STAT 641 Fall 2021
Solutions for ASSIGNMENT 8

(P1) (8 pts.)

(S1) Matched pairs - both algorithms are applied to the same problems

(S2) Independent samples - There are two independent random samples, one from inner city schools and the other from suburban schools.

(S3) Matched pairs - Each of the 250 were observed under both stimuli.

(S4) Matched pairs - The two viruses were applied to the same leaf, one half to Virus 1 and the other half to Virus 2.

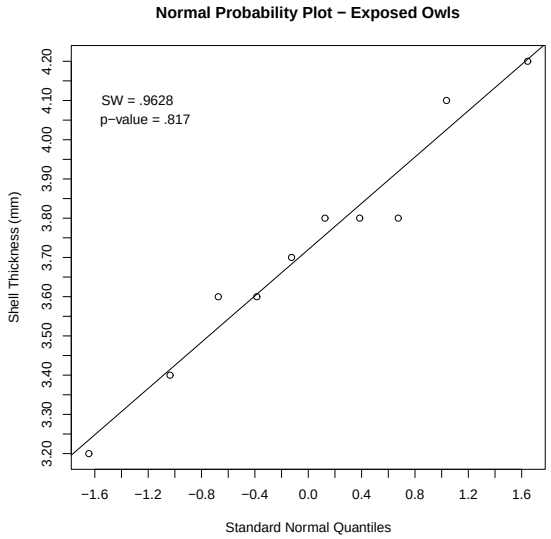
(P2) (8 pts.)

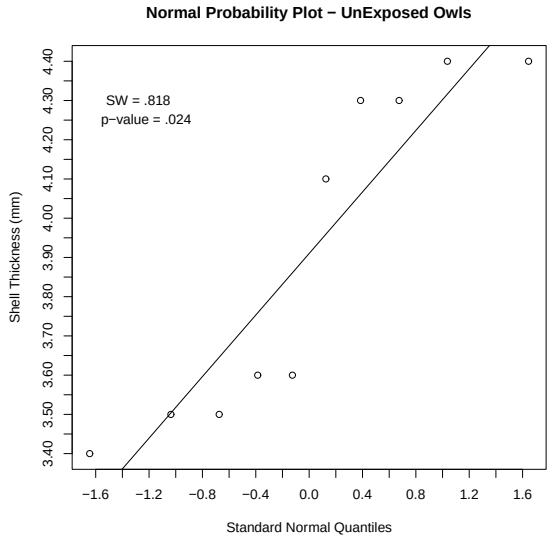
1. Test $H_o : \mu_{exp} \geq \mu_{unexp}$ vs $H_o : \mu_{exp} < \mu_{unexp}$. A separate variance t-test will be implemented because the p-value from the BFL test is .0265 (see part (E) for details) implies there is sufficient evidence to conclude that there is a difference in the two population's variances. From the data, the $C = \frac{(.2974)^2/10}{(.4228)^2/10} = .4948$ and $df = \frac{(.4948+1)^2(10-1)(10-1)}{(.4948)^2(10-1)+(10-1)} = 16.154$

$$t = \frac{3.72 - 3.91}{\sqrt{(.2974)^2/10 + (.4228)^2/10}} = -1.1623 > -1.745 = -t_{.05,16.154} \Rightarrow$$

$$\text{p-value } = P[t_{16.154} \leq -1.1623] = pt(-1.1623, 16.154) = .131$$

with 95% Upper Bound $(-\infty,\ .095)$ $\Rightarrow$ Fail to reject H_o and conclude that there is not significant evidence that the average shell thickness for eggs from PCB exposed owls is less than for unexposed owls. For the t-test to be valid both the exposed and unexposed shell thickness populations would need to have normal distributions. From the exposed data we have that the Shapiro-Wilk's test has p-value=.817 and the unexposed data has p-value =.024 . Thus, we would conclude that the data indicates that the exposed shell thickness have a normal distribution but the unexposed shell thickness do not have a normal distribution. This is confirmed by the following normal reference distribution plots:





Therefore, the p-value for the t-test may not be valid.

2. Because the distribution for the Unexposed shell thicknesses was not a normal distribution, the following calculations are not very reliable:

Let $\Delta = \frac{\mu_{exp}-\mu_{unexp}}{\sigma\sqrt{1/10+1/10}} = \frac{k\sigma}{\sigma\sqrt{2/10}} = k\sqrt{5}$, where k= 0, -.5, -1, -1.5, -2

$$\begin{aligned} P[\text{Type II error at } \mu_{exp}-\mu_{unexp}=k\sigma] &= P[\text{Fail to Reject } H_o \text{ at } \mu_{exp}-\mu_{unexp}=k\sigma] \\ &= P[t_{18,\Delta} > -1.734] \\ &= 1 - pt(-1.734, 18, \Delta] \end{aligned}$$

$\mu_{exp}-\mu_{unexp}$	0	$-.5\sigma$	-1.0σ	-1.5σ	-2.0σ
Δ	0	$-.5\sqrt{5}$	$-1.0\sqrt{5}$	$-1.5\sqrt{5}$	$-2.0\sqrt{5}$
P[Type II Error]	0	.7152	.3064	.0571	.0040

3. Using the normal based procedure with an estimated common variance of

$\hat{\sigma}^2 = \frac{(10-1)(.2974)^2+(10-1)(.4228)^2}{20-1} = (.3655)^2$, even though it is of questionable validity due to the conclusion of unequal variance and lack of normality,

$$m = \left(\frac{3+1}{3}\right)\frac{(\hat{\sigma})^2(Z_\alpha+Z_\beta)^2}{(\delta)^2} = \left(\frac{3+1}{3}\right)\frac{(.3655)^2(1.645+.84)^2}{(.3)^2} = 12.22 \Rightarrow m = 13 \text{ and } n = 3m = 39.$$

4. Using the Wilcoxon Rank Sum test (even though the distributions of the exposed and unexposed egg thicknesses are not in the same family of distributions), we obtain the following ranks:

Exposed	3.6	3.2	3.8	3.6	4.1	3.8	4.2	3.4	3.7	3.8
Ranks	7.5	1.0	12.0	7.5	14.5	12.0	16.0	2.5	10.0	12.0
UnExposed:	4.3	4.4	3.6	3.5	4.4	3.5	3.4	3.6	4.1	4.3
Ranks	17.5	19.5	7.5	4.5	19.5	4.5	2.5	7.5	14.5	17.5

The sum of the ranks for the Exposed owls is $W_1 = 95$, with

$p - value = pwilcox(W_1 - (10)(11)/2, 10, 10) = .2406$ which would imply that there is not sufficient evidence to conclude that the egg thickness for the exposed owls is shifted to the left of the egg thicknesses for the Unexposed owls.

