

Josh Rhoades

HW4

1.

6.4

Test of children with convulsive disorder

prop.test(c(82, 118), c(200, 200))

2-sample test for equality of proportions with continuity correction

data: c(82, 118) out of c(200, 200)

X-squared = 12.25, df = 1, p-value = 0.0004653

alternative hypothesis: two.sided

95 percent confidence interval:

-0.28139756 -0.07860244

sample estimates:

prop 1 prop 2

0.41059

binom.test(c(82, 118), c(200, 200), p=0.05)

Exact binomial test

data: c(82, 118)

number of successes = 82, number of trials = 200, p-value <

2.2e-16

alternative hypothesis: true probability of success is not equal to 0.05

95 percent confidence interval:

0.3411306 0.4815784

sample estimates:

probability of success

0.41

Test of siblings

prop.test(c(121, 156), c(277, 277), conf.level = 0.9)

2-sample test for equality of proportions with continuity correction

data: c(121, 156) out of c(277, 277)

X-squared = 8.3466, df = 1, p-value = 0.003864

alternative hypothesis: two.sided

90 percent confidence interval:

-0.19928694 -0.05342064

sample estimates:

prop 1 prop 2

0.4368231 0.5631769

binom.test(c(121, 156), c(277, 277), p = 0.1)

Exact binomial test

data: c(121, 156)

number of successes = 121, number of trials = 277, p-value < 2.2e-16

alternative hypothesis: true probability of success is not equal to 0.1

95 percent confidence interval:

0.3775627 0.4974497

sample estimates:

probability of success

0.4368231

6.7

prop.test(c(118, 156), c(200, 277), conf.level = 0.9)

2-sample test for equality of proportions with continuity correction

data: c(118, 156) out of c(200, 277)

X-squared = 0.2409, df = 1, p-value = 0.6236

alternative hypothesis: two.sided

90 percent confidence interval:

-0.05281585 0.10646206

sample estimates:

prop 1 prop 2

0.5900000 0.5631769

> binom.test(c(118, 156), c(200, 277), p = 0.1)

Exact binomial test

data: c(118, 156)

number of successes = 118, number of trials = 274, p-value < 2.2e-16

alternative hypothesis: true probability of success is not equal to 0.1

95 percent confidence interval:

0.3712342 0.4915959

sample estimates:

probability of success

0.4306569

2.

6.17

a.

nonwhite

> binom.test(c(3, 3), c(14, 12), p=0.05)

Exact binomial test

data: c(3, 3)

number of successes = 3, number of trials = 6, p-value = 0.00223

alternative hypothesis: true probability of success is not equal to 0.05

95 percent confidence interval:

0.1181172 0.8818828

sample estimates:

probability of success

0.5

married

> binom.test(c(8, 10), c(49, 56), p=0.05)

Exact binomial test

data: c(8, 10)

number of successes = 8, number of trials = 18, p-value = 1.086e-06

alternative hypothesis: true probability of success is not equal to 0.05

95 percent confidence interval:

0.2153015 0.6924283

sample estimates:

probability of success

0.4444444

15-29

> binom.test(c(5, 33), c(12, 90), p=0.05)

Exact binomial test

data: c(5, 33)

number of successes = 5, number of trials = 38, p-value = 0.03973

alternative hypothesis: true probability of success is not equal to 0.05

95 percent confidence interval:

0.04413744 0.28086385

sample estimates:

probability of success
0.1315789

b.

```
nonwhite
> (3/14)/(3/12)
[1] 0.8571429
married
> (8/49)/(10/56)
[1] 0.9142857
15-29
> (5/12)/(33/90)
[1] 1.136364
```

c.

```
nonwhite
prop.test(c(3, 3), c(11, 9), conf.level = 0.9)
2-sample test for equality of proportions with continuity
correction
data: c(3, 3) out of c(11, 9)
X-squared = 0, df = 1, p-value = 1
alternative hypothesis: two.sided
90 percent confidence interval:
-0.4611955 0.3399834
sample estimates:
prop 1 prop 2
0.2727273 0.3333333
Warning message:
In prop.test(c(3, 3), c(11, 9), conf.level = 0.9) :
Chi-squared approximation may be incorrect
married
> prop.test(c(8, 10), c(41, 46), conf.level = 0.9)
2-sample test for equality of proportions with continuity
correction
data: c(8, 10) out of c(41, 46)
X-squared = 0, df = 1, p-value = 1
alternative hypothesis: two.sided
90 percent confidence interval:
-0.1872624 0.1427237
sample estimates:
prop 1 prop 2
0.1951220 0.2173913
15-29
> prop.test(c(5, 33), c(7, 57), conf.level = 0.9)
2-sample test for equality of proportions with continuity
correction
data: c(5, 33) out of c(7, 57)
X-squared = 0.0786, df = 1, p-value = 0.7792
alternative hypothesis: two.sided
90 percent confidence interval:
-0.2456102 0.5162869
sample estimates:
prop 1 prop 2
0.7142857 0.5789474
Warning message:
In prop.test(c(5, 33), c(7, 57), conf.level = 0.9) :
Chi-squared approximation may be incorrect
3.
tree<-read.table('treedata.txt', header=T)
a.
```

```
table(tree$SPP,tree$y)
```

```
0 1
```

```
A 130 306
```

```
PB 407 90
```

