

Test #1

Please, write clearly and justify your work to receive credit. If you use R, you need to report the R command you entered with the complete list of parameters. You also need to report the R output that you used to draw your conclusions.

(1) [5Pts] *The following data are the oxygen uptakes (milliliters) during incubation of a random sample of 9 cell suspensions:*

13.1, 12.5, 13.2, 11.2, 13.0, 12.2, 11.1, 13.7, 13.2

(a) *Under the assumption that data are normally distributed, do these data provide sufficient evidence at the 0.01 level of significance that the population mean is not 12 ml? When you solve the problem, you must state the hypothesis testing problem you are solving and justify your conclusion.*

(b) *Find the sample size n that is necessary to achieve 0.90 power of the test at the alternative hypothesis $\mu_1 = 13$. Note: for this problem, assume data are normally distributed with unknown mean and variance given by the sample variance computed in part (a).*

(a) We test $H_0 : \bar{x} \leq 12$ against $H_1 : \bar{x} > 12$ with $\alpha = 0.01$.

From the data: $\bar{x} = 12.578$, $s^2 = 0.839$, $s = 0.916$, $n = 9$.

Test statistic (Student t pdf):

$$t = \frac{\bar{x}_r - x_0}{\sqrt{\frac{s^2}{n}}} = \frac{12.578 - 12.000}{\sqrt{\frac{0.839}{9}}} = 2.819$$

Rejection region: $t > t_{0.01;8} \Rightarrow qt(1 - 0.01, 8) = 2.896$

Conclusion: since $t < t_{0.01;8}$, then H_0 is NOT REJECTED.

R solution

```
> x=c(13.1, 12.5, 13.2, 11.2, 13.0, 12.2, 11.1, 13.7, 13.2)
```

```
> t.test(x,mu=12,alternative="greater" )
```

```
One Sample t-test
```

```
data: x
```

```
t = 1.8918, df = 8, p-value = 0.04758
```

```
alternative hypothesis: true mean is greater than 12
```

```
Conclusion: Since p-value is less than 0.01, then  $H_0$  is NOT REJECTED.
```

(b) $n = \sigma^2 \frac{(z_\alpha + z_\beta)^2}{(\mu_0 - \mu_1)^2} = 0.839 * (z_{0.01} + z_{0.1})^2 = 0.839 * (qnorm(0.99) + qnorm(0.9))^2 = 10.92$

We need at least $n = 11$ samples to achieve 0.90 power of the test at the alternative hypothesis $\mu_1 = 13$

(2) [4Pts] *A study about the effects of reminiscence therapy for older women with depression considers a sample of 10 women residing in an assisted living long-term care facility. For this study, depression was measured by the Geriatric Depression Scale (GDS). Higher scores indicate more severe depression symptoms. The participants received reminiscence therapy. Pre-treatment and posttreatment depression scores are given in the following table.*

Pre-GDS: 12, 10, 16, 2, 12, 18, 11, 16, 16, 10

Post-GDS: 11, 10, 11, 3, 9, 13, 8, 14, 14, 10

Can we conclude that subjects who participate in reminiscence therapy experience, on average, a decline in GDS depression scores? Let $\alpha = 0.01$. When you solve the problem, you must state the hypothesis testing problem you are solving and justify your conclusion.

We apply a Paired t-test. We set $d = x_{pre} - x_{post}$.

We test $H_0 : \mu_d \leq 0$ against $H_1 : \mu_d > 0$ with $\alpha = 0.01$.

Data: $n = 10$, $\bar{d} = \frac{1}{10} \sum_{i=1}^{15} d_i = 2$, $s_d = 2.055$.

Test statistic (Student t pdf):

$$t = \frac{\bar{d} - \mu_d}{s_{\bar{d}}} = \frac{\bar{d} - \mu_d}{s_d/\sqrt{n}} = \frac{2}{\frac{2.055}{\sqrt{10}}} = 3.078$$

Rejection region: $t > t_{0.005;9} = 2.821$

Since $t > t_{0.005;9}$, then H_0 is REJECTED.

R solution

```
> x=c(12, 10, 16, 2, 12, 18, 11, 16, 16, 10)
> y=c(11, 10, 11, 3,9, 13, 8, 14, 14, 10)
> t.test(x,y,alternative = "greater", paired = TRUE,var.equal = TRUE)
```

Paired t-test

data: x and y

```
t = 3.0779, df = 9, p-value = 0.006592
```

```
alternative hypothesis: true mean difference is greater than 0
```

Conclusion: Since p-value is less than 0.01, then H_0 is REJECTED.