Using the R-function: **wilcox.test(ex,uex,alternative="l",paired=FALSE)** we obtain

```
        Wilcoxon rank sum test with continuity correction
data:  ex and uex
W = 40, p-value = 0.2347
alternative hypothesis: true location shift is less than 0
Warning message:
In wilcox.test.default(ex, uex, alternative = "l", paired = FALSE) :
  cannot compute exact p-value with ties
```

5. There is not a valid test for testing $H_o : \sigma_{exp} \leq \sigma_{unexp}$ versus $H_1 : \sigma_{exp} > \sigma_{unexp}$ because the distribution of the shell thicknesses from the Unexposed owls have a non-normal distribution. We can test $H_o : \sigma_{exp} = \sigma_{unexp}$ versus $H_1 : \sigma_{exp} \neq \sigma_{unexp}$ using the Brown-Forsythe-Levene test (SAS) which yields a p-value of .0265 which would indicate there is sufficient evidence to conclude there is a difference in the variability of the two populations of egg thicknesses.

6. Based on the lack of normality in the data for the unexposed egg thicknesses, the t-test would not appear to be a valid procedure, especially considering the small sample sizes. Therefore, I would be more confident in using the results from the Wilcoxon Rank Sum test, although, the conditions for using this test are not valid either. However, the Wilcoxon Rank Sum test is much more robust against deviations from its conditions than is the t-test.

(P3) (8 pts.) Let $\tilde{\mu}_1$ and $\tilde{\mu}_2$ be the medians of Vitamin B and Placebo groups, respectively.

Test $H_0 : \tilde{\mu}_1 \leq \tilde{\mu}_2$ vs $H_1 : \tilde{\mu}_1 > \tilde{\mu}_2$.

Let $D = VitB - Placebo$. The values of D and the ranks of their magnitudes $|D_i|$ are given below:

Pair	1	2	3	4	5	6	7	8	9	10	11	12
$Y = X_1 - X_2$	6	8	9	5	-7	5	3	3	-12	3	0	1
Rank	7	9	10	5.5	8	5.5	3	3	11	3	*	1

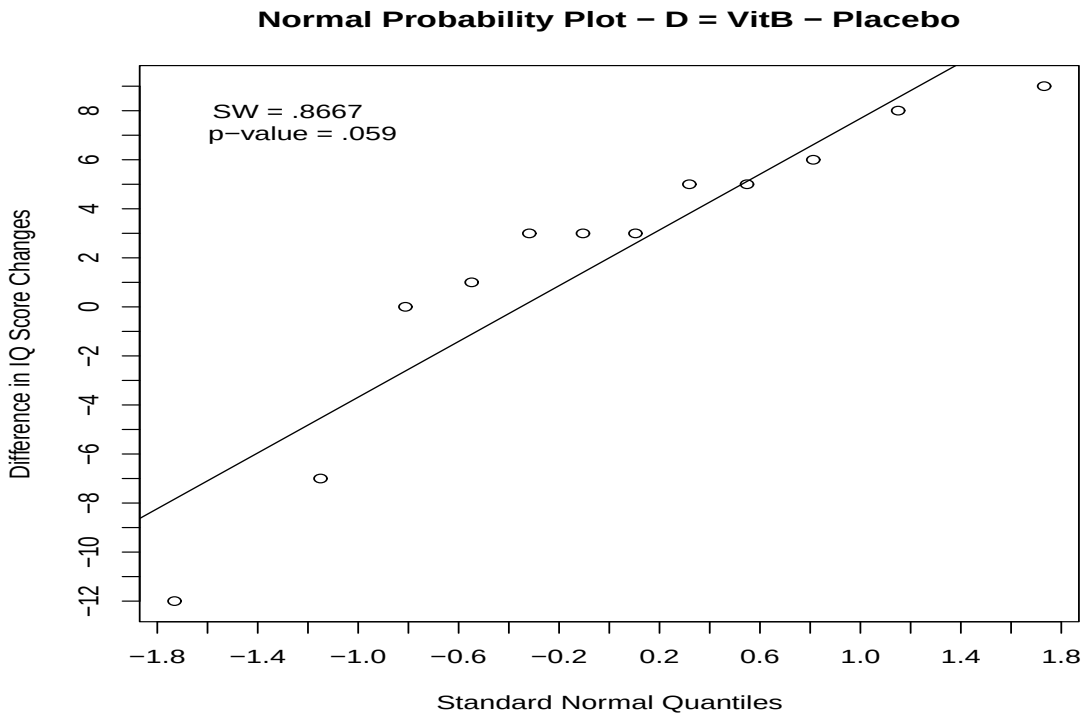
- **t-test:** $t = \frac{\bar{D}}{S_D/\sqrt{12}} = \frac{2}{6.0603/\sqrt{12}} = 1.143$ with $p-value = P[t_{12} \geq 1.143] = 1 - pt(1.143, 12) = .138$.
  Therefore, fail to reject H_o and conclude there is insufficient evidence that the median change in IQ score for the Vitamin B group is larger than the median change in IQ score for the Placebo group.

