# Chi-Square Tests

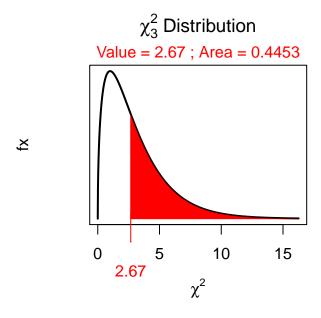
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# First Commands

> library(NCStats)

# Chi-Square Distribution Calculations

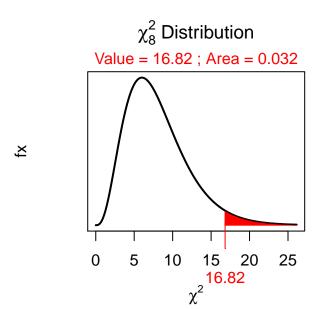
An example of computing the p-value  $\chi^2=2.67$  and df=3.



## [1] 0.4453496

An example of computing the p-value if  $\chi^2=16.82$  and df=8.

```
> ( distrib(16.82,distrib="chisq",df=8,lower.tail=FALSE) )
```



[1] 0.03203895

chinook salmon

# Chi-Square Test

### From Summarized Observed Table

Do the dominant food items in lake trout and chinook salmon differ at the 5% level? The summarized observed table was given in class.

```
> freq <- c(32,10,8,18,18,4)
> ( obs <- matrix(freq,nrow=2,byrow=TRUE) )</pre>
     [,1] [,2] [,3]
[1,]
       32
             10
[2,]
       18
             18
> rownames(obs) <- c("lake trout", "chinook salmon")</pre>
> colnames(obs) <- c("lake herring", "smelt", "mysis")</pre>
> obs
                lake herring smelt mysis
lake trout
                           32
chinook salmon
                           18
                                  18
> chi1 <- chisq.test(obs,correct=FALSE)</pre>
> chi1$expected
                lake herring
                                  smelt
                                           mysis
lake trout
                    27.77778 15.55556 6.666667
```

22.2222 12.44444 5.333333

```
> chi1$expected >= 5
               lake herring smelt mysis
                       TRUE TRUE TRUE
lake trout
                       TRUE TRUE TRUE
chinook salmon
> chi1
Pearson's Chi-squared test with obs
X-squared = 6.5083, df = 2, p-value = 0.03861
> chi1$residuals
               lake herring
                                smelt
                                           mysis
lake trout
                  0.8011103 -1.408590 0.5163978
chinook salmon
                 -0.8956686 1.574852 -0.5773503
> percTable(obs,margin=1,digits=1)
               lake herring smelt mysis Sum
lake trout
                         64
                               20
                                     16 100
chinook salmon
                         45
                               45
                                     10 100
> (obs2 < -obs[,-2])
               lake herring mysis
lake trout
                         32
                         18
                                4
chinook salmon
> ( chi2 <- chisq.test(obs2,correct=FALSE) )</pre>
Warning in chisq.test(obs2, correct = FALSE): Chi-squared approximation may be incorrect
Pearson's Chi-squared test with obs2
X-squared = 0.0301, df = 1, p-value = 0.8624
> chi2
Pearson's Chi-squared test with obs2
X-squared = 0.0301, df = 1, p-value = 0.8624
```

