**BIOS 6611**

**Biostatistical Methods I**

**Self-assessment Homework #6**

1. As a geneticist interested in human populations, you have been studying growth patterns in U.S. males since 1900. A monograph written in 1902 states that the mean height of adult U.S. males is 67.5 inches with a standard deviation (σ) of 3.2 inches. You decide to compare these values with the current measures, and you draw a sample of 100 adult males. You find an average of 69.2 inches and SD (s) of 4.1 inches.
2. Test the hypothesis at the 0.01 level that the current mean height has not changed from the 1902 value, using the 1902 population standard deviation (σ) of 3.2 inches. Apply both the critical value method and the p-value method to draw a conclusion.

Assuming the underlying distribution is symmetric, with n > 30 the CLT applies to the sampling distribution for Xbar

H0: The current mean height of U.S. adult males has not changed since the 1902 value.

H1: The current mean height of U.S. adult males is different than the 1902 value.

Set α = 0.01

Critical value method:

Fail to reject:

p-value method:

Area beyond 5.3125 = 5.407 × 10-8

p-value = 5.407 × 10-8 + 5.407 × 10-8 = 1.0814 × 10-7

Since p = 1.0814 × 10-7 < α = 0.01, we reject H0 in favor of H1.

1. Repeat (a) using the sample s.d. (s) of 4.1 inches.

H0: The current mean height of U.S. adult males has not changed since the 1902 value.

H1: The current mean height of U.S. adult males is different than the 1902 value.

Set α = 0.01

Critical value method:

Fail to reject:

p-value method:

Area beyond 4.146 = 7.140 × 10-7

p-value = 7.140 × 10-7 + 7.140 × 10-7 = 1.42 × 10-6

Since p = 1.42 × 10-6 < α = 0.01, we reject H0 in favor of H1.

1. Repeat (a) and (b) using an *upper* one-sided test. Note: Best practice is to use α/2 so as not to be anti-conservative when using a one-sided test

H0: The current mean height of U.S. adult males has not changed since the 1902 value.

H1: The current mean height of U.S. adult males is different than the 1902 value.

Set α = 0.01

Critical value method using σ:

Fail to reject:

p-value method using σ:

Area beyond 5.3125 = 5.407 × 10-8

p-value = 5.407 × 10-8

Since p = 5.407 × 10-8 < α/2 = 0.005, we reject H0 in favor of H1.

H0: The current mean height of U.S. adult males has not changed since the 1902 value.

H1: The current mean height of U.S. adult males is different than the 1902 value.

Set α = 0.01

Critical value method using s:

Fail to reject:

p-value method using s:

Area beyond 4.146 = 3.574 × 10-5

p-value = 3.574 × 10-5

Since p = 3.574 × 10-5 < α/2 = 0.005, we reject H0 in favor of H1.

d. In this situation, which hypothesis (one-sided or two-sided) seems more appropriate?

The one sided seems more appropriate since it is assumed that the mean height of adult males in the U.S. has not decreased. However, I think it would be best to use the one-sided test with a more conservative significance level, e.g. since that will give the same upper rejection region as the two-sided test. Note: A one-sided test with full alpha is ok, too, but some mention should be made of anti-conservatism of that approach

e. Sometimes investigators would like to apply a one-sided test and to calculate the p-value in the direction of the observed difference.

i. In general, how does the p-value of a one-sided test relate to the p-value of the corresponding two-sided test?

In general the p-value of the one-sided test is lower than the p-value of the two-sided test, making it more likely that the null hypothesis will be rejected. Consequently, a one-sided test is more likely to lead to rejection of the null hypothesis.

ii. In general, which test, one-sided or two-sided, is more likely to lead to rejection (i.e., a significant result) based on a specific level test?

The one-sided test would be more likely to reject the null hypothesis if the same alpha level is used for both tests.

iii. A one-sided test with a specific directional alternative hypothesis should be declared a priori - before ever looking at the data - and should be based on substantive area reasoning.

1. Do you think it is appropriate to allow a result to be declared significant based on p-value < α level, if the observed difference is in the opposite direction of the stated alternative? Why or why not?

No it Is not appropriate since that means that the hypothesis test is being driven by the data and not by the hypothesis itself.

1. What would you expect to happen to the probability of a Type I error if the p-value for a one-sided test were always calculated based on the direction of the observed difference?

Since the test would reject the null hypothesis more often, I would expect the Type I error to be larger than the stated alpha level.

1. Refer back to the Rosner dataset BETACAR.DAT. This dataset was used in Homework 6 Problem 3.
2. Using R code in Lecture 11-12, obtain the 90%, 95% and 99% CI for the mean betacarotene levels of each preparation at Week 12. Assuming unknown variance.

They can read the data into R, obtain, means by group and then write code *like* the code below, or they can use the means they got in SAS and the code below – either way is ok but reading data into R preferred

library(moments)

by(betacart$week12adj,betacart$prep, mean)

by(betacart$week12adj,betacart$prep, sd)

library(base)

# For prep = SOL

sqrtn<- sqrt(6)

t90 <- c(qt(0.05, df = 5), qt(0.95, df = 5))

ci<-117.5 + t90 \* (87.31724/sqrtn)

etc.

b. Look for packages and functions in R that can automatically obtain the CI in (a) above and apply one of them.

t.test(data, conf.level=a) gives a x 100% CI

c. For each preparation, using SAS, test the hypothesis that the mean change in betacarotene is 0 mcg/dl vs. the alternative that the mean change does not equal 0 mcg/dl. Use  = 0.10, 0.05, and 0.01. Summarize your conclusions.