- **Signed Rank Test:** Let W_+ be sum of the ranks of positive differences.
  Note that the sample size is reduced to $n^* = 12 - 1$ due to one of the pairs having D=0.
  $W_+ = 47$ and $p - value = P[W_+ \geq 47] > P[W_+ \geq 48] = 0.103$ from Table A.10 in Textbook
  $p - value = P[W_+ \geq 47] = psignrank(46, 11, FALSE) = 0.120$ using R-function
  An approximate p–value is obtained using the Central Limit Theorem for W_+:
  $Z = \frac{W_+ - 0.5 - 33}{\sqrt{(11)(23)/2}} \sim N(0,1)$ approximately for large n

  $$p-value = P[W_+ \geq 47] \approx P\left[Z \geq \frac{47 - 0.5 - 33}{\sqrt{(11)(23)/2}}\right] = 1 - pnorm\left(\frac{47 - 0.5 - 33}{\sqrt{(11)(23)/2}}\right) = 1 - pnorm(1.20) = 0.115$$

  The following R code can be used to obtain the same results as above:

```
x = c(14,26,2,4,-5,14,3,-1,1,6,3,4)
y = c(8,18,-7,-1,2,9,0,-4,13,3,3,3)

t.test(x,y,alternative=c("greater"),paired=TRUE)

wilcox.test(x,y,alternative=c("greater"),paired=TRUE)

OUTPUT From R:
        Paired t-test

data:  V and P
t = 1.1432, df = 11, p-value = 0.1386
alternative hypothesis: true difference in means is greater than 0
95 percent confidence interval:
 -1.141826       Inf
sample estimates:
mean of the differences 2


OUTPUT From R:
       Wilcoxon signed rank test with continuity correction

data:  x and y
V = 47, p-value = 0.1144
alternative hypothesis: true location shift is greater than 0
```



- The Wilcoxon Signed Rank test provides a more reliable p-value than the paired t-test because the t-test requires that the differences have a normal distribution. From the normal reference distribution plot of the 12 differences, it would appear that a normal distribution is not a very good fit and the Shapiro-Wilk's test has p-value .059.

(P4) (8 pts.) (1.) Let p_1 be the probability that a Normal patient will have Low Excretions and p_2 be the probability that a Diabetic patient will have Low Excretions. We want to test $H_0 : p_1 = p_2$ vs $H_1 : p_1 \neq p_2$.

(2.) The $E'_{ij}s$ would be given by

$\hat{E}_{11} = (14)(12)/24 = 7,\ \hat{E}_{21} = (14)(12)/24 = 7,\ \hat{E}_{12} = (10)(12)/24 = 5,\ \hat{E}_{22} = (10)(12)/24 = 5$

We could use the Chi-square test because $E_{ij} \geq 5$ for all (i, j).

$$\chi^2 = \sum_{i=1}^{2}\sum_{j=1}^{2}(O_{ij} - \hat{E}_{ij})^2/\hat{E}_{ij} = \frac{(10-7)^2}{7} + \frac{(4-7)^2}{7} + \frac{(2-5)^2}{5} + \frac{(8-5)^2}{5} = 6.171$$

With the two of the four expected values at 5, the Fisher Exact test will also be calculated:

$$p(x_0) = \frac{\binom{12}{x_0}\binom{12}{14-x_0}}{\binom{24}{14}} \quad \Rightarrow \quad p(10) = \frac{\binom{12}{10}\binom{12}{14-10}}{\binom{24}{14}} = dhyper(10, 12, 12, 14) = 0.0167.$$

For the Pearson Chi-squared Test: $p - value = P[\chi^2_1 > 6.171] = 1 = pchisq(6.171, 1) = .013$

For the Fisher Exact Test: p-value=$\sum_{x\in\Omega_0} p(x) = 0.0361$,

where $\Omega_0 = \{x : p(x) \leq p(x_0)\}$ and $p(x) = \frac{\binom{12}{x}\binom{12}{14-x}}{\binom{24}{14}} = dhyper(x, 12, 12, 14)$ for $2 \leq x \leq 12$.

x	2	3	4	5	6	7	8	9	10	11	12
p(x)	0.00003	0.00135	0.01666	0.08884	0.23321	0.31983	0.23321	0.08884	0.01666	0.00135	0.00003

Because of the small values of expected counts and the discrepancies between the two p-values, we will use the values from the Fisher Exact Test:

p-value $= .00003 + .00135 + .01666 + .01666 + .00135 + .00003 = 0.03608 < 0.05$,

Therefore, we reject H_0 and conclude that there is significant evidence (p-value=.036) of a difference in the urinary thromboglobulin excretion between normal and diabetic persons.

(P5) 8 pts.

1. $H_o : p_{1.} = p_{.1}$ vs $H_a : p_{1.} \neq p_{.1}$,

   where $p_{1.}, p_{.1}$ are the probabilities that drug 1 and drug 2 remained anesthetized, respectively.

   Because the data consists of the two responses from the same individual, the McNemar's test statistic is appropriate.

   The Pearson chi-square or Fisher Exact test would be inappropriate due to the correlation in the two responses.

2. $p - value = 2min(P[B \leq n_{12}], P[B \geq n_{12}]) = 2min(P[B \leq 13], P[B \geq 13]) = 2min(.9979, .0106) = .0212$,

   where B has a $Bin(m, .5) = Bin(3 + 13, .5) = Bin(16, .5)$ distribution.

   There is significant evidence (p-value=.0212) of a difference in the two drugs' probabilities that the membrane remained anesthetized.

(P6) 8 pts. Let p_1 = proportion of offspring that are Tall, cut-leaf,

p_2 = proportion of offspring that are Dwarf, cut-leaf,

p_3 = proportion of offspring that are Tall, potato-leaf,

p_4 = proportion of offspring that are Dwarf, potato-leaf.

Test the hypotheses

$H_0 : p_1 = \frac{9}{16}, \;\; p_2 = \frac{3}{16}, \;\; p_3 = \frac{3}{16}, \;\; p_4 = \frac{1}{16}$ vs H_1 : at least one of the p_i's differs from its specified value.

This is a multinomial distribution so we can use the chi-square goodness of fit test from Handout 9 to test the hypotheses as we did for testing the fit of a discrete distribution.