(3) [5+2Pts] A study of Marfan syndrome (a genetic disorder affecting connective tissue) reported the following severity scores of patients with no dural ectasia (NO), mild dural ectasia (MI) and marked dural ectasia (MA):

NO : 18, 18, 20, 21, 23, 23, 24, 26, 26, 27, 28, 20, 29, 21, 20, 21, 20, 18

MI : 10, 16, 22, 22, 23, 26, 28, 28, 28, 29, 29, 30, 31, 32, 32, 33, 33, 38, 39, 40, 47

MA : 17, 24, 26, 27, 29, 30, 30, 33, 34, 35, 35, 36, 39

(a) May we conclude, on the basis of these data, that mean severity scores differ among the three populations represented in the study? Use a significance level $\alpha = 0.05$.

(b) If needed, apply the Tukey's HSD procedure to test for significant differences among individual pairs of sample means.

(c)[Extra credit] Verify that normality of the data and homogeneity of the variance are satisfied using appropriate statistical tests.

```
> severity <-c(18, 18, 20, 21, 23, 23, 24, 26, 26, 27, 28, 20, 29, 21, 20, 21, 20, 18, 10,
16, 22, 22, 23, 26, 28, 28, 28, 29, 29, 30, 31, 32, 32, 33, 33,38, 39, 40, 47,17, 24, 26,
27, 29, 30, 30, 33, 34, 35, 35, 36, 39)
> group <-factor(c(rep("NO",len=18),rep("MI",len=21),rep("MA",len=13)))
> Data <- data.frame(severity, group)
> str(Data)
'data.frame': 52 obs. of 2 variables:
 $ severity: num 18 18 20 21 23 23 24 26 26 27 ...
 $ group : Factor w/ 3 levels "MA","MI","NO": 3 3 3 3 3 3 3 3 3 3 ...
```

Alternatively, if data are loaded from the file test1.csv

```
> Data <- read.csv("C:/Users/dlabate/Desktop/Teaching/ma4310/test1.csv")
> Data$group <- factor(Data$group, levels = c(1,2,3),labels = c("NO", "MI","MA"))
> res.aov <- aov(severity ~ group, data = Data)
> str(test1)
'data.frame': 52 obs. of 2 variables:
 $ severity: int 18 18 20 21 23 23 24 26 26 27 ...
 $ group : Factor w/ 3 levels "NO","MI","MA": 1 1 1 1 1 1 1 1 1 1 ...
```

(a)

```
> res.aov <- aov(severity ~ group, data = Data)
> summary(res.aov)
```

	<i>Df</i>	<i>SumSq</i>	<i>MeanSq</i>	<i>Fvalue</i>	<i>Pr(> F)</i>	
<i>group</i>	2	644.1	322.0	7.937	0.00103	**
<i>Residuals</i>	49	1988.0	40.6			

Conclusion: Since p-value is less than 0.05, then H_0 is REJECTED, that is, mean severity scores differ among the three populations.

(b)

```
> TukeyHSD(res.aov)
Tukey multiple comparisons of means
95% family-wise confidence level
```

```
Fit: aov(formula = severity ~ group, data = Data)
```

<i>\$group</i>	<i>diff</i>	<i>lwr</i>	<i>upr</i>	<i>padj</i>
<i>MI - MA</i>	-1.051282	-6.484201	4.381637	0.8867111
<i>NO - MA</i>	-7.995726	-13.599080	-2.392373	0.0032883
<i>NO - MI</i>	-6.944444	-11.889390	-1.999499	0.0038543

Conclusion: only the differences NO-MA and NO-MI are significant but the difference MI-MA is not.

(c)

We test normality first:

```
> aov_residuals <- residuals(object = res.aov)
> shapiro.test(x = aov_residuals)
```

```
Shapiro-Wilk normality test
data: aov_residuals
W = 0.96338, p-value = 0.1097
```

Since the p-value is above 0.05, we can assume normality of the data.

Finally we test homogeneity.

```
> library(car)
> leveneTest(severity ~ group, data = Data)
```

```
Levene's Test for Homogeneity of Variance (center = median)
```

	<i>Df</i>	<i>Fvalue</i>	<i>Pr(> F)</i>
<i>group</i>	2	2.4294	0.09863
	49		

Since the p-value is above 0.05, can assume the homogeneity of variances.