ST 502 Final

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2022-12-04

Introduction

This report will explore the Chi-Square test for homogeneity in detail. We will derive the likelihood ratio test (LRT) statistic used to conduct this test and explain the Pearson Chi-Square statistic that can be used as an approximation. Once the theory is well established, we then conduct a simulation. The goal is to determine how well the asymptotic rejection region performs at controlling the alpha level of the Pearson Chi-Square test and to determine the power of the asymptotic test when comparing certain alternative hypotheses.

The Chi-Square test for homogeneity is used in a specific case: comparing J multinomials with I classes (with $I, J \in \mathbb{N}$), where the researcher is interested in determining if the probabilities of each cell are the same across every multinomial. In practice, this test can be used to see if identifying factors (sex/age/etc.) have an impact on factors a researcher is interested in studying. For example, a medical research group may want to know if sex has a relationship with the probability that specific, unrelated illnesses are contracted. They could sample a large independent population, creating a multinomial for males and females with observed and expected counts. By performing the Chi-Square test for homogeneity, the research group would be able to determine the likelihood that sex has a relationship illnesses of interest.

It is worth mentioning that the Chi-Square test for independence is similar to the test for homogeneity. The chi-square test statistic is derived through a different approach, but is ultimately the same. However the use cases are

Data Example

Use hospital data given to conduct a χ^2 test for homogeneity.

```
#create and print matrix of hospital data
rows <- rbind(a=c(41, 27, 51), b=c(36,3,40), c=c(169, 106, 109))
(hospDat <- matrix(data=rows, nrow = 3, ncol = 3,
                   dimnames = list(c("A", "B", "C"),
                                   c("Surgical Site Infections",
                                     "Pneumonia Infections",
                                     "Bloodstream Infections"))))
```

```
##   Surgical Site Infections Pneumonia Infections Bloodstream Infections
## A                       41                   27                     51
## B                       36                    3                     40
## C                      169                  106                    109
```

```
summary(hospDat)
```

```
##  Surgical Site Infections Pneumonia Infections Bloodstream Infections
##  Min.   : 36.0            Min.   :  3.00       Min.   : 40.00
##  1st Qu.: 38.5            1st Qu.: 15.00       1st Qu.: 45.50
##  Median : 41.0            Median : 27.00       Median : 51.00
##  Mean   : 82.0            Mean   : 45.33       Mean   : 66.67
##  3rd Qu.:105.0            3rd Qu.: 66.50       3rd Qu.: 80.00
```

```
##  Max.   :169.0            Max.   :106.00       Max.   :109.00
```

Now we will conduct a Chi-Square test for homogeneity using this sample data.
H_0: The distribution of infections is the same for each hospital
H_1: The distribution of infections is **not** the same for each hospital.

```
x = chisq.test(hospDat)
x
```

```
##
##  Pearson's Chi-squared test
##
## data:  hospDat
## X-squared = 30.696, df = 4, p-value = 3.531e-06
```

```
x$expected
```

```
##   Surgical Site Infections Pneumonia Infections Bloodstream Infections
## A                 50.29897             27.80756               40.89347
## B                 33.39175             18.46048               27.14777
## C                162.30928             89.73196              131.95876
```

The p-value of our chi-square test statistic is extremely small, indicating that we reject the null hypothesis. The data in this example provides support for the alternative hypothesis that the multinomials from these hospitals are not homogeneous.

Deriving the Likelihood Ratio Test

The goal of this section is to derive the likelihood ratio test for a generalized case comparing J independent multinomial distributions, each with I categories.

Let there be J independent multinomial distributions, each with I categories, where $I, J \in \mathbb{N}$. We want to test the hypothesis $H_0 = \pi_{11} = \pi_{12} = ... = \pi_{1J}, \pi_{21} = \pi_{22} = ... = \pi_{1J}, \pi_{I1} = \pi_{I2} = ... = \pi_{IJ}$ vs. H_a : at least one probability differs.

To determine if there is a difference between the probability's associated with each multinomial being tested, we look at the difference between the expected and observed counts $Obs_{ij} - Exp_{ij}$, where the expected counts assume the null hypothesis to be true. We need to look at the likelihood function, which is given by the product of the J multinomials.

The likelihood function is given by $L(\pi'_{ij}s) = \prod_{j=1}^{J} \binom{J}{n} \cdot \pi_{ij}^{n_{ij}} \cdot \pi_{2j}^{n_{2j}} \cdot ... \cdot \pi_{IJ}^{n_{IJ}} \propto \prod_{j=1}^{J} \prod_{i=1}^{I} \pi_{ij}^{n_{ij}}$. This likelihood function is subject to the constraint $\sum_{i=1}^{I} \pi_i = 1, \forall i \in I \forall j \in J$.

Taking the natural log of the likelihood, we get the log-likelihood function $l \propto ln(\prod_{j=1}^{J} \prod_{i=1}^{I} \pi_{ij}^{n_{ij}}) = \sum_{j=1}^{J} \sum_{i=1}^{I} n_{ij} \cdot \pi_{ij}$

Note that the constraint dictates that the degrees of freedom of the whole space is given by $dim(\Omega) = J \cdot (I-1)$ with the dimension of each multinomial given by $dim(\omega) = (I-1)$. The degrees of freedom are therefore:$df = J(I-1) - (I-1) = (I-1)(J-1)$. The expected counts under H_0 are $E(ij) = \frac{n_{\cdot j} n_{i\cdot}}{n}$.