$\widehat{E}_1 = (1611)\left(\frac{9}{16}\right) = 906.1875, \;\; \widehat{E}_2 = \widehat{E}_3 = (1611)\left(\frac{3}{16}\right) = 302.0625, \;\; \widehat{E}_4 = (1611)\left(\frac{1}{16}\right) = 100.6875.$

i. T.S: $\chi^2 = \sum_{i=1}^{4} \frac{(O_i - \widehat{E}_i)^2}{\widehat{E}_i} = \frac{(926-906.1875)^2}{906.1875} + \frac{(293-302.0625)^2}{302.0625} + \frac{(288-302.0625)^2}{302.0625} + \frac{(104-100.6875)^2}{100.6875} = 1.4687$ with df=4-1=3

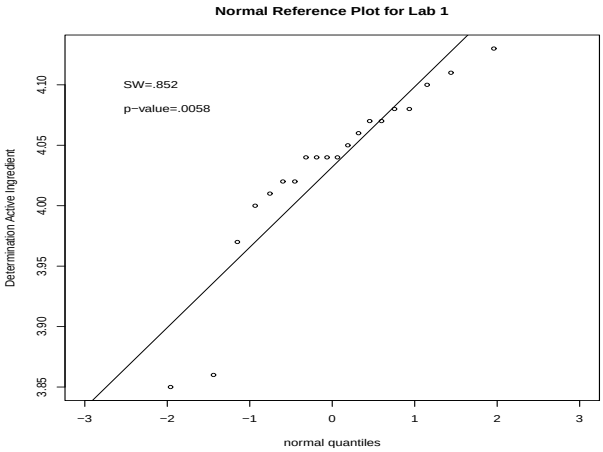
ii. p-value$=Pr(\chi^2_3 \geq 1.4687) = 1 - pchisq(1.4687, 3) = 0.6895 > 0.05 \quad \Rightarrow$ fail to reject H_0.

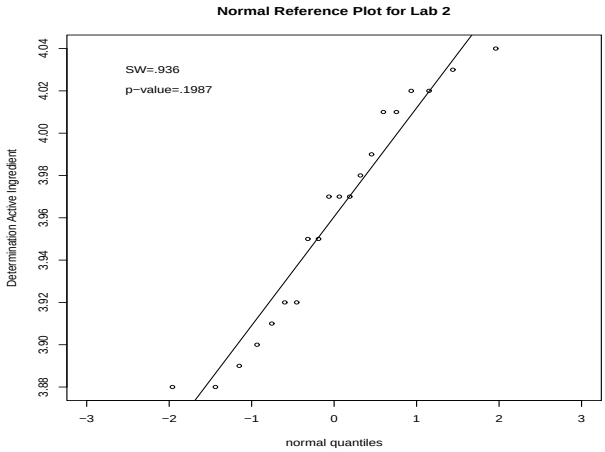
We conclude that there is not significant evidence (p-value=.6895) in the data that the tomato plants deviated from the current theory.

(P7) 14 pts.

1. Lab 1: plotted points are not close to the line and p-value=0.0058 from Shapiro-Wilk which implies that the normal distribution provides a poor fit to the data.

   Lab 2: plotted points are close to the line and p-value=0.1987 from Shapiro-Wilk which implies that the normal distribution provides a good fit to the data





2. $H_0 : \sigma_1^2 = \sigma_2^2$ vs $H_1 : \sigma_1^2 \neq \sigma_2^2$.

   From the data we have $\hat{\sigma}_1^2 = .005133$; $\hat{\sigma}_2^2 = .002752$

   From part 1. we have Lab 1 data has a non-normal distribution and therefore use BFL - test.

```
library(car)
y1 = c(4.13,4.07,4.04,4.07,4.05,4.04,4.02,4.06,4.10,3.86,
                  3.85,4.08,4.11,4.08,4.01,4.02,4.04,3.97,4.00,4.04)
y2 = c(3.88,4.02,4.01,4.01,4.04,3.99,4.03,3.97,3.98,4.02,
                 3.88,3.91,3.95,3.92,3.97,3.92,3.90,3.89,3.97,3.95)
y=c(y1,y2)
grp=as.factor(c(rep(1,20),rep(2,20)))
leveneTest(y, grp, center=median)
p-value=0.799
```

   The BFL test yields p-value=0.799 and hence we would fail to reject H_o.

   Thus, we conclude that there is not significant evidence that the two labs have different levels of variability.

- Note that the positive correlation for the data from Lab 2 found in part 3., would somewhat invalidate this conclusion.

3. Test the hypotheses: H_0 : Data not correlated vs H_1: Data is correlated
   i. $\hat{\rho}_1 = 0.260$ and $\hat{\rho}_2 = 0.313$ which indicates mild positive correlation in the readings from both labs
   ii. Because the data for Lab 1 was determined to be non-normally distributed, a Runs test will be used (see plots on next page)

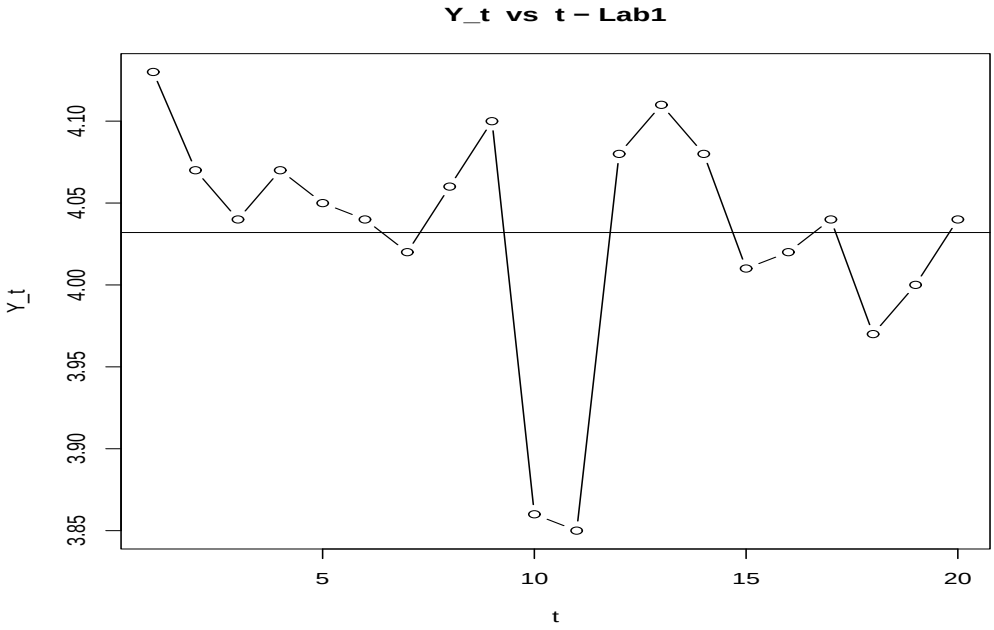
Runs test for Lab 1:
T.S: $r = \#$ of runs $= 9$.
$n_1 = 13,\ n_2 = 7 \quad \Rightarrow \quad$ From Table in Handout 13: $r_L = 5,\ r_U = 15$.
Because $r_L < r < r_U$, fail to reject H_0.

