Ma 322: Biostatistics
Solutions to Homework Assignment 8

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Due Friday, March 30th, 2018

Read Chapter 14, “Hypothesis Testing,” pages 240–262 of our text.

1. Following are 14 samples from a normal population with unknown mean and unknown standard deviation:

2.59 2.67 2.16 1.95 2.61 1.11 2.62 2.06 2.06 1.66 2.16 3.35 2.46 2.55

(a) Estimate the mean $\mu$, the standard deviation $\sigma$, and the variance $\sigma^2$ from this sample.
(b) Test the hypothesis $H_0 : \mu = 2.0$, using the significance level $\alpha = 0.05$.
(c) Test the hypothesis $H_0 : \mu \leq 2.0$, using the significance level $\alpha = 0.05$.

Solution: (a) Use the following R code:

```r
x<-c(2.59, 2.67, 2.16, 1.95, 2.61, 1.11, 2.62, 2.06, 2.06, 1.66, 2.16, 3.35, 2.46, 2.55);
mean(x); sd(x); var(x);
```

That yields the values $\mu \approx 2.286429$, $\sigma \approx 0.5342228$, and $\sigma^2 \approx 0.2853940$.

(b) Use the following R code:

```r
x<-c(2.59, 2.67, 2.16, 1.95, 2.61, 1.11, 2.62, 2.06, 2.06, 1.66, 2.16, 3.35, 2.46, 2.55);
t.test(x, mu=2.0)
```

1
That yields the following values: \( p\text{-value} = 0.06611 \), so \textbf{Do not reject} \( H_0 \).

c) Use the following \texttt{R} code:

\[
\begin{align*}
\text{x} &\leftarrow \text{c}(2.59, 2.67, 2.16, 1.95, 2.61, 1.11, 2.62, 2.06, 2.06, \\
&\quad 1.66, 2.16, 3.35, 2.46, 2.55); \\
\text{t.test(x, mu=2.0, alternative="greater")}
\end{align*}
\]

That performs the one-sided test with \( H_A : \mu > 2.0 \) and yields the result \( p\text{-value} = 0.03306 \), so \textbf{Reject} \( H_0 \). \( \square \)

2. Using the sample standard deviation from Exercise 1 and a significance level of \( \alpha = 0.05 \), determine:

(a) The power \( 1 - \beta \) of the \textit{t}-test to reject the two-sided null hypothesis on the mean in Exercise 1b when there is a true difference \( \delta = 0.4 \).

(b) The power \( 1 - \beta \) of the \textit{t}-test to reject the one-sided null hypothesis on the mean in Exercise 1c when there is a true difference \( \delta = 0.4 \).

(c) The number of samples needed to get a power \( 1 - \beta = 99\% \) in the \textit{t}-test of the two-sided null hypothesis on the mean in Exercise 1b when there is a true difference \( \delta = 0.4 \).

(d) The number of samples needed to get a power \( 1 - \beta = 99\% \) in the \textit{t}-test of the one-sided null hypothesis on the mean in Exercise 1c when there is a true difference \( \delta = 0.4 \).

\textbf{Solution:} First enter the data and compute the sample standard deviation:

\[
\begin{align*}
\text{x} &\leftarrow \text{c}(2.59, 2.67, 2.16, 1.95, 2.61, 1.11, 2.62, 2.06, 2.06, \\
&\quad 1.66, 2.16, 3.35, 2.46, 2.55); \\
\text{sd(x)}
\end{align*}
\]

That yields the value \( \text{sd(x)} = 0.5342228 \). Now use \texttt{power.t.test()}:

(a)

\[
\text{power.t.test(n=length(x), sd=sd(x), delta = 0.4, sig.level = 0.05,} \\
\text{power = NULL,} \\
\text{strict=TRUE, type="one.sample", alternative="two.sided"};}
\]

We get the result \( \text{power} = 0.7357849 \).