Under the null hypothesis,$\pi_{11} = \pi_{12} = ... = \pi_{1J}$, so we will replace these with a common value π_1. Similarly, we will continue forward considering the common values $\pi_1, ..., \pi_I$. There is one restriction on these probabilities to make them valid, which is $\sum \pi_i = 1$

We look at the likelihood ratio $\lambda = \frac{L(H_0)}{L(H_1)} = \frac{\prod_{j=1}^{J} \prod_{i=1}^{I} \pi_{ij}^{n_{ij}}}{\prod_{j=1}^{J} \prod_{i=1}^{I} \pi_{ij}^{n_{ij}}}$

Using the Lagrange Multiplier technique, we can find the maximized value for the likelihood ratio.

The likelihood ratio test for the homogeneity hypothesis being tested is therefore given by $LRT = 2\sum_{j=1}^{J}\sum_{i=1}^{I} Obs_{ij} \cdot ln(\frac{Obs_{ij}}{Exp_{ij}})$

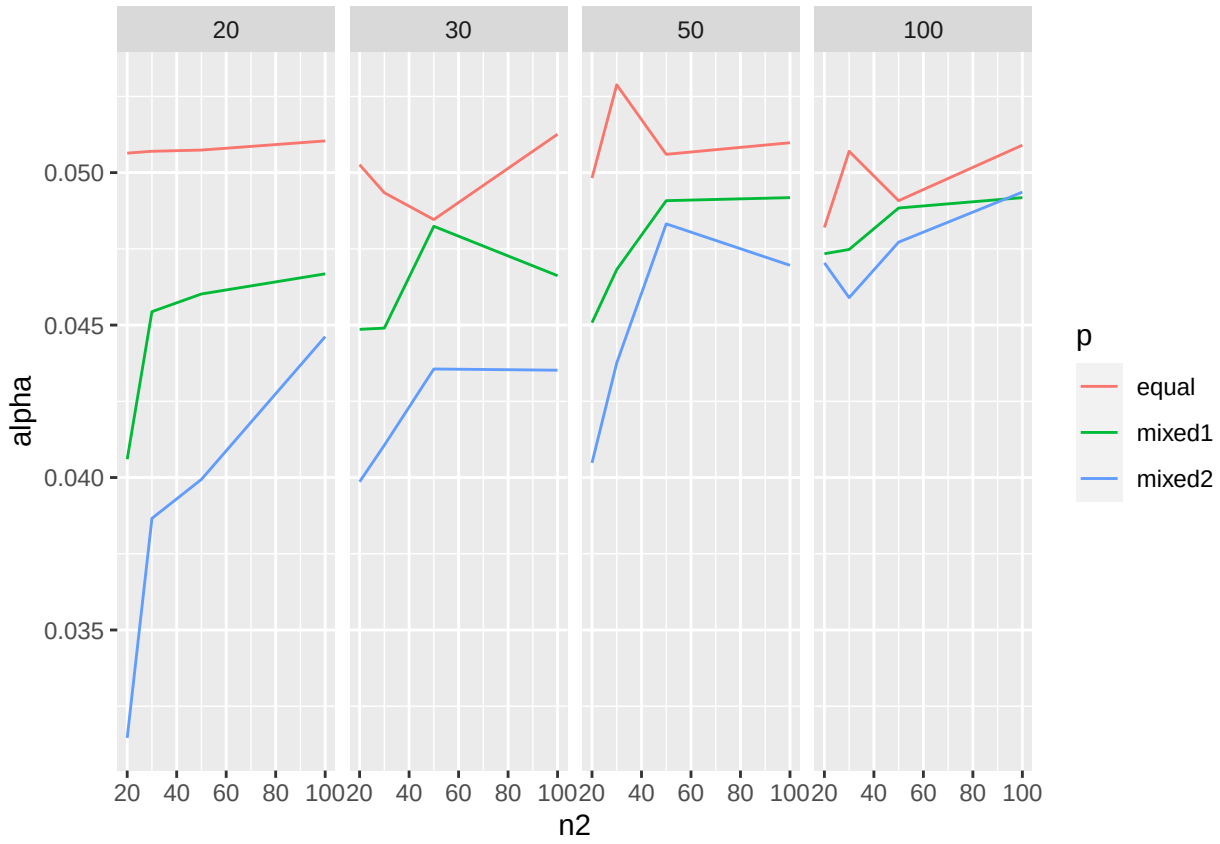
Simulation

Goal: - Determine how well the asymptotic rejection region performs at controlling α. - Determine the power of the asymptotic test when comparing certain alternative situations.