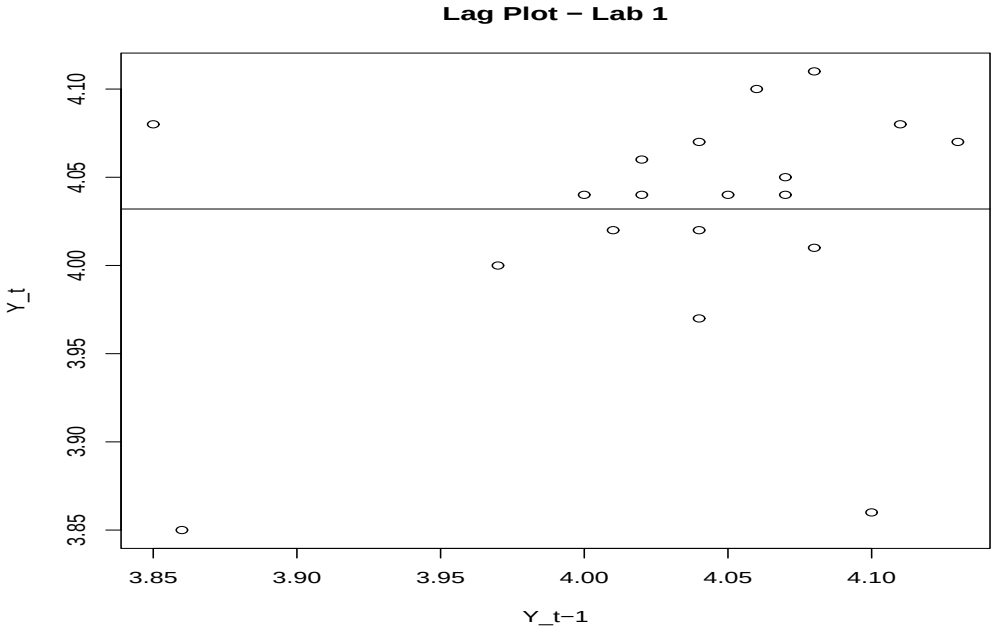
iii. Because there is a strong indication that the data is normally distributed, the von Neumann test will be used to evaluate correlation.
Reject H_o : Data is not correlated if $Q < Q_{P,.05} = 1.368$. From the data $\hat{\rho} = .3126$ and $Q = 1.314 < 1.368$. Conclude that there is sufficient evidence of correlation in the 20 observations from Lab 2.
Alternatively: Runs test for Lab 2:
$r = \#$ of runs $= 7$.
$n_1 = 11,\ n_2 = 9 \quad \Rightarrow \quad$ From Table in Handout 13: $r_L = 6,\ r_U = 16$.
Because $r_L < r < r_U$, fail to reject H_0.
When the data is from a normal distribution, the von Neumann test is more powerful that the Runs test and hence less likely to commit a Type II error.

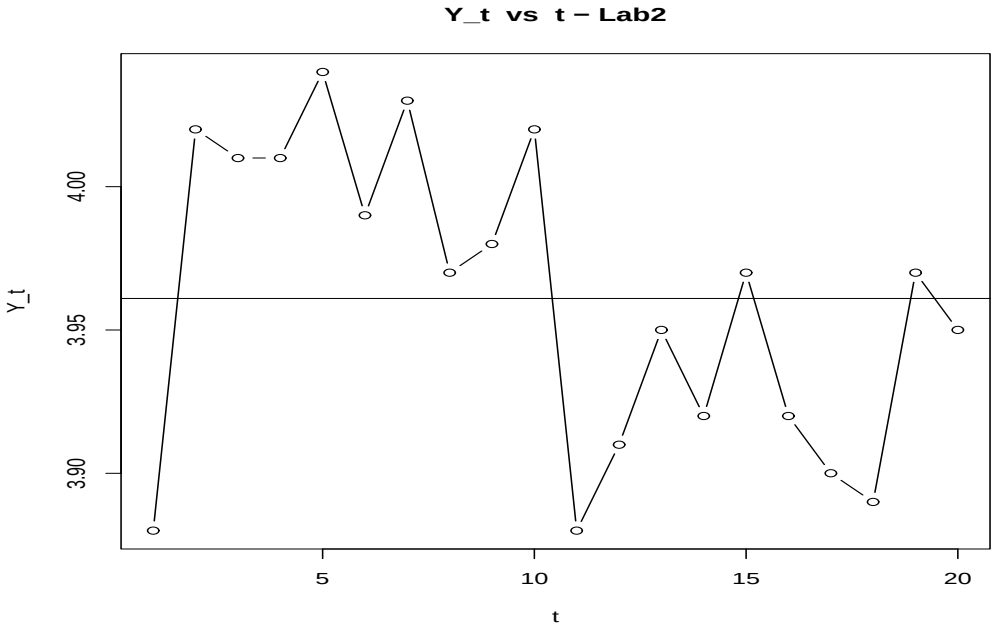
Thus we conclude that there is not significant evidence that the daily determinations within Lab 1 are correlated but there is mild positive correlation in the Lab 2 data.

