Josh Rhoades	alternative hypothesis: two.sided
HW4	90 percent confidence interval:
1.	-0.05281585 0.10646206
6.4	sample estimates:
Test of children with convulsive disorder	prop 1 prop 2
prop.test(c(82, 118), c(200, 200))	0.5900000 0.5631769
2-sample test for equality of proportions with continuity	> binom.test(c(118, 156), c(200, 277), p = 0.1)
correction	Exact binomial test
data: c(82, 118) out of c(200, 200)	data: c(118, 156)
X-squared = 12.25, df = 1, p-value = 0.0004653	number of successes = 118, number of trials = 274, p-value <
alternative hypothesis: two.sided	2.2e-16
95 percent confidence interval:	alternative hypothesis: true probability of success is not equal
-0.28139756 -0.07860244	to 0.1
sample estimates:	95 percent confidence interval:
prop 1 prop 2	0.3712342 0.4915959
0.410.59	sample estimates:
binom.test(c(82, 118), c(200, 200), p=0.05)	probability of success
Exact binomial test	0.4306569
data: c(82, 118)	2.
number of successes = 82, number of trials = 200, p-value <	6.17
2.2e-16	a.
alternative hypothesis: true probability of success is not equal	
to 0.05	> binom.test(c(3, 3), c(14, 12), p=0.05)
95 percent confidence interval:	Exact binomial test
0.3411306 0.4815784	data: c(3, 3)
sample estimates:	number of successes = 3, number of trials = 6, p-value =
probability of success	0.00223
0.41	alternative hypothesis: true probability of success is not equal
Test of siblings	to 0.05
prop.test(c(121, 156), c(277, 277), conf.level = 0.9)	95 percent confidence interval:
2-sample test for equality of proportions with continuity	0.1181172 0.8818828
correction	sample estimates:
data: c(121, 156) out of c(277, 277)	probability of success
X-squared = 8.3466, df = 1, p-value = 0.003864	0.5
alternative hypothesis: two.sided	married
90 percent confidence interval:	> binom.test(c(8, 10), c(49, 56), p=0.05)
-0.19928694 -0.05342064	Exact binomial test
-0.19926094 -0.05342004 sample estimates:	
•	data: c(8, 10)
prop 1 prop 2 0.4368231 0.5631769	number of successes = 8, number of trials = 18, p-value = 1.086e-06
binom.test(c(121, 156), c(277, 277), p = 0.1)	alternative hypothesis: true probability of success is not equal
Exact binomial test	to 0.05
data: c(121, 156)	95 percent confidence interval:
number of successes = 121, number of trials = 277, p-value < 2.26, 16	
2.2e-16	sample estimates:
alternative hypothesis: true probability of success is not equal	
to 0.1	0.4444444
95 percent confidence interval:	15-29
0.3775627 0.4974497	> binom.test(c(5, 33), c(12, 90), p=0.05)
sample estimates:	Exact binomial test
probability of success	data: c(5, 33)
0.4368231	number of successes = 5, number of trials = 38, p-value =
6.7	0.03973
prop.test(c(118, 156), c(200, 277), conf.level = 0.9)	alternative hypothesis: true probability of success is not equal
2-sample test for equality of proportions with continuity	to 0.05
correction	95 percent confidence interval:
data: c(118, 156) out of c(200, 277)	0.04413744 0.28086385
X-squared = 0.2409, df = 1, p-value = 0.6236	sample estimates:

```
probability of success
                                                             table(tree$SPP,tree$y)
       0.1315789
                                                                 0 1
                                                              A 130 306
b.
nonwhite
                                                              PB 407 90
> (3/14)/(3/12)
[1] 0.8571429
                                                             treereg<-glm(SPP~y, family=binomial,data=tree)
married
                                                             > treereg
                                                             Call: glm(formula = SPP \sim y, family = binomial, data = tree)
> (8/49)/(10/56)
[1] 0.9142857
                                                             Coefficients:
15-29
                                                             (Intercept)
                                                                          -2.365
> (5/12)/(33/90)
                                                                1.141
[1] 1.136364
                                                             Degrees of Freedom: 932 Total (i.e. Null); 931 Residual
                                                             Null Deviance:
                                                                               1289
nonwhite
                                                             Residual Deviance: 1019
                                                                                           AIC: 1023
prop.test(c(3, 3), c(11, 9), conf.level = 0.9)
                                                             summary(treereg)
2-sample test for equality of proportions with continuity
                                                             Call:
                                                             glm(formula = SPP ~ y, family = binomial, data = tree)
     correction
data: c(3, 3) out of c(11, 9)
                                                             Deviance Residuals:
X-squared = 0, df = 1, p-value = 1
                                                               Min
                                                                        1Q Median
                                                                                        3Q
                                                                                               Max
                                                             -1.6843 -0.7181 0.7446 0.7446 1.7214
alternative hypothesis: two.sided
90 percent confidence interval:
                                                             Coefficients:
-0.4611955 0.3399834
                                                                    Estimate Std. Error z value Pr(>|z|)
sample estimates:
                                                             (Intercept) 1.1413 0.1007 11.33 <2e-16 ***
 prop 1 prop 2
                                                                     -2.3651 0.1566 -15.10 <2e-16 ***
0.2727273 0.3333333
                                                             Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' '1
Warning message:
In prop.test(c(3, 3), c(11, 9), conf.level = 0.9):
                                                             (Dispersion parameter for binomial family taken to be 1)
 Chi-squared approximation may be incorrect
                                                               Null deviance: 1289.4 on 932 degrees of freedom
married
                                                             Residual deviance: 1018.9 on 931 degrees of freedom
> prop.test(c(8, 10), c(41, 46), conf.level = 0.9)
                                                             AIC: 1022.9
2-sample test for equality of proportions with continuity
                                                             Number of Fisher Scoring iterations: 4
                                                             4.