## From Raw Data

On the GSS, respondents were asked to state their opinion on how true the following statement was "All radioactivity is made by humans." Respondents were also categorized by their highest educational degree. Use the results in the SciTest1.csv data file to determine, at the 5% level, if the response to the question differs among levels of education

```
> setwd("C:/aaaWork/Web/GitHub/NCMTH107/lecture/HOs")
> ST1 <- read.csv("SciTest1.csv")</pre>
> str(ST1)
              2549 obs. of 2 variables:
'data.frame':
 $ degree : Factor w/ 5 levels "bach","grad",..: 5 5 5 5 5 5 5 5 5 5 5 ...
 $ scitest: Factor w/ 4 levels "def.not", "def.true",..: 2 2 2 2 2 2 2 2 2 2 ...
> levels(ST1$degree)
[1] "bach" "grad" "hs"
                            "jc"
                                    "lt.hs"
> ST1$fdegree <- factor(ST1$degree,levels=c("lt.hs","hs","jc","bach","grad"))</pre>
> levels(ST1$scitest)
[1] "def.not"
                "def.true" "prob.not" "prob.true"
> ST1$fscitest <- factor(ST1$scitest,levels=c("def.not","prob.not","prob.true","def.true"))
> ( freq.tbl <- xtabs(~fdegree+fscitest,data=ST1) )</pre>
       fscitest
fdegree def.not prob.not prob.true def.true
  lt.hs
            52
                    112
                               155
                                         70
  hs
            366
                     451
                               437
                                        114
  jс
             60
                      44
                                36
                                         12
  bach
            214
                     135
                                78
  grad
            123
                      57
                                18
> ST1.chi <- chisq.test(freq.tbl,correct=FALSE)</pre>
> ST1.chi$expected
       fscitest
fdegree def.not prob.not prob.true def.true
  lt.hs 124.37623 121.93448 110.48882 32.20047
  hs
       437.39506 428.80816 388.55708 113.23970
        47.64025 46.70498 42.32091 12.33386
  iс
  bach 140.36289 137.60730 124.69047 36.33935
       65.22558 63.94508 57.94272 16.88662
> ST1.chi$expected >= 5
       fscitest
fdegree def.not prob.not prob.true def.true
  lt.hs
           TRUE
                    TRUE
                              TRUE
                                       TRUE
  hs
           TRUE
                    TRUE
                              TRUE
                                       TRUE
           TRUE
                   TRUE
                              TRUE
                                       TRUE
  ic
  bach
           TRUE
                   TRUE
                              TRUE
                                       TRUE
  grad
           TRUE
                    TRUE
                              TRUE
                                       TRUE
```

```
> all(chi1$expected >= 5)
[1] TRUE
> ST1.chi
Pearson's Chi-squared test with freq.tbl
X-squared = 288.2331, df = 12, p-value < 2.2e-16
> ST1.chi$residuals
      fscitest
fdegree
           def.not
                    prob.not prob.true
                                           def.true
  lt.hs -6.4897392 -0.8996675 4.2345762 6.6612431
  hs
        -3.4137460 1.0716718 2.4575530 0.0714471
  jс
         1.7906992 -0.3958064 -0.9716327 -0.9492868
         6.2154218 -0.2222643 -4.1813025 -4.0375730
  bach
        7.1536326 -0.8685073 -5.2473280 -2.6492428
  grad
> percTable(freq.tbl,margin=1,digits=1)
```

#### fscitest

```
fdegree def.not prob.not prob.true def.true
  lt.hs
           13.4
                     28.8
                               39.8
                                         18.0 100.0
  hs
           26.8
                     33.0
                               31.9
                                          8.3 100.0
  jс
           40.3
                     29.5
                               24.2
                                          6.0 100.0
  bach
           48.7
                     30.8
                               17.8
                                          2.7 100.0
           60.3
                     27.9
                                8.8
                                          2.9 99.9
  grad
```

## Goodness-of-Fit Test

Four-o'clocks (Mirabilis jalapa) are plants native to tropical America. Individual four-o'clocks can have red, white, or pink flowers. Flower color in this species is thought to controlled by a single gene locus with two alleles experssing incomplete dominance, so that heterozygotes are pink-flower, while homozygotes for one allele are white-flowered and homozygotes for the other allele are red-flowered. According to Mendelian genetic principles, self-pollination of pink-flowered plants should produce progeny that have red, pink, and white flowers in a 1:2:1 ratio. A horticulturist self-pollinates several pink-flowered plants and produces 240 progeny with 55 that are red-flowered, 132 that are pink-flowered, and 53 that are white-flowered. Use the results to determine, at the 5% level, if the theoretical 1:2:1 ratio is upheld with these data (This is example 11.1 from Glover, T. and K. Mitchell. 2008. An Introduction to Biostatistics, 2nd edition. Waveland Press).

```
> obs <- c(red=55,pink=132,white=53)
> exp.p <- c(red=1/4,pink=2/4,white=1/4)
> chi1 <- chisq.test(obs,p=exp.p,rescale=TRUE,correct=FALSE)
> chi1$expected
```

```
red pink white 60 120 60
```

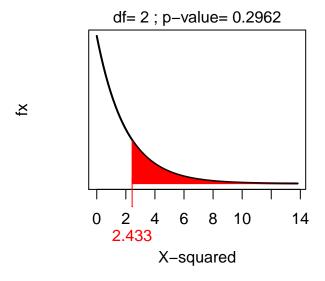
## > chi1\$observed

```
red pink white 55 132 53
```

#### > chi1

Chi-squared test for given probabilities with obs X-squared = 2.4333, df = 2, p-value = 0.2962

## > plot(chi1)



## > gofCI(chi1,digits=3)

p.obs p.LCI p.UCI p.exp red 0.229 0.181 0.286 0.25 pink 0.550 0.487 0.612 0.50 white 0.221 0.173 0.277 0.25