

Chi-Square Tests

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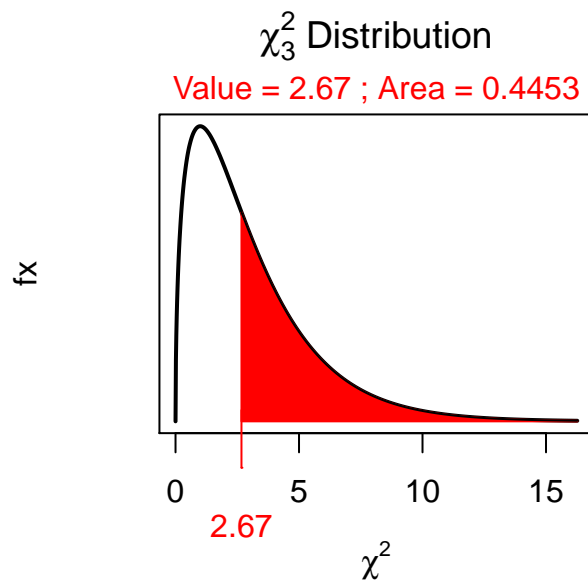
First Commands

```
> library(NCStats)
```

Chi-Square Distribution Calculations

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

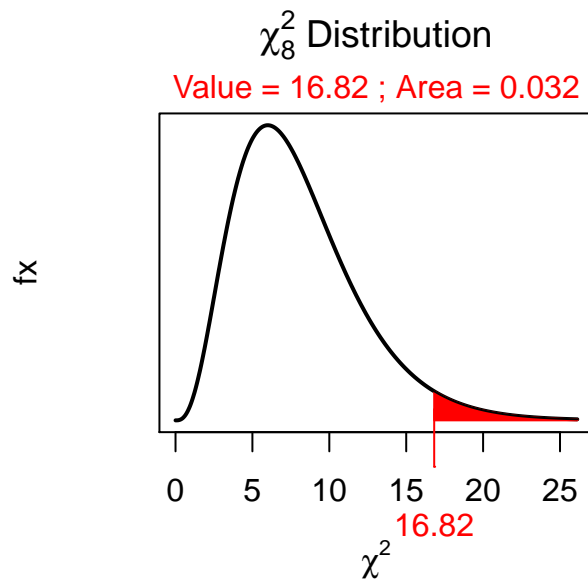
```
> ( distrib(2.67,distrib="chisq",df=3,lower.tail=FALSE) )
```



```
[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
```

Chi-Square Test

From Summarized Observed Table

When [Chinook Salmon](#) (*Oncorhynchus tshawytscha*) were first introduced to Lake Superior there was concern that they would compete with native [Lake Trout](#) (*Salvelinus namaycush*) for [Cisco](#) (*Coregonus artedii*). Preliminarily, fisheries biologists classified the dominant food items (Cisco, [Smelt](#) (*Osmerus mordax*) (another type of fish), or [Mysis](#) (an invertebrate)) in the diets of 50 Lake Trout and 40 Chinook Salmon. They found that 32, 10, and 8 Lake Trout diets were dominated by Cisco, Smelt, and *Mysis*, respectively. Similarly, 18, 18, and 4 Chinook Salmon diets were dominated by Cisco, Smelt, and *Mysis*, respectively. Test (at the 10% level) if the distribution of dominant food items differs at the 5% level?

```
> 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("Cisco","Smelt","Mysis")
> obs
```

```
      Cisco Smelt Mysis
Lake Trout      32    10     8
Chinook Salmon  18    18     4
```

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

	Cisco	Smelt	Mysis
Lake Trout	27.77778	15.55556	6.66667
Chinook Salmon	22.22222	12.44444	5.33333

```
> chi1$expected >= 5
```

	Cisco	Smelt	Mysis
Lake Trout	TRUE	TRUE	TRUE
Chinook Salmon	TRUE	TRUE	TRUE

```
> chi1
```

Pearson's Chi-squared test with obs
X-squared = 6.5083, df = 2, p-value = 0.03861

```
> chi1$residuals
```

	Cisco	Smelt	Mysis
Lake Trout	0.8011103	-1.408590	0.5163978
Chinook Salmon	-0.8956686	1.574852	-0.5773503

```
> percTable(obs,margin=1,digits=1)
```

	Cisco	Smelt	Mysis	Sum
Lake Trout	64	20	16	100
Chinook Salmon	45	45	10	100

```
> ( obs2 <- obs[, -2] )
```

	Cisco	Mysis
Lake Trout	32	8
Chinook Salmon	18	4

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

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

The [General Social Survey](#) (GSS) is a nationwide survey that has been administered since 1972 to gather data on contemporary American society in an attempt to monitor and explain trends in attitudes, behaviors, and attributes of American society. One part of that survey asked respondents 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. The results from this portion of the GSS is in [SciTest1.csv](#). Use these data to determine, at the 5% level, if the distribution of responses to this statement differs among levels of education.

```
> setwd("C:/aaaWork/Web/GitHub/NCMTH107/resources/class/H0s")
> ST1 <- read.csv("SciTest1.csv")
> 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 ...
 $ scitest: Factor w/ 4 levels "def.not","def.true",...: 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	124.37623	121.93448	110.48882	32.20047
hs	437.39506	428.80816	388.55708	113.23970
jc	47.64025	46.70498	42.32091	12.33386
bach	140.36289	137.60730	124.69047	36.33935
grad	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
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 = 288.2331, 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
jc       1.7906992 -0.3958064 -0.9716327 -0.9492868
bach     6.2154218 -0.2222643 -4.1813025 -4.0375730
grad     7.1536326 -0.8685073 -5.2473280 -2.6492428

```

```
> 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 be controlled by a single gene locus with two alleles expressing incomplete dominance, so that heterozygotes are pink-flowered, 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 allowed several pink-flowered plants to self-pollinate and produce 240 progeny with 55 that were red-flowered, 132 that were pink-flowered, and 53 that were white-flowered. Use the results to determine, at the 5% level, if the theoretical 1:2:1 ratio is upheld with these data.

```
> 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
```

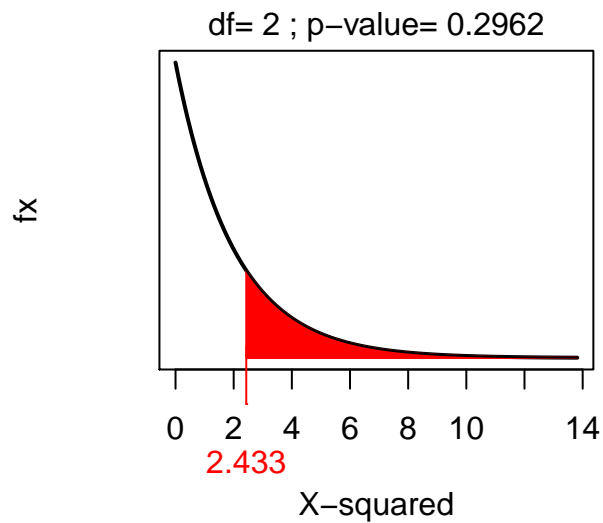
```
> chi1$observed
```

```
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