(b)
power.t.test(n=length(x), sd=sd(x), delta = 0.4, sig.level = 0.05, power = NULL, strict=TRUE, type="one.sample", alternative="one.sided");

We get the result \( \text{power} = 0.8429093 \).

(c)

\[
\text{power.t.test(n=NULL,}
\text{sd=sd(x), delta = 0.4, sig.level = 0.05, power = 0.99,}
\text{strict=TRUE, type="one.sample", alternative="two.sided";)
\]

We get the result \( n = 34.76837 \), so we would take 35 samples.

(d)

\[
\text{power.t.test(n=NULL,}
\text{sd=sd(x), delta = 0.4, sig.level = 0.05, power = 0.99,}
\text{strict=TRUE, type="one.sample", alternative="one.sided";)
\]

We get the result \( n = 29.55045 \), so we would take 30 samples.

3. (a) Using the following data, and assuming that both populations are normal with equal variance, test the null hypothesis that male and female turtles have the same mean serum cholesterol concentrations.

<table>
<thead>
<tr>
<th>Serum cholesterol (mg/100 ml) of turtles.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Male</td>
</tr>
<tr>
<td>Female</td>
</tr>
</tbody>
</table>

(b) The following data were found in Table 1 of C. M. Holcomb, C. G. Jackson, Jr., and M. M. Jackson, “Serum Cholesterol Values in Three Species of Turtles,” J. Wildlife Diseases 8(1972), pp.181–182. <www.jwildlifedis.org/cgi/reprint/8/2/181.pdf>

<table>
<thead>
<tr>
<th>Serum cholesterol (mg/100 ml) in turtles.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Species</td>
</tr>
<tr>
<td>---------</td>
</tr>
<tr>
<td>C. scripta</td>
</tr>
<tr>
<td>T. carolina</td>
</tr>
</tbody>
</table>

Assuming that both populations are normal with equal variance, test the alternative hypothesis that \( T. carolina \) has higher mean serum cholesterol concentrations than \( C. scripta \).
Solution:  (a) Denote the male and female turtle serum cholesterol population means by $\mu_m$ and $\mu_f$. The hypotheses are: $H_0 : \mu_m = \mu_f$ versus $H_A : \mu_m \neq \mu_f$. Test these with a two-tailed two-sample $t$-test. The R commands are:

```r
male <- c(248, 329, 223, 313, 271, 324, 255, 255, 423, 332, 311, 264);
female <- c(341, 311, 362, 371, 419, 366, 246, 273, 312, 331);
t.test(male, female, var.equal=TRUE);
```

The default specification for $H_A$ is `alternative="two.sided"` and need not be invoked in this case. However, we must specify the non-default assumption of equal population variances. The $p$ value is 0.1113, so do not reject the null hypothesis. NOTE: for this experiment, assuming unequal variances and thus using Welch’s approximation gives a $p$ value of 0.1092 from `t.test(male, female)`, so again we would not reject $H_0$.

(b) Denote the two species by subscripts of 1 (for $C.\scriptta$) and 2 (for $T.\ carolina$). The hypotheses are: $H_0 : \mu_1 \geq \mu_2$ versus $H_A : \mu_1 < \mu_2$.

This is a one-tailed, two-sample $t$-test from reduced data. Prepare the test statistic from the given data as follows. Compute the two sample standard deviations from the published standard errors:

$$s_1 = SE_1 \sqrt{n_1} = 119.6; \quad s_2 = SE_2 \sqrt{n_2} = 86.86.$$  

The homoscedasticity assumption allows us to compute the pooled variance using these sample standard deviations:

$$s_p^2 = \frac{\nu_1 s_1^2 + \nu_2 s_2^2}{\nu_1 + \nu_2} = 8825,$$

where $\nu_1 = n_1 - 1 = 7$ and $\nu_2 = n_2 - 1 = 30$. We now use Welch’s approximation to compute the variance of the difference of the means:

$$s_{\bar{X}_1 - \bar{X}_2}^2 = s_p^2 \left( \frac{1}{n_1} + \frac{1}{n_2} \right) = 1388.$$  