The UNIVARIATE Procedure

Variable: **SOL**

Tests for Location: Mu0=0

Test -Statistic- -----p Value------

Student's t t 3.2962 Pr > |t| 0.0216

Sign M 2 Pr >= |M| 0.2188

Signed Rank S 9.5 Pr >= |S| 0.0625

Variable: **ROCHE**

Tests for Location: Mu0=0

Test -Statistic- -----p Value------

Student's t t 2.59933 Pr > |t| 0.0483

Sign M 2 Pr >= |M| 0.2188

Signed Rank S 9.5 Pr >= |S| 0.0625

Variable: **BASF30**

Tests for Location: Mu0=0

Test -Statistic- -----p Value------

Student's t t 6.601942 Pr > |t| 0.0027

Sign M 2.5 Pr >= |M| 0.0625

Signed Rank S 7.5 Pr >= |S| 0.0625

Variable: **BASF60**

Tests for Location: Mu0=0

Test -Statistic- -----p Value------

Student's t t 3.238475 Pr > |t| 0.0230

Sign M 3 Pr >= |M| 0.0313

Signed Rank S 10.5 Pr >= |S| 0.0313

H0: The mean change in betacarotene is 0 mcg/dl.

H1: The mean change in betacarotene does not equal 0 mcg/dl.

Whether or not we can reject the null hypothesis depends on the preparation we are analyzing and the level we choose to use. The BASF30 preparation has a p-value of 0.0027. With such a low p-value, we can reject the null hypothesis in favor of the alternative hypothesis at α = 0.10, 0.05 or 0.01, since the p-value is less than 0.10, 0.05 and 0.01. Therefore, the result is significant at the 10%, 5% and 1% level.

The SOL, BASF30, and BASF60 have p-values of 0.0216, 0.0483, and 0.0230, respectively. With these p-values we can reject the null hypothesis in favor of the alternative hypothesis at α = 0.10 and 0.05, since all three p-values are less than 0.05. However, unlike with the BASF60 preparation, we cannot reject the null hypothesis at α = 0.01 because all three p-values are > 0.01. Therefore, the result for the SOL, ROCHE30 and ROCHE60 preparations is only significant at the 10% and 5% level.

Code for part c:

\*Bring in the data;

FILENAME betacar 'E:\BIOS 6611\BETACAR.DAT'; \* Location of raw data;

LIBNAME myname 'E:\'; \* Save the data to this directory - on your own thumb drive!;

**DATA** myname.betacar; \* Save the data as a SAS system dataset;

INFILE betacar;

INPUT Preparation Subject FirstBaseline SecondBaseline Week6

Week8 Week10 Week12; \* Read in the raw data;

**RUN**;

\*Create change variable;

**Data** myname.betacar;

set myname.betacar;

Change=Week12-((FirstBaseline+SecondBaseline)/**2**);

**Run**;

\*Label the Preparations and assign change to each;

**DATA** myname.betacar;

SET myname.betacar;

IF Preparation = **1** THEN SOL = Change;

IF Preparation = **2** THEN ROCHE = Change;

IF Preparation = **3** THEN BASF30 = Change;

IF Preparation = **4** THEN BASF60 = Change;

**RUN**;

\*Generate the p-values;

**proc** **univariate** data = myname.betacar;

var SOL ROCHE BASF30 BASF60;

**run**;

d. Relate your conclusions for the hypothesis tests to the respective confidence intervals you obtained in Homework 6 Problem 3.

My conclusions for the above hypothesis tests are in agreement with the confidence intervals created on the previous homework assignment. The confidence intervals calculated previously are presented in the table below.



As can be seen above, only the BASF30 preparation shows a mean change greater than zero for all confidence levels. This is in agreement with the p-value calculated above (0.0027) which is below all levels of α. Additionally, the confidence intervals for the SOL, ROCHE and BASF60 preparations all exclude zero at the 90% and 95% confidence intervals, but include zero at the 99% confidence level. This is also in agreement with the p-value calculated above because all three preparations had p-values < 0.05, but > 0.01.

e. State what the Type I and Type II errors are for these tests and describe the relationship between their respective probabilities of occurring and the various α-levels in (c).

The type I error for these tests is the probability of rejecting the null hypothesis, H0, when it is actually true. So for this test it would be concluding that the mean change of betacarotene is not zero, when in fact it is zero. The probability of type I error is simply the α-level that we decide to use. In contrast, the type II error for these tests is the probability of failing to reject H0, when it is actually false. So for this test it would simply be concluding that the mean change in betacarotene is zero, when in fact it actually is not zero. The probability of type II error is represented by β.

The probability of type I error and type II error are negatively correlated, that is, as type I error (α-level) increases, type II error decreases, and vise versa.