One Sample Tests Two Sample Tests Tests for Categorical Data Nonparametric Tests Simple Linear Regression

R Examples from BIOST 511 - Set 7 and 8

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Disclaimer

All of the following slides and functions are to be used when given sample descriptive statistics

For raw data, refer to the documentation for ttest() and other functions given on http://www.emersonstatistics.com/R

Test of Proportions

Use the prop.test() function from the stats package (automatically loaded into R along with the base package)

```
prop.test(110, 200, p=.3, alternative="two.sided")

1-sample proportions test with continuity correction

data: 110 out of 200, null probability 0.3

X-squared = 58.3393, df = 1, p-value = 2.206e-14
alternative hypothesis: true p is not equal to 0.3

95 percent confidence interval:
0.4782703 0.6197775

sample estimates:
p
0.55
```

If we want a different test, we change the alternative argument

t-test using Sample Descriptive Statistics

Use the ttesti() function from the uwIntroStats package

```
ttesti(24, 175, 35, 43, null.hyp=230)
One-sample t-test
   Obs Mean Std. Error SD 95 %CI
x 24 175 7.1443     35 160.221 189.779
t-statistic = -7.698396 , df = 23
Ho: mean = 230
Ha: mean != 230 , Pr(|T| > |t|) = 8.24e-08
```

Again, if we want a different test, we change the alternative argument

Binomial Test

Use the binom.test() function from the stats package

```
binom.test(110, 200, p=.3, alternative="two.sided")

Exact binomial test

data: 110 and 200
number of successes = 110, number of trials = 200, p-value = 3.125e-13
alternative hypothesis: true probability of success is not equal to 0.3
95 percent confidence interval:
0.4782493 0.6202464
sample estimates:
probability of success
0.55
```

 Again, if we want a different test, we change the alternative argument

Group 1 and Group 2 One-Sample Tests

```
## One sample t-test for Group 1
ttesti(obs=10, mean=-1.6, sd=1.5, null.hvp=0)
One-sample t-test
 Obs Mean Std. Error SD 95 %CI
x 10 -1.6 0.4743 1.5 -2.673 -0.527
t-statistic = -3.373096 , df = 9
 Ho: mean = 0
Ha: mean != 0 , Pr(|T| > |t|) = 0.0082165
## For Group 2
ttesti(obs=30, mean=-.7, sd=2.1, null.hyp=0)
One-sample t-test
 Obs Mean Std. Error SD 95 %CI
x 30 -0.7 0.3834
                     2.1 -1.484 0.084
t-statistic = -1.825742 , df = 29
Ho: mean = 0
Ha: mean != 0 , Pr(|T| > |t|) = 0.078203
```

Difference of Means with Sample Descriptive Statistics Unequal Variances

Use the ttesti() function in the uwIntroStats package For the Group 1 Group 2 example,

Proportions

Use the binom.test() function in the stats package

```
## Exact binomial test
binom.test(7, 26, .5)

Exact binomial test

data: 7 and 26
number of successes = 7, number of trials = 26, p-value = 0.02896
alternative hypothesis: true probability of success is not equal to 0.5
95 percent confidence interval:
    0.1157322 0.4778748
sample estimates:
probability of success
    0.2692308
```

Chi-squared Test

Use the chisq.test() function in the stats package If given raw data, use the tabulate() function in the uwIntroStats package

The correct=FALSE argument tells R to NOT use Yates' continuity correction

For this small data example, you will get a warning from R, because the expected cell counts are too small for a reliable Chi-squared test

```
chisq.test(matrix(c(2,23,5,30), nrow=2, byrow=T), correct=FALSE)
Pearson's Chi-squared test
data: matrix(c(2, 23, 5, 30), nrow = 2, byrow = T)
X-squared = 0.5591, df = 1, p-value = 0.4546
```

Fisher's Exact Test

Use the fisher.test() function in the stats package If given raw data, use the tabulate() function in the uwIntroStats package with the correct arguments

```
fisher.test(matrix(c(2,23,5,30), nrow=2, byrow=T))

Fisher's Exact Test for Count Data

data: matrix(c(2, 23, 5, 30), nrow = 2, byrow = T)
p-value = 0.6882
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
0.04625243 3.58478157
sample estimates:
odds ratio
0 527113
```

Chi-squared Goodness of Fit Test

Use the chisq.test() function in the stats package Simply enter in a vector rather than a matrix and a goodness of fit test will be performed

Homogeneity Test

Use the chisq.test() function in the stats package If given raw data, use the tabulate() function in the uwIntroStats package with the correct arguments

Independence Test

One Sample Tests Two Sample Tests Tests for Categorical Data Nonparametric Tests Simple Linear Regression

Sign Test

No direct analog for this test in R Since it ignores a lot of information, use the binomial test or McNemar's test