    correction
data: c(8, 10) out of c(41, 46)
X-squared = 0, df = 1, p-value = 1
                                                             > ((130/436)/(1-(130/436)))/((407/497)/(1-(407/497)))
alternative hypothesis: two.sided
                                                             [1] 0.09394421
90 percent confidence interval:
                                                             \ln(((130/436)/(1\text{-}(130/436)))/((407/497)/(1\text{-}(407/497))))
-0.1872624 0.1427237
sample estimates:
                                                             +1.96(((1/130)+(1/306)+(1/407)+(1/90))^{-1})
  prop 1 prop 2
                                                             -2.36505418354759 + 79.9073885869975776 =
0.1951220 0.2173913
                                                             77.5423344034499876
                                                             -2.36505418354759 - 79.9073885869975776 =
> prop.test(c(5, 33), c(7, 57), conf.level = 0.9)
                                                             -82.2724427705451676
2-sample test for equality of proportions with continuity
                                                             95% CI is 77.5423344034499876 to -82.2724427705451676
    correction
data: c(5, 33) out of c(7, 57)
                                                             ((1/130+1/306+1/407+1/90))^{-1}
X-squared = 0.0786, df = 1, p-value = 0.7792
                                                             [1] 40.76908
alternative hypothesis: two.sided
                                                             The standard error is much different.
90 percent confidence interval:
-0.2456102 0.5162869
sample estimates:
                                                             admit<-read.csv('admitdata.csv', header=T)
 prop 1 prop 2
                                                             > admitgpa.glm<-
0.7142857 0.5789474
                                                             glm(factor(gpa)~factor(admit),family=binomial,data=admit)
Warning message:
                                                             > admitgpa.glm
In prop.test(c(5, 33), c(7, 57), conf.level = 0.9):
                                                             Call: glm(formula = factor(gpa) ~ factor(admit), family =
 Chi-squared approximation may be incorrect
                                                             binomial,
                                                               data = admit)
tree<-read.table('treedata.txt', header=T)
                                                             Coefficients:
                                                               (Intercept) factor(admit)1
a.
```

5.606 16.960 Estimate Std. Error z value Pr(>|z|)5.606 Degrees of Freedom: 399 Total (i.e. Null); 398 Residual (Intercept) 1.002 5.596 2.2e-08 \*\*\* Null Deviance: factor(admit)1 16.960 4276.716 0.004 0.997 13.98 Residual Deviance: 13.22 AIC: 17.22 > summary(admitgpa.glm) Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' '1 (Dispersion parameter for binomial family taken to be 1) Call:  $glm(formula = factor(gpa) \sim factor(admit), family = binomial,$ Null deviance: 13.980 on 399 degrees of freedom data = admit) Residual deviance: 13.215 on 398 degrees of freedom Deviance Residuals: AIC: 17.215 10 Median Number of Fisher Scoring iterations: 21 Min 3Q Max -3.3495 0.0000 0.0857 0.0857 0.0857 Coefficients: admitboth.glm<-glm(factor(gre + Estimate Std. Error z value Pr(>|z|)gpa)~factor(admit),family=binomial,data=admit) 1.002 5.596 2.2e-08 \*\*\* (Intercept) 5.606 admitboth.glm factor(admit)1 16.960 4276.716 0.004 0.997 Call:  $glm(formula = factor(gre + gpa) \sim factor(admit), family$ = binomial, Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' '1 data = admit) (Dispersion parameter for binomial family taken to be 1) Coefficients: Null deviance: 13.980 on 399 degrees of freedom (Intercept) factor(admit)1 Residual deviance: 13.215 on 398 degrees of freedom 5.606 16.960 Degrees of Freedom: 399 Total (i.e. Null); 398 Residual AIC: 17.215 Number of Fisher Scoring iterations: 21 Null Deviance: 13.98 admitgre.glm<-Residual Deviance: 13.22 AIC: 17.22 glm(factor(gre)~factor(admit),family=binomial,data=admit) summary(admitboth.glm) > admitgre.glm Call: Call: glm(formula = factor(gre) ~ factor(admit), family = glm(formula = factor(gre + gpa) ~ factor(admit), family = binomial, binomial, data = admit) data = admit)Coefficients: Deviance Residuals: (Intercept) factor(admit)1 Min 10 Median 3Q Max 5.606 16.960 -3.3495 0.0000 0.0857 0.0857 0.0857 Degrees of Freedom: 399 Total (i.e. Null); 398 Residual Coefficients: Null Deviance: Estimate Std. Error z value Pr(>|z|)13.98 Residual Deviance: 13.22 AIC: 17.22 (Intercept) 5.606 1.002 5.596 2.2e-08 \*\*\* > summary(admitgre.glm) factor(admit)1 16.960 4276.716 0.004 0.997 glm(formula = factor(gre) ~ factor(admit), family = binomial, Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' '1 data = admit) (Dispersion parameter for binomial family taken to be 1) Deviance Residuals: Null deviance: 13.980 on 399 degrees of freedom 1Q Median Min 3Q Max Residual deviance: 13.215 on 398 degrees of freedom -3.3495 0.0000 0.0857 0.0857 0.0857 AIC: 17.215 Coefficients: Number of Fisher Scoring iterations: 21