R Handout - Chi-Square Tests

Fall 2014, MTH107 Statistics

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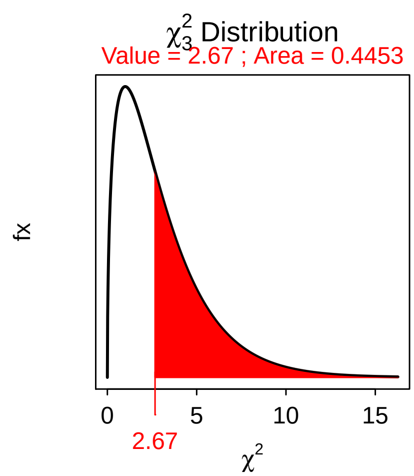
First Commands

```
> library(NCStats)
```

Chi-Square Distribution Calculations

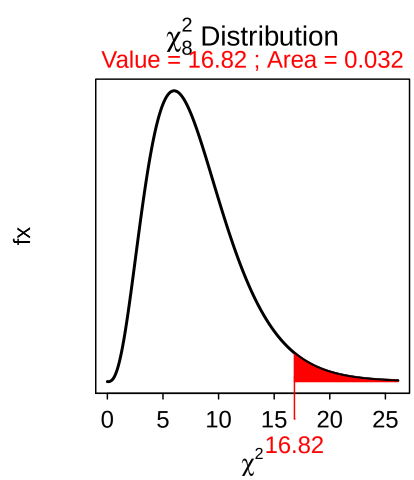
An example of computing the p-value χ^2=2.67 and df=3.

```
> ( distrib(2.67,distrib="chisq",df=3,lower.tail=FALSE) )
[1] 0.4453
```



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

```
> ( distrib(16.82,distrib="chisq",df=8,lower.tail=FALSE) )
[1] 0.03204
```



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) )

     [,1] [,2] [,3]
[1,]   32   10    8
[2,]   18   18    4

> rownames(obs) <- c("lake trout","chinook salmon")
> colnames(obs) <- c("lake herring","smelt","mysis")
> obs

               lake herring smelt mysis
lake trout               32    10     8
chinook salmon           18    18     4

> chi1 <- chisq.test(obs,correct=FALSE)
> chi1$expected

               lake herring smelt mysis
lake trout            27.78 15.56 6.667
chinook salmon        22.22 12.44 5.333

> chi1$expected >= 5

               lake herring smelt mysis
lake trout             TRUE  TRUE  TRUE
chinook salmon         TRUE  TRUE  TRUE

> chi1

Pearson's Chi-squared test with obs
X-squared = 6.508, df = 2, p-value = 0.03861

> chi1$residuals

               lake herring  smelt   mysis
lake trout           0.8011 -1.409  0.5164
chinook salmon      -0.8957  1.575 -0.5774

> 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     8
chinook salmon           18     4

> ( chi2 <- chisq.test(obs2,correct=FALSE) )

Warning:  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.txt data file to determine, at the 5% level, if the response to the question differs among levels of education

```
> setwd("C:/aaaWork/Class Materials/MTH107/Lecture/HOs")
> ST1 <- read.table("SciTest1.txt",head=TRUE)
> str(ST1)

'data.frame': 2549 obs. of  2 variables:
 $ degree : Factor w/ 5 levels "bach","grad",..: 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"))
> 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"))
```

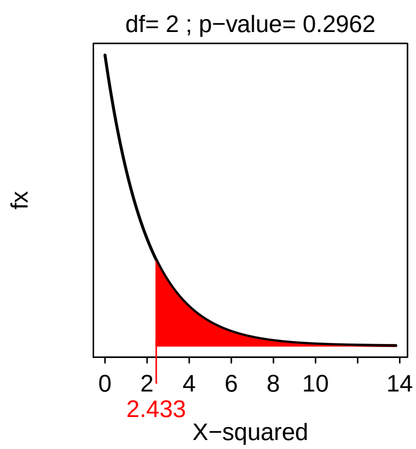
```
> ( freq.tbl <- xtabs(~fdegree+fscitest,data=ST1) )

       fscitest
fdegree def.not prob.not prob.true def.true
  lt.hs      52      112       155       70
  hs        366      451       437      114
  jc         60       44        36        9
  bach      214      135        78       12
  grad      123       57        18        6

> ST1.chi <- chisq.test(freq.tbl,correct=FALSE)
> ST1.chi$expected

       fscitest
fdegree def.not prob.not prob.true def.true
  lt.hs  124.38   121.93    110.49    32.20
  hs     437.40   428.81    388.56   113.24
  jc      47.64    46.70     42.32    12.33
  bach   140.36   137.61    124.69    36.34
  grad    65.23    63.95     57.94    16.89

> 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
  jc       TRUE     TRUE      TRUE     TRUE
  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 = 288.2, df = 12, p-value < 2.2e-16
```

```
> ST1.chi$residuals
       fscitest
fdegree  def.not prob.not prob.true def.true
  lt.hs -6.48974 -0.89967   4.23458  6.66124
  hs    -3.41375  1.07167   2.45755  0.07145
  jc     1.79070 -0.39581  -0.97163 -0.94929
  bach   6.21542 -0.22226  -4.18130 -4.03757
  grad   7.15363 -0.86851  -5.24733 -2.64924
> percTable(freq.tbl,margin=1,digits=1)
       fscitest
fdegree def.not prob.not prob.true def.true   Sum
  lt.hs    13.4     28.8      39.8     18.0 100.0
  hs       26.8     33.0      31.9      8.3 100.0
  jc       40.3     29.5      24.2      6.0 100.0
  bach     48.7     30.8      17.8      2.7 100.0
  grad     60.3     27.9       8.8      2.9  99.9
```

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[1].

```
> 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 = 2.433, 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
```

[1]This is example 11.1 from Glover, T. and K. Mitchell. 2008. An Introduction to Biostatistics, 2nd edition. Waveland Press.