Thus $s_{\bar{X}_1 - \bar{X}_2} = \sqrt{s_{\bar{X}_1 - \bar{X}_2}^2} = 37.25$. From this and the two means, we form the difference statistic:

$$t = \frac{\bar{X}_1 - \bar{X}_2}{s_{\bar{X}_1 - \bar{X}_2}} = -1.33.$$  

This negative $t$-statistic allows us to use the area under the lower tail as the one-tailed probability of that value or worse, given $H_0$. There are $\nu = \nu_1 + \nu_2 = n_1 - 1 + n_2 - 1 = 37$ total degrees of freedom, so the $p$-value for a one-tailed test of these hypotheses is given by the cdf $pt(t, \ df=37) \approx 0.095$. Using a significance level $\alpha = 0.05$, we do not reject the null hypothesis.

The R commands are:
n1<-8; n2<-31; nu1<-n1-1; nu2<-n2-1; nu<-nu1+nu2;
SE1 <- 42.3; SE2<-15.6; s1 <- SE1*sqrt(n1); s2<-SE2*sqrt(n2);
s2p <- (nu1*s1**2+nu2*s2**2)/nu; s1; s2; s2p;
s2xbar<-s2p*(1/n1+1/n2); s2xbar; sxbar<-sqrt(s2xbar); sxbar;
m1<-290.0; m2<-339.7; t<-(m1-m2)/sxbar; t; p<- pt( t, df=nu ); p;

Alternatively, generate fake data with the same means and variances with the program faker() on the class website, then use t.test():

source("faker.R") # or cut/paste the function into this console
SE1 <- 42.3; n1 <- 8; s1 <- SE1*sqrt(n1); m1<-290.0;
SE2 <- 15.6; n2 <- 31; s2 <- SE2*sqrt(n2); m2<-339.7;
x1 <- faker(n1, mu=m1, sd=s1); # fake C.scripta data
x2 <- faker(n2, mu=m2, sd=s2); # fake T.carolina data
t.test(x1, x2, var.equal=TRUE, alt="less")

4. Use a paired-sample $t$-test at the 5% significance level to compare the marksmanship of fathers and their daughters, with the hypotheses $H_0$: Fathers and daughters have the same scores, versus $H_A$: they have different scores, using the data in the following table:

<table>
<thead>
<tr>
<th>Team Number</th>
<th>Father</th>
<th>Daughter</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>120</td>
<td>160</td>
</tr>
<tr>
<td>2</td>
<td>155</td>
<td>160</td>
</tr>
<tr>
<td>3</td>
<td>184</td>
<td>158</td>
</tr>
<tr>
<td>4</td>
<td>190</td>
<td>172</td>
</tr>
<tr>
<td>5</td>
<td>125</td>
<td>185</td>
</tr>
<tr>
<td>6</td>
<td>88</td>
<td>134</td>
</tr>
<tr>
<td>7</td>
<td>155</td>
<td>155</td>
</tr>
</tbody>
</table>

**Solution:** First state the hypotheses: $H_0$: Fathers and daughters have the same scores, versus $H_A$: they have different scores.

Use the following R commands:

fathers <-c(120,155,184,190,125, 88,155);
daughters<-c(160,160,158,172,185,134,155);
t.test(fathers,daughters,paired=TRUE)
This yields \( p = 0.2719 \). Thus, do not reject \( H_0 \) at the 0.05 significance level. Conclude that fathers and daughters are about equal marksmen. 

5. For a fair coin, expect a binomial distribution with “heads” probability \( p = 1/2 \). A certain guilder coin is tossed 1100 times and comes up heads just 510 times.

(a) Rosencrantz does not believe that this guilder is a fair coin. Use the experimental data and a significance threshold of \( \alpha = 0.01 \) to test Rosencrantz’s one-sided hypothesis \( H_A \): heads are less likely than tails in a toss of that coin.