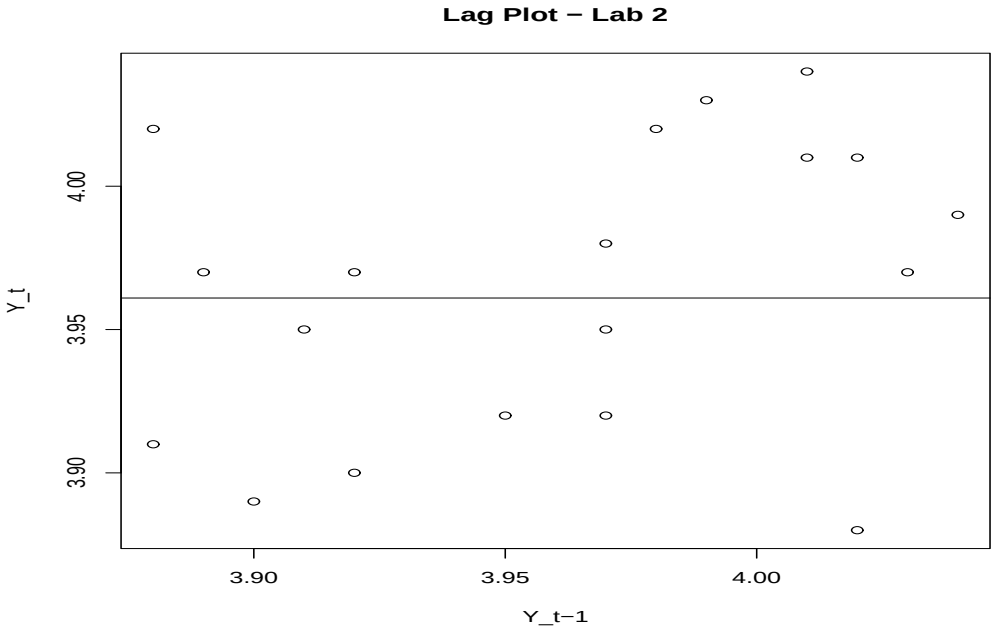
The graphs on the following pages display the plot of the data along with a lag plot. In the lag plot for Lab 1 there is no distinct pattern but a somewhat positive trend appears in the plot for Lab 2.

4. From part 1. we have that Lab 1 data is non-normal distributed and n_1 is relatively small. So, use Wilcoxon Rank sum test.
   i. Let $\tilde{\mu}_1$ and $\tilde{\mu}_2$ be the location parameters of the distributions for Lab 1 and Lab 2, respectively.
   Test: $H_0 : \tilde{\mu}_1 = \tilde{\mu}_2$ vs $H_1 : \tilde{\mu}_1 \neq \tilde{\mu}_2$.
   ii. T.S: Let W_1 and W_2 be sums of ranks from Lab 1 data and Lab 2 data, respectively, $W_1 = 541.5$ and $W_2 = 278.5$.
   iii. p-value$=2Pr(W_1 \geq w_{\max}) = 2Pr(W_1 \geq 541.5) = 2(1 - pwilcox(541 - 210, 20, 20) = .00020 < \alpha = 0.05 \quad \Rightarrow$ reject H_0.
   We conclude there is significant evidence that the two labs have the different average determinations.
   - Note that the positive correlation for the data from Lab 2 would somewhat invalidate this conclusion.


Y_t vs t – Lab1
Y_t
t
3.85
3.90
3.95
4.00
4.05
4.10
5
10
15
20


Lag Plot – Lab 1
Y_t
Y_t−1
3.85
3.90
3.95
4.00
4.05
4.10





5. Because the data from Lab 1 appears non-normal and the sample size, $n_1 = 20$ is small, we could report a distribution-free confidence interval on the medians instead of the mean:

   From Table VII.3 on page 32 in Handout 11, we have that with k=6, a 95.9% C.I. on the median determination is $(X_{(6)},\ X_{(15)})$

   For Lab 1, a 95.9% C.I. on the median determination is (4.02, 4.07)

   Alternatively, we could perform a studentized bootstrap to get an approximate C.I. on the mean. Using the provided code, the resulting interval is (3.98, 4.06)

   For Lab 2, a 95% C.I. based on studentized bootstrap is (3.93, 3.98)

The distribution-free 95.9% C.I. on the median determination for Lab 2 is $(X_{(6)},\ X_{(15)}) = (3.92,\ 4.01)$

(P8) 8 pts. Let p_{ij} be the probability that a randomly selected child has the ith level of Tonsil Size and jth level of Carrier Status.

Test for Independence between Tonsil Size and Carrier Status:

$H_0 : p_{ij} = p_{i\cdot}p_{\cdot j}$ for all pairs (i,j) vs $H_1 : p_{ij} \neq p_{i\cdot}p_{\cdot j}$ for some (i,j)

$$\widehat{E}_{11} = \frac{516)(72)}{1398} = 26.58, \quad \widehat{E}_{12} = \frac{516)(1326)}{1398} = 489.42, \quad \widehat{E}_{21} = \frac{589)(72)}{1398} = 30.33,$$
$$\widehat{E}_{22} = \frac{589)(1326)}{1398} = 558.67, \quad \widehat{E}_{31} = \frac{293)(72)}{1398} = 15.09, \quad \widehat{E}_{32} = \frac{293)(1326)}{1398} = 277.91$$

$\chi^2 = \sum_{i=1}^{3}\sum_{j=1}^{2} \frac{(O_{ij}-\widehat{E}_{ij})^2}{\widehat{E}_{ij}} = 7.885$ with $df = (3-1)(2-1) = 2 \quad \Rightarrow$

p-value=$Pr(\chi^2_2 \geq 7.885) = 1 - pchisq(7.885, 2) = 0.0194 < 0.05 \quad \Rightarrow$ reject H_0.

We thus conclude that there is significant evidence (p-value=.0194) that Tonsil Size and Carrier Status are associated.

(P9) (16 points) Multiple Choice.

MC1 **C** because of the strong positive correlation in the data.

