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STATS449/Green

Homework 5

1. 1. McNemar’s test :

Null Hypothesis: **12 =**

Test Statistic = Z^2 = **43.58**

43.58 > Chisq(.95) = **3.84** (critical value)

We reject the null hypothesis at alpha = 0.05. The probability of people agreeing with “Let Patient Die” at the time of the first survey is not equal to the probability of people agreeing with “Suicide” on the second survey.

* 1. Confidence Interval:

p1+ - p+1 +/- 1.96 \* se(p1+ - p+1)

(.71-.65) +/- 1.96 \* 0.0093

**(0.42,0.62)**

The probability of approval was between about 0.43 and 0.62 higher at the first survey than the second. These results are significant as 0 is not in the interval.

1. 2. McNemar’s Z^2 test:

(3-1)^2 / 3 + 1 = **1**

Mantel-Haenszel chi-squared test without continuity

correction

data: x and y and z

Mantel-Haenszel X-squared = **1**, df = 1, p-value =

0.3173

alternative hypothesis: true common odds ratio is not equal to 1

95 percent confidence interval:

0.3120602 28.8405896

sample estimates:

common odds ratio

3

As seen above, the test statistics of McNemar’s test and the Mantel-Haenszel statistic are equal.

Code Used:

z <- gl(8,2)

y <- c(1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,0)

y <- factor(y)

x <- factor(c(1,0,1,0,1,0,1,1,1,1,1,1,0,0,0,1))

mantelhaen.test(x,y,z, correct= F)

* 1. Var(x + y) => var(x) + var(y) + 2cov(x,y) => 1 + 2 + 2(1) = **5**
  2. Var(y – z) => var(y) + var(z) – 2cov(y,z) => 2 + 3 – 2(-1) = **7**
  3. Var(2x + z) => var(2x) + var(z) => 2(var(x)) + var(z) + 2cov(x,z) => 2(1) + 3 + 2(-0.5) = **4**
  4. Null hypothesis: **B2 = B4 = 0**

Test Statistic = **2.7894**

Critical value = **5.99**

P – value = **0.248**

The large p-value leads us to fail to reject the null hypothesis.

* 1. Confidence interval:

B-hat3 – B-hat2 +/- 1.96 \* se(B-hat3 – B-hat2)

1.0047 +/- 1.96 (.062 + (-.160) – 2(.017))

**(.74598,1.26342)**

Code Used:

data <- read.csv("bindat.csv")

View(data)

summary(data)

m1 <- glm(y ~ x1 + x2 + x3 + x4, family= binomial, data = data)

summary(m1)

m0 <- glm(y ~ 1, family= binomial, data= data)

m0 <- glm(y~ x1 + x3, family = binomial, data= data)

anova(m0,m1)

1 - pchisq(2.7894,2)

summary(m1)

m2 <- glm(y ~ x3 + x2, family= binomial, data = data)

summary(m2)

vcov(m2)