(b) Guildenstern does not share Rosencrantz’s suspicions about the coin. Use the experimental data and a significance threshold of \( \alpha = 0.01 \) to test Guildenstern’s two-sided hypothesis \( H_0 \): heads and tails are equally likely in a toss of that coin.

Solution: (a) Rosencrantz’s hypothesis test is one-tailed: \( H_0 : p \geq 1/2 \) versus \( H_A : p < 1/2 \). The R command to perform this test is:

\[
\text{binom.test(x=510,n=1100,p=1/2,alternative="less");}
\]

This yields \( p\text{-value} = 0.0086 \). With significance threshold of \( \alpha = 0.01 \), we therefore reject the null hypothesis in favor of Rosencrantz’s alternative that heads are less likely than tails in a toss of the guilder coin.

(b) Guildenstern’s hypothesis test is two-tailed: \( H_0 : p = 1/2 \) versus \( H_A : p \neq 1/2 \). The R command to perform this test can use the default \( \text{alternative="two.sided"} \):

\[
\text{binom.test(x=510,n=1100,p=1/2)}
\]

This yields \( p\text{-value} = 0.017 \). With significance threshold of \( \alpha = 0.01 \), we therefore do not reject the null hypothesis that heads and tails are equally likely in a toss of the guilder coin.

6. (a) Using the data for Problem 3, part a, test the null hypothesis that male and female turtles have the same serum cholesterol variance.

(b) Using the data for Problem 3, part b, test the alternative hypothesis that \( C. \ scripta \) has a higher serum cholesterol variance than \( T. \ carolina \).

Solution: (a) This is a two-tailed test of the hypotheses \( H_0 \): male and female turtles have the same serum cholesterol variance, versus \( H_A \): male and female turtles have different serum cholesterol variance. It is performed with an \( F \)-test of the variance ratio, all done by the following R commands:
male <-c(248,329,223,313,271,324,255,255,423,332,311,264);
female<-c(341,311,362,371,419,366,246,273,312,331);
var.test(male,female)

This returns p-value = 0.8392, so with a significance threshold of $\alpha = 0.05$ we certainly do not reject $H_0$.

NOTE: the default in `var.test()` is to test the two-sided alternative hypothesis $H_A: \sigma_1 \neq \sigma_2$. For a one-sided $H_A$ such as $H_A: \sigma_1 > \sigma_2$, we would call `var.test( male, female, alternative="greater")`.

(b) This is a one-tailed test of the hypotheses $H_0: \sigma_1 \leq \sigma_2$ (C. scripta has no higher serum cholesterol variance than T. carolina), versus $H_A: \sigma_1 > \sigma_2$ (C. scripta has a higher serum cholesterol variance than T. carolina).

To perform the test, we must construct the $F$ statistic from the reduced data. So, first recover the two sample standard deviations from the published standard errors:

$$s_1 = SE_1 \sqrt{n_1} = 119.6; \quad s_2 = SE_2 \sqrt{n_2} = 86.86.$$ 

Note that $s_1 > s_2$, which is the ordering consistent with $H_A$, so compute the $F$ statistic with the species 1 quantities in the numerator:

$$F = \frac{s_1^2}{s_2^2} = 1.897.$$ 

The numerator degrees of freedom are $\nu_1 = n_1 - 1 = 7$, and the denominator degrees of freedom are $\nu_2 = n_2 - 1 = 30$. The $p$ value for the variance ratio is computed by $pf(F, \nu_1, \nu_2) \approx 0.105$. Since this is greater than the significance threshold $\alpha = 0.05$, do not reject the null hypothesis.

The R commands are:

```r
SE1 <- 42.3; SE2<-15.6; n1<-8; n2<-31; nu1<-n1-1; nu2<-n2-1;
s1 <- n1*SE1**2; s2<-n2*SE2**2; F <- s1/s2; s1; s2; F;
p<-pf(F, df1=nu1, df2=nu2, lower.tail=FALSE); p
```

NOTE: We must specify the non-default lower.tail=FALSE when placing the larger variance in the numerator of the $F$ ratio to perform the one-tailed test $H_A$: numerator $>$ denominator.