MC2 **D** because $t = \frac{\bar{X}-53}{S/\sqrt{200}} > \frac{\bar{X}-53}{\widehat{SE}(\bar{X})} = t^* \ \Rightarrow\ P[t_{199} \geq t] < P[t_{199} \geq t^*]$

MC3 **C** See HO 12 discussion on the robustness of the test of variances

MC4 **B** Testing $H_o : \sigma \leq 2.5$ vs $H_1 : \sigma > 2.5$. Size of the test is the height of the curve when $\sigma = 2.5$

MC5 **A** P[Type II error at $\sigma = 3.5$] $= 1 - \gamma(3.5) = 1 - .79 = .21$

MC6 **C** With $n = 40,\ \alpha = .01$, Reject H_o when $\frac{(n-1)S^2}{(2.5)^2} \geq \chi^2_{39,.01} = qchisq(.99, 39) = 62.43$

P[Type II error at $\sigma = 2.775$] $= P\left[\frac{(n-1)S^2}{(2.5)^2} < \chi^2_{39,.01} \text{ when } \sigma = 2.775\right] =$

$P\left[\frac{(n-1)S^2}{(2.755)^2} < \frac{(2.5)^2}{(2.775)^2}\chi^2_{39,.01} \text{ when } \sigma = 2.775\right] =$

$P[\chi^2_{39} < \frac{(2.5)^2}{(2.775)^2}62.43] = P[\chi^2_{39} < 50.66] = pchisq(50.66, 39) = .90$

MC7 **B** Using Table A11 from Handout 12, the value of n is 27.
Using the R function:
power.t.test(n=,delta=.2,sd=.4,sig.level=.05,power=.8,type=c("one.sample"),alternative=c("one.sided")), n = 27
Using the formula for the Z-test, $n = \frac{(.4)^2[1.645+.84]^2}{(3-2.8)^2} = 24.7$, thus this simple formula underestimates the necessary sample size. The power using n=25, is .783, whereas, using n=27, the power is .812.