b.

```
treereg<-glm(SPP~y, family=binomial,data=tree)
> treereg
Call: glm(formula = SPP ~ y, family = binomial, data = tree)
Coefficients:
(Intercept)          y
      1.141      -2.365
Degrees of Freedom: 932 Total (i.e. Null); 931 Residual
Null Deviance: 1289
Residual Deviance: 1019 AIC: 1023
summary(treereg)
Call:
glm(formula = SPP ~ y, family = binomial, data = tree)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.6843 -0.7181  0.7446  0.7446  1.7214
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.1413    0.1007   11.33  <2e-16 ***
y           -2.3651    0.1566  -15.10  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
Null deviance: 1289.4 on 932 degrees of freedom
Residual deviance: 1018.9 on 931 degrees of freedom
AIC: 1022.9
Number of Fisher Scoring iterations: 4
4.
a.
> ((130/436)/(1-(130/436)))/((407/497)/(1-(407/497)))
[1] 0.09394421
b.
ln(((130/436)/(1-(130/436)))/((407/497)/(1-(407/497))))
+1.96(((1/130)+(1/306)+(1/407)+(1/90))^-1)
-2.36505418354759 + 79.9073885869975776 =
77.5423344034499876
-2.36505418354759 - 79.9073885869975776 =
-82.2724427705451676
95% CI is 77.5423344034499876 to -82.2724427705451676
c.
((1/130+1/306 + 1/407 + 1/90))^-1
[1] 40.76908
The standard error is much different.
5.
a.
admit<-read.csv('admitdata.csv', header=T)
> admitgpa.glm<-
glm(factor(gpa)~factor(admit),family=binomial,data=admit)
> admitgpa.glm
Call: glm(formula = factor(gpa) ~ factor(admit), family =
binomial,
data = admit)
Coefficients:
(Intercept) factor(admit)1
```

```

5.606      16.960
Degrees of Freedom: 399 Total (i.e. Null); 398 Residual
Null Deviance: 13.98
Residual Deviance: 13.22 AIC: 17.22
> summary(admitgpa.glm)
Call:
glm(formula = factor(gpa) ~ factor(admit), family = binomial,
     data = admit)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.3495  0.0000  0.0857  0.0857  0.0857
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)    5.606     1.002  5.596 2.2e-08 ***
factor(admit)1 16.960    4276.716  0.004  0.997
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
Null deviance: 13.980 on 399 degrees of freedom
Residual deviance: 13.215 on 398 degrees of freedom
AIC: 17.215
Number of Fisher Scoring iterations: 21
admitgre.glm<-
glm(factor(gre)~factor(admit),family=binomial,data=admit)
> admitgre.glm
Call: glm(formula = factor(gre) ~ factor(admit), family =
binomial,
          data = admit)
Coefficients:
(Intercept) factor(admit)1
    5.606      16.960
Degrees of Freedom: 399 Total (i.e. Null); 398 Residual
Null Deviance: 13.98
Residual Deviance: 13.22 AIC: 17.22
> summary(admitgre.glm)
Call:
glm(formula = factor(gre) ~ factor(admit), family = binomial,
     data = admit)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.3495  0.0000  0.0857  0.0857  0.0857
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)    5.606     1.002  5.596 2.2e-08 ***
factor(admit)1 16.960    4276.716  0.004  0.997
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
Null deviance: 13.980 on 399 degrees of freedom
Residual deviance: 13.215 on 398 degrees of freedom
AIC: 17.215
Number of Fisher Scoring iterations: 21

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```

            Estimate Std. Error z value Pr(>|z|)
(Intercept)    5.606     1.002  5.596 2.2e-08 ***
factor(admit)1 16.960    4276.716  0.004  0.997
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
Null deviance: 13.980 on 399 degrees of freedom
Residual deviance: 13.215 on 398 degrees of freedom
AIC: 17.215
Number of Fisher Scoring iterations: 21
b.
admitboth.glm<-glm(factor(gre +
gpa)~factor(admit),family=binomial,data=admit)
admitboth.glm
Call: glm(formula = factor(gre + gpa) ~ factor(admit), family =
binomial,
          data = admit)
Coefficients:
(Intercept) factor(admit)1
    5.606      16.960
Degrees of Freedom: 399 Total (i.e. Null); 398 Residual
Null Deviance: 13.98
Residual Deviance: 13.22 AIC: 17.22
summary(admitboth.glm)
Call:
glm(formula = factor(gre + gpa) ~ factor(admit), family =
binomial,
     data = admit)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.3495  0.0000  0.0857  0.0857  0.0857
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)    5.606     1.002  5.596 2.2e-08 ***
factor(admit)1 16.960    4276.716  0.004  0.997
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
Null deviance: 13.980 on 399 degrees of freedom
Residual deviance: 13.215 on 398 degrees of freedom
AIC: 17.215
Number of Fisher Scoring iterations: 21

```