

```
t <- (x.bar-25)/s*sqrt(10)
t
```

```
## [1] -3.980063
```

```
alpha=0.05
#p-test
p.value <-pt(t,10-1)
p.value
```

```
## [1] 0.001602748
```

```
#rejection area
t.alpha <- c(qt(0.05,10-1))
```

```
t.alpha
```

```
## [1] -1.833113
```

```
#confidence interval
ci <- x.bar-t.alpha*s/sqrt(10)
ci
```

```
## [1] -45.50299
```

```
t.test(TBBMC[1:10],TBBMC[11:20],alternative="less",mu=25,paired=T, conf.level=0.95)
```

```
##
##  Paired t-test
##
## data:  TBBMC[1:10] and TBBMC[11:20]
## t = -3.9801, df = 9, p-value = 0.001603
## alternative hypothesis: true difference in means is less than 25
## 95 percent confidence interval:
##      -Inf -45.50299
## sample estimates:
## mean of the differences
##                 -105.7
```

We reject null hypothesis since $p = 0.001602748 < \alpha = 0.05$, rejection interval $(-\infty, -1.833113)$does include test statistics -3.980063 , confidence interval $(-\infty, -45.50299)$ does not contain mean 25.

   b) Calculate an upper confidence bound using a 95% confidence level for the true average difference between TBBMC during post weaning and during lactation.

We did this in part (a).

   c) Does the (incorrect) use of the two-sample t test to test the hypotheses suggested in (a) lead to the same conclusion that you obtained there? Explain.

```
n1 <- 10
n2 <- 10
s1 <- sd(TBBMC[1:10])
s2 <-sd(TBBMC[11:20])
a1<-s1^2/n1
a2<-s2^2/n2
sd<-sqrt(a1+a2)
sd
```

```
## [1] 179.5411
```

```
df<-(a1+a2)^2/((a1^2/(n1-1))+(a2^2/(n2-1)))
df
```

```
## [1] 17.99011
```

```
t=x.bar/sd #test statistics
t
```

```
## [1] -0.588723
```

```
alpha=0.05
#p-test
p.value <-pt(t,df)
p.value
```

```
## [1] 0.2816834
```
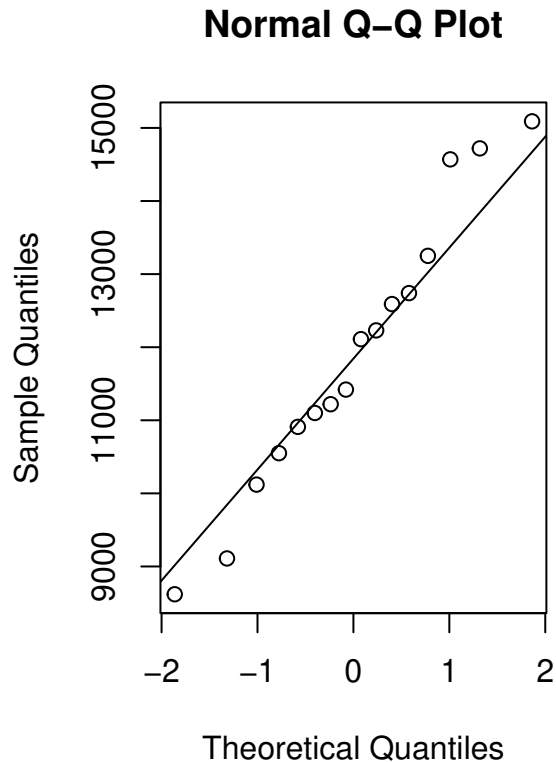```r
#rejection area
t.alpha <- c(qt(0.05,df))
t.alpha
```
```
[1] -1.734115
```
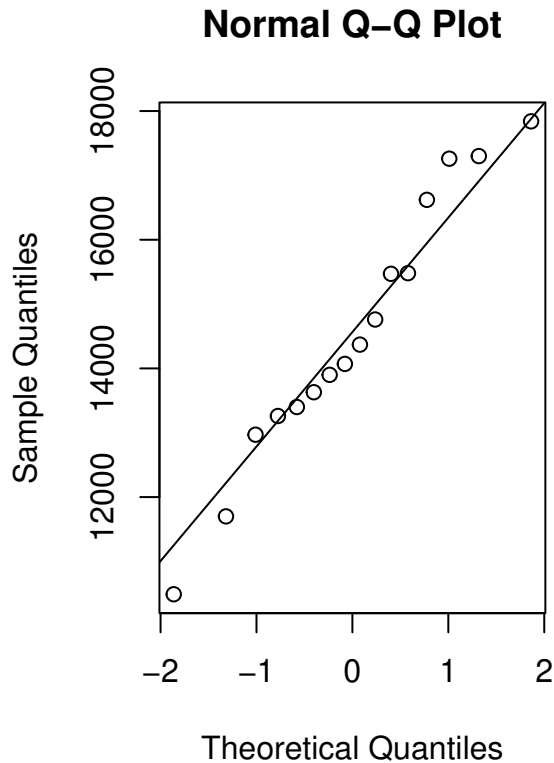```r
#confidence interval
ci <-x.bar-t.alpha*sd
ci
```
```
## [1] 205.645
```
```r
detach(ex40)
```

Here, $p = 0.281634 > \alpha = 0.05$, rejection area $(-\infty, -1.734115)$ does not include t statistic value -0.588723, confidence interval $(-\infty, 205.645)$ does include mean 25, so if we mistakenly do this hypothesis with above method then our result would be accepting null hypothesis.