Wilcoxon Signed Rank Test

Use the wilcoxon function from the uwIntroStats package First you must have data vectors, so create them if necessary

```
cf <- c(1153, 1132, 1165, 1460, 1162, 1493, 1358, 1453, 1185, 1824, 1793, 1930, 2075) healthy <- c(996, 1080, 1182, 1452, 1634, 1619, 1140, 1123, 1113, 1463, 1632, 1614, 1836) wilcoxon(cf, healthy, paired=TRUE)
```

```
Wilcoxon signed rank test
        obs sum ranks expected
positive 10
                          45.5
                   71
                          45.5
negative
                   20
         0
                          0.0
zero
                    0
all
         13
                   91
                          91.0
unadjusted variance
                     204.75
adjustment for ties
                      0.00
adjustment for zeroes 0.00
adjusted variance
                     204.75
                   HO Ha
Hypothesized Median 0 two.sided
 Test Statistic p-value
V 71
                0.080322
7. 1. 7821
                0.037368
```

Wilcoxon Rank Sum Test

Use the wilcoxon function from the uwIntroStats package First you must have data vectors, so create them if necessary

```
ebv <- c(2.9, 12.1, 2.6, 2.5, 2.8, 15.8, 3.2, 1.8, 7.8,
         2.9, 3.2, 8.0, 1.5, 6.3, 1.2, 3.5, 4.5, 1.3,
         1.0, 1.0, 1.3, 1.9, 1.3, 2.1, 2.1, 1.0)
sero \leftarrow c(rep(1.16), rep(0.10))
data <- cbind(ebv. sero)
wilcoxon(data[sero==1], data[sero==0])
Wilcoxon rank sum test
         obs rank sum expected
combined
unadjusted variance 2826,666667
adjustment for ties
                       2.968326
adjusted variance
                    2823.698341
                     HO Ha
Hypothesized Median 0 two.sided
  Test Statistic p-value
                 0.001828
Warning message:
In wilcoxon.do(x = y, y = x, alternative = alternative, mu = mu, :
  cannot compute exact p-value with ties
```

The warning message means that there are tied values, so the p-values are approximate

Systolic Blood Pressure Example

Create the data set by saving it as a text file, then load it into R and attach it

```
systolic <- read.table("P:/TA/systolic.txt", header=TRUE, quote="\"", stringsAsFactors=FALSE)
```

Next regress systolic (the y-variable) vs age using the regress() function, with first argument "mean"

```
regress("mean", systolic$systolic, model=uModel(systolic$age))
Call:
regress(fnctl = "mean", v = systolic$systolic, model = uModel(systolic$age))
Residuals:
             10 Median
-7.1395 -2.3314 -0.2163 2.1872 5.8605
Coefficients:
                Estimate Naive SE Robust SE 67.68 3.191 2.440
Intercept
systolic$age
                  6.153
                             0.9283
                                       0.6511
                                                    4.757
                                                               7.550
                                                                               89.32 1 < 0.00005
Residual standard error: 3.403 on 14 degrees of freedom
Multiple R-squared: 0.7584, Adjusted R-squared: 0.7411
F-statistic: 43.94 on 1 and 14 DF, p-value: 1.135e-05
```

The uModel() function gives the correct names and allows multiple variables to be listed in the model argument

Prediction of the mean

Again use the regress() function We will need items from the list it returns, so get the predicted \hat{y} 's with \$linearPredictor and the standard deviation with \$sigma:

```
vhat <- svsRegress$linearPredictor</p>
## get standard error about line
se <- svsRegress$sigma/sqrt(14)
## calculate confidence interval around the line using the quantile of the t distribution
lower <- vhat - gt(.975, 14)*se
upper <- vhat + qt(.975, 14)*se
cbind(round(lower, 3), round(yhat, 3), round(upper,3))
 [1.] 84.189 86.140 88.090
 [2.] 90.342 92.293 94.244
 [3,] 84,189 86,140 88,090
 [4.] 78.035 79.986 81.937
 [5,] 90,342 92,293 94,244
 [6,] 96,496 98,447 100,397
 [7,] 78,035 79,986 81,937
 [8,] 84,189 86,140 88,090
 [9.] 96.496 98.447 100.397
[10,] 90.342 92.293 94.244
[11,] 78.035 79.986 81.937
[12,] 84.189 86.140 88.090
[13,] 84.189 86.140 88.090
[14,] 90.342 92.293 94.244
[15.] 84.189 86.140 88.090
[16.] 84.189 86.140 88.090
```

Prediction of a new value

Again use the regress() function

```
vhat <- sysRegress$linearPredictor
## get standard error about line
se <- sysRegress$sigma*sqrt(1+1/16+(systolic$age-mean(systolic$age))^2/(sd(systolic$age)^2))
## calculate confidence interval around the line using the quantile of the t distribution
lower <- yhat - qt(.975, 14)*se
upper <- yhat + qt(.975, 14)*se
cbind(round(lower, 3), round(yhat, 3), round(upper,3))
        [,1] [,2]
 [1,] 78,240 86,140 94,039
 [2,] 83,090 92,293 101,497
 [3,] 78,240 86,140 94,039
 [4.] 67.375 79.986 92.597
 [5.] 83.090 92.293 101.497
 [6,] 83.416 98.447 113.478
 [7,] 67.375 79.986 92.597
 [8,] 78.240 86.140 94.039
 [9,] 83.416 98.447 113.478
[10,] 83.090 92.293 101.497
[11.] 67.375 79.986 92.597
[12.] 78.240 86.140 94.039
[13.] 78.240 86.140 94.039
[14.] 83.090 92.293 101.497
[15.] 78.240 86.140 94.039
[16.] 78.240 86.140 94.039
```