NOTE: Perform the two-tailed test, $H_A$: numerator $\neq$ denominator, by using two calls to `pf()`, one with $F$ and one with $1/F$ as the first argument.

Alternatively, generate fake data with the same variances with the program `faker()` on the class website, then use `var.test()`: 7
source("faker.R") # or cut/paste the function into this console
SE1 <- 42.3; n1 <- 8; s1 <- SE1*sqrt(n1); s1 # C.scripta, smaller
SE2 <- 15.6; n2 <- 31; s2 <- SE2*sqrt(n2); s2 # T.carolina, bigger
var.test(faker(n1,sd=s1),faker(n2,sd=s2), alt="greater")

NOTE: the population means are not used by `var.test()`; they are set to 0 by default in the fake data when `faker(n,mu,sd)` is called without specifying `mu`.

7. (a) Use the Mann-Whitney (or Wilcoxon) rank test to compare male and female turtle cholesterol, using the data for Problem 3, part a, without the normality and equivariance assumptions.

(b) Use the Mann-Whitney (or Wilcoxon) rank test to compare the marksmanship of fathers and their daughters, using the data for Problem 4, without the normality and equivariance assumptions.

**Solution:**  (a) First state the hypotheses: $H_0$: male and female turtles have the same serum cholesterol levels, versus $H_A$: they have significantly different serum cholesterol levels.

To apply the Mann-Whitney rank test, use the following R commands:

```r
male <- c(248, 329, 223, 313, 271, 324, 255, 255, 423, 332, 311, 264);
female<-c(341,311,362,371,419,366,246,273,312,331);
wilcox.test(male,female);
```

This gives $p = 0.09907$, so **do not reject** the null hypothesis.

(b) First state the hypotheses: $H_0$: Fathers and daughters have the same scores, versus $H_A$: they have different scores.

Use the following R commands:

```r
fathers <- c(120, 155, 184, 190, 125, 88, 155);
daughters<-c(160,160,158,172,185,134,155);
wilcox.test(fathers,daughters,paired=TRUE);
```

This yields $p=0.2945$. Thus, **do not reject** $H_0$ at the 0.05 significance level. Conclude that fathers and daughters are about equal marksmen.  

\[\square\]
8. (a) Test the hypothesis that nucleotides a,c,g,t are equally likely in the GenBank sequence NM_005369, using the $\chi^2$ goodness-of-fit method. Use significance level $\alpha = 0.01$.

(b) Test the hypothesis that nucleotides a,c,g,t are equally likely in the GenBank sequence NM_005367, using the $\chi^2$ goodness-of-fit method. Use significance level $\alpha = 0.01$.

**Solution:** Use the following R code to install the APE package:

```r
install.packages("ape"); require(ape);
```

The command `install.packages()` and subsequent commands `read.GenBank()` must be executed on an internet-connected computer.

(a) Obtain sequence "NM_005369" and perform the test:

```r
ref<-c("NM_005369"); data<-read.GenBank(ref);
counts<-base.freq(data,freq=TRUE); counts; chisq.test(counts);
```

This finds counts of 1244 As, 639 Cs, 812 Gs, and 1106 Ts, yielding X-squared = 238.397, df = 3, p-value < 2.2e-16, indicating that we should definitely reject the null hypothesis $H_0$: all 4 nucleotides are equally likely, in favor of $H_A$: some of the nucleotides are more likely than others.

(b) Obtain sequence "NM_005367" and perform the test with slightly different function calls:

```r
ref<-c("NM_005367"); data<-read.GenBank(ref, as.character=TRUE);
table(data); chisq.test(table(data));
```

This finds counts of 430 As, 397 Cs, 443 Gs, and 408 Ts, yielding X-squared = 3.1013, df = 3, p-value = 0.3763, so we do not reject the null hypothesis $H_0$: all 4 nucleotides are equally likely.