Problem 4: Calculate and interpret an upper confidence bound for the true average difference between 1 minute modulus and 4 week modulus; first check the plausibility of any necessary assumptions.

```r
ex46 <- read.csv("ex9-46.csv")
attach(ex46)
par(mfrow=c(1,2))
onemin<- elasticity[1:16]
fourmin<- elasticity[17:32]
# check for normality
qqnorm(onemin)
qqline(onemin)
qqnorm(fourmin)
qqline(fourmin)
```

Normal Q–Q Plot

Sample Quantiles / Theoretical Quantiles

Normal Q–Q Plot

Sample Quantiles / Theoretical Quantiles

As we see, both graphs representing a normal distribution. Next, we introduce $H_0 : \mu_2 - \mu_1 = 0$ and $H_a : \mu_2 - \mu_1 \neq 0$. We have two dependent samples with $n = n_1 = n_2 = 16$. So, we will use the following

```
delta <-elasticity[1:16]-elasticity[17:32]
x.bar <- mean(delta)    # calculate sample statistics
s<-sd(delta)
s
```

```
## [1] 508.6448
```

```
t <- (x.bar)*sqrt(16) /s
t
```

```
## [1] 20.72664
```

```
alpha=0.05
p.value <- pt(-t,16-1)+pt(t,16-1,lower.tail=F)    # p-value (two sided)
p.value
```

```
## [1] 1.880121e-12
```

```
t.alpha <- c(qt(0.025,16-1),qt(0.975,16-1)) # rejection region (two sided)
t.alpha
```

```
## [1] -2.13145  2.13145
```

```
ci <- x.bar+t.alpha*s/sqrt(16) # confidence interval (two sided)
ci
```

```
## [1] 2364.587 2906.663
```

Thus, the upper confidence bound for the true average difference bewteen 1 minute and 4 weeks modulus is 2906.663. Also, note that since p values is less than 0.05, rejection area does $(-\infty, -2.13145) \cup (2.13145, \infty)$ does include $t = 20.72664$, and $CI = [2364.587, 2906.663]$ does not include mean zero, we reject null hypothesis.

Problem 5: Recent incidents of food contamination have caused great concern among consumers. The article "How Safe Is That chicken?" (Consumer Reports, Jan. 2010: 19–23) reported that 35 of 80 randomly selected Perdue brand broilers tested positively for either campylobacter or salmonella (or both), the leading bacterial causes of food-borne disease, whereas 66 of 80 Tyson brand broilers tested positive.

a) Does it appear that the true proportion of noncontaminated Perdue broilers differs from that for the Tyson brand? Carry out a test of hypotheses using a significance level .01.

Hypotheses are: $H_0 : p_1 - p_2 = 0$ and $H_1 : p_1 - p_2 \neq 0$. Let p_1 be the proportion of non-contaminated Perdue broilers and p_2 be the proportion of non-contaminated Tyson broilers.

```
p1.hat<-45/80
p2.hat<-14/80
n1<-80
n2<-80
p.hat <- (45+14)/(80+80)
p.hat
```

```
## [1] 0.36875
```

```
z <- (p1.hat-p2.hat)/sqrt(p.hat*(1-p.hat)*(1/80+1/80))   # test statistic
z
```

```
## [1] 5.079664
```

```
p.value=pnorm(-z)+pnorm(z,lower.tail=F)    # p-value
p.value
```

```
## [1] 3.781029e-07
```

```
z.alpha <- qnorm(c(0.005,0.995))    # rejection region
z.alpha
```

```
## [1] -2.575829  2.575829
```

```
ci <- (p1.hat-p2.hat)+z.alpha*sqrt(p.hat*(1-p.hat)*(1/80+1/80)) ci
```

```
## [1] 0.191004 0.583996
```

```
tab <- matrix(0,2,2)    # create table with rows = aspirin, no aspirin, columns = lived, died
tab[1,] <- c(45,80-45)
tab[2,] <- c(14,80-14)
tab
```

```
##      [,1] [,2]
## [1,]   45   35
## [2,]   14   66
```

```
prop.test(tab,alternative="two.sided",conf.level=0.99,correct=F)
```

```
##
##  2-sample test for equality of proportions without continuity
##  correction
##
## data:  tab
## X-squared = 25.803, df = 1, p-value = 3.781e-07
## alternative hypothesis: two.sided
## 99 percent confidence interval:
##  0.2075445 0.5674555
## sample estimates:
```

```
## prop 1 prop 2
## 0.5625 0.1750
```

Since $p = 3.781029e - 07 < \alpha = 0.01$, rejection area $(-\infty, -2.575829) \cup (2.575829, \infty)$ does include $z = 5.079664$, $CI = [0.191004, 0.583996]$ does not include difference of proportion value zero, we reject null hypothesis. So, there is a difference.

   b) If the true proportions of non-contaminated chickens for the Perdue and Tyson brands are .50 and .25, respectively, how likely is it that the null hypothesis of equal proportions will be rejected when a .01 significance level is used and the sample sizes are both 80?

We have $p_1 = 0.5, p_2 = 0.25$.

```
p1=0.5
p2=0.25
n=80
sd=sqrt((p1*(1-p1)/n)+(p2*(1-p2)/n))
p.bar=(n*p1+n*p2)/(n+n)
p.bar
```

```
## [1] 0.375
```

```
q.bar=1-p.bar
z.alpha=-qnorm(0.01/2)
selected.term=z.alpha*sqrt(p.bar*q.bar*((1/80)+(1/80)));
beta=pnorm((selected.term-(p1-p2))/sd)-pnorm((-selected.term-(p1-p2))/sd)
beta
```

```
## [1] 0.237496
```

```
(1-beta)*100
```

```
## [1] 76.2504
```

Thus, there is a 76.25% chance that the null hypothesis of equal proportions will be rejected at a 0.01 significance level.