MC8 **B or D** Pairing increases the power of the paired t-test over the independent samples t-test only when there is a strong positive correlation between the responses within each of the n pairs of experimental units.

```
####
#### (2)
####

x_exp <- c(3.6, 3.2, 3.8, 3.6, 4.1, 3.8, 4.2, 3.4, 3.7, 3.8)
x_nexp <- c(4.3, 4.4, 3.6, 3.5, 4.4, 3.5, 3.4, 3.6, 4.1, 4.3)
n <- length(x_exp)

##
## (1)
##

## Are the data Normally distributed? Not the not-exposed data apparently.
shapiro.test(x_exp)
shapiro.test(x_nexp)

## Are the variances equal? BFL test p-value = 0.0265.
library(car)

x_all <- c(x_exp, x_nexp)
grp <- factor(rep(1:2, each = n))

leveneTest(x_all, grp)

## Go ahead and use an unequal-variance t-test.
t.test(x_exp, x_nexp, alt = "less", var.equal = FALSE)

## Compute approximate df for unequal-variance t-test.
s_1 <- sd(x_exp)
s_2 <- sd(x_nexp)
CC <- (s_1 ^ 2 / n) / (s_2 ^ 2 / n)
nu <- ((CC + 1) ^ 2 * (n - 1) * (n - 1)) / (CC ^ 2 * (n - 1) + n - 1)

##
## (2)
##

## Probability of Type II error for pooled t-test
s_p <- sqrt(((n - 1) * var(x_exp) + (n - 1) * var(x_nexp)) / (n + n - 2))
k <- c(0, -0.5, -1, -1.5, -2)
Delta <- k * sqrt(5)

qt(0.05, 18)

## The probability of a Type II error when Delta = 0 is actually 0
for(i in 1:length(k))
  print(1 - pt(-1.734064, 18, Delta[i]))

##
## (3)
##

delta <- -0.3
m <- ((3 + 1) / 3) * (s_p * (qnorm(0.95) + qnorm(0.8)) / delta) ^ 2
```

```
##
## (4)
##

x_all <- c(x_exp, x_nexp)
rk_all <- rank(x_all)
W_1 <- sum(rk_all[1:n])
p_val <- pwilcox(W_1 - n * (n + 1) / 2, n, n)

wilcox.test(x_exp, x_nexp, alt = "less", paired = FALSE)

##
## (5) See above use of 'leveneTest'
##

####
#### (3)
####

x_vit <- c(14, 26, 2, 4, -5, 14, 3, -1, 1, 6, 3, 4)
x_pla <- c(8, 18, -7, -1, 2, 9, 0, -4, 13, 3, 3, 3)
d <- x_vit - x_pla
n <- length(x_vit)

## Paired differences normal?
qqnorm(d); qqline(d)
shapiro.test(d)

## Do both paired T-test and Wilcoxon signed rank test.
t.test(d, alt = "greater")
wilcox.test(x_vit, x_pla, alt = "greater", paired = TRUE)

####
#### (4)
####

## Chi-square test
N <- 24
R_1 <- 14
R_2 <- 10
n_1 <- 12
n_2 <- 12
p_0 <- R_1 / N

O_11 <- 10
O_12 <- 2
O_21 <- 4
O_22 <- 8
E_11 <- n_1 * p_0
E_12 <- n_1 * (1 - p_0)
E_21 <- n_2 * p_0
E_22 <- n_2 * (1 - p_0)
OO <- c(O_11, O_12, O_21, O_22)
```

```
EE <- c(E_11, E_12, E_21, E_22)

chi_sq <- sum((OO - EE) ^ 2 / EE)
p_val <- 1 - pchisq(chi_sq, 1)

## Fisher's Exact test
p_x <- dhyper(0:12, 12, 12, 14)
p_val <- sum(p_x[p_x <= p_x[11]])

M <- matrix(c(O_11, O_21, O_12, O_22), nrow = 2)
fisher.test(M, alternative = "two.sided")

####
#### (5)
####

## McNemar's test
m <- 16
n_12 <- 13
p_val <- 2 * min(1 - pbinom(n_12 - 1, m, 0.5), pbinom(n_12, m, 0.5))

####
#### (6)
####

## Chi-square GOF test for completely specified distribution
OO <- c(926, 293, 288, 104)
N <- sum(OO)
p_0 <- c(9 / 16, 3 / 16, 3 / 16, 1 / 16)
EE <- N * p_0

chi_sq <- sum((OO - EE) ^ 2 / EE)
p_val <- 1 - pchisq(chi_sq, 3)

####
#### (7)
####

x_1 <- c(4.13, 4.07, 4.04, 4.07, 4.05, 4.04, 4.02, 4.06, 4.10, 3.86, 3.85, 4.08, 4.11,
  4.08, 4.01, 4.02, 4.04, 3.97, 4.00, 4.04)
x_2 <- c(3.88, 4.02, 4.01, 4.01, 4.04, 3.99, 4.03, 3.97, 3.98, 4.02, 3.88, 3.91, 3.95,
  3.92, 3.97, 3.92, 3.90, 3.89, 3.97, 3.95)
n <- length(x_1)

##
## (1)
##

## Reference distribution plots
x_1_sort <- sort(x_1)
x_2_sort <- sort(x_2)
u <- (1:n - 0.5) / n
Q <- qnorm(u)
```

```
plot(Q, x_1_sort, xlab = "Normal Quantiles", ylab = "Sample Quantiles", main = "Lab 1")
abline(lm(x_1_sort ~ Q))

plot(Q, x_2_sort, xlab = "Normal Quantiles", ylab = "Sample Quantiles", main = "Lab 2")
abline(lm(x_2_sort ~ Q))

## Shapiro-Wilks tests
shapiro.test(x_1)
shapiro.test(x_2)

##
## (2)
##

require(car)

## BFL test
x <- c(x_1, x_2)
grp <- factor(rep(1:2, each = n))

leveneTest(x, grp, center = median)

##
## (3)
##

## Sample autocorrelation estimates
x_bar_1 <- mean(x_1)
x_bar_2 <- mean(x_2)
rho_1 <- sum((x_1[2:n] - x_bar_1) * (x_1[1:(n - 1)] - x_bar_1)) /
  sum((x_1 - x_bar_1) ^ 2)
rho_2 <- sum((x_2[2:n] - x_bar_2) * (x_2[1:(n - 1)] - x_bar_2)) /
  sum((x_2 - x_bar_2) ^ 2)

## Runs test for Lab 1
x_1_c <- x_1 - x_bar_1
n_1 <- sum(x_1_c > 0)
n_2 <- sum(x_1_c < 0)

numb_runs <- 1
for(j in 2:n) {
  if(sign(x_1_c[j]) != sign(x_1_c[j - 1]))
    numb_runs <- numb_runs + 1
}

## von Neumann test for Lab 2
Q <- (1 / (n - 1)) * sum((x_2[2:n] - x_2[1:(n - 1)]) ^ 2) /
  ((1 / n) * sum((x_2 - x_bar_2) ^ 2))

## Time series plots
x_ts_1 <- ts(x_1, start = 1, frequency = 1)
x_ts_2 <- ts(x_2, start = 1, frequency = 1)
plot.ts(x_ts_1, type = "b", xlab = "t", ylab = "x_t", main = "Lab 1 Time Series Plot")
abline(x_bar_1, 0)
```

```
plot.ts(x_ts_2, type = "b", xlab = "t", ylab = "x_t", main = "Lab 2 Time Series Plot")
abline(x_bar_2, 0)

## Lag plots
plot(x_1[1:(n - 1)], x_1[2:n], xlab = "x_t-1", ylab = "x_t", main = "Lab 1 Lag Plot")
abline(x_bar_1, 0)
plot(x_2[1:(n - 1)], x_2[2:n], xlab = "x_t-1", ylab = "x_t", main = "Lab 2 Lag Plot")
abline(x_bar_2, 0)

##
## (4)
##

## Wilcoxon Rank Sum test
x_all <- c(x_1, x_2)
x_all_r <- rank(x_all)
x_1_r <- x_all_r[1:n]
x_2_r <- x_all_r[(n + 1):(2 * n)]

W_1 <- sum(x_1_r)
W_2 <- sum(x_2_r)
p_val <- 2 * min(1 - pwilcox(W_1 - n * (n + 1) / 2 - 1, n, n),
  pwilcox(W_1 - n * (n + 1) / 2, n, n))

wilcox.test(x_1, x_2, alternative = "t", paired = FALSE)

##
## (5)
##

## Since Lab 1 did not appear to be Normally distributed, could do distribution-free CI
## on median. Alternatively, could do studentized bootstrap CI on mean.
B <- 9999
theta_1 <- mean(x_1)
V_1 <- var(x_1) / n

Z_star <- numeric(B)
for(b in 1:B) {
  x_b <- sample(x_1, replace = TRUE)
  theta_b <- mean(x_b)
  V_b <- var(x_b) / n
  Z_star[b] <- (theta_b - theta_1) / sqrt(V_b)
}
Z_star_o <- sort(Z_star)
theta_1 - sqrt(V_1) * Z_star_o[9750]
theta_1 - sqrt(V_1) * Z_star_o[250]

## Repeat studentized bootstrap on Lab 2.
theta_2 <- mean(x_2)
V_2 <- var(x_2) / n

Z_star <- numeric(B)
for(b in 1:B) {
  x_b <- sample(x_2, replace = TRUE)
```

```
  theta_b <- mean(x_b)
  V_b <- var(x_b) / n
  Z_star[b] <- (theta_b - theta_2) / sqrt(V_b)
}
Z_star_o <- sort(Z_star)
theta_2 - sqrt(V_2) * Z_star_o[9750]
theta_2 - sqrt(V_2) * Z_star_o[250]

####
#### (8)
####

## Chi square test of independence
N <- 1398

O_11 <- 19
O_12 <- 497
O_21 <- 29
O_22 <- 560
O_31 <- 24
O_32 <- 269

n_1_dot <- 516
n_2_dot <- 589
n_3_dot <- 293
n_dot_1 <- 72
n_dot_2 <- 1326
p_i_dot <- c(n_1_dot, n_2_dot, n_3_dot) / N
p_dot_i <- c(n_dot_1, n_dot_2) / N

E_11 <- N * p_i_dot[1] * p_dot_i[1]
E_12 <- N * p_i_dot[1] * p_dot_i[2]
E_21 <- N * p_i_dot[2] * p_dot_i[1]
E_22 <- N * p_i_dot[2] * p_dot_i[2]
E_31 <- N * p_i_dot[3] * p_dot_i[1]
E_32 <- N * p_i_dot[3] * p_dot_i[2]

OO <- c(O_11, O_12, O_21, O_22, O_31, O_32)
EE <- c(E_11, E_12, E_21, E_22, E_31, E_32)
chi_sq <- sum((OO - EE) ^ 2 / EE)
p_val <- 1 - pchisq(chi_sq, 2)

## Using chisq.test()
M <- matrix(c(O_11, O_21, O_31, O_12, O_22, O_32), nrow = 3)
chisq.test(M)
```