Process: For the simulation process, we will do the case of 2 multinomials each with 3 classes. We will generate many, many tables of these multinomial pairs, each of varying sample sizes, and from 3 cases of probabilities: the equal probability case, and two mixed cases. After generating our tables, we will then conduct a theoretical χ^2 test and obtain a proportion of times we reject H_0 over all tests for each combination of sample sizes under each probability case. This is our approximated α. Similarly, we will look at the power of the test by comparing multinomials of varying sample sizes with different probability cases: equal case vs the first mixed case, equal case vs the second mixed case, first mixed case vs the second mixed case. For both the α control and the power inspection, we will graph the comparisons.

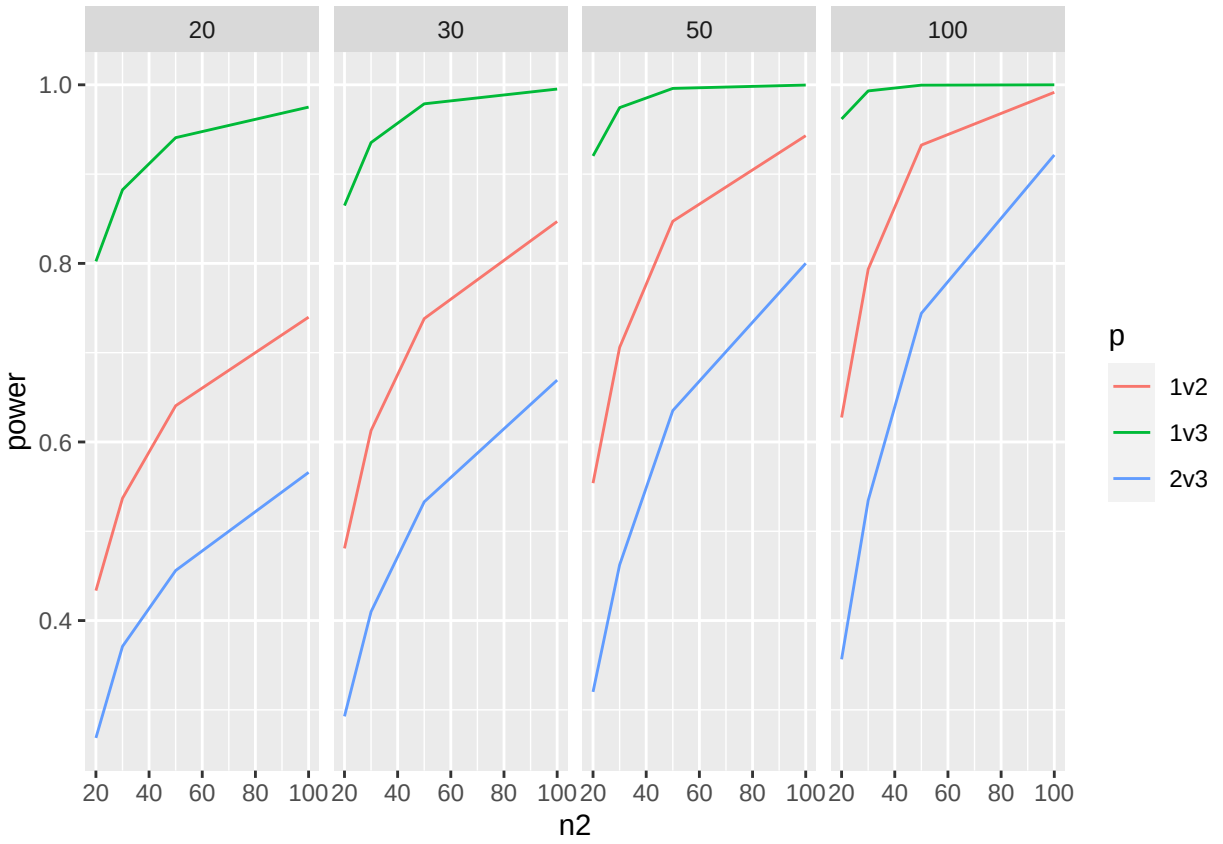
```
#set seed for reproduction
set.seed(17)

#sample sizes
n1 <- c(20,30,50,100)
n2 <- n1

#probabilities - three cases being tested
p1 <- c(1/3, 1/3, 1/3) #equal
p2 <- c(0.1, 0.3, 0.6) #mixed 1
p3 <- c(0.1, 0.1, 0.8) #mixed 2


#Use N=50000 random tables (start lower, end up here)
N <- 50000

#number of classes & multinomials being compared
#classes I = 3
#multinomials J = 2

# function to create two multinomials,using sample size and probabilities input
### sampleSize: (int)
### probs: (list of doubles) length of p split determines number of classes. All = 3 for this simulatio
### returns the approximate alpha values from simulated multinomials

#create function to generate tables like in hospital example
multGenerate <- function(size1, size2, prob) {
  #generate multinomials
  mult1 <- rmultinom(1, size1, prob)
  mult2 <- rmultinom(1, size2, prob)
  #combine multinomials into table
  multTab <- cbind(mult1, mult2)
  #transpose table to have multinomials as the rows
  multTrans = t(multTab)
  #return table
  return(multTrans)
}
```

```r
#testing in wrapper function
wrapAlpha <- function(size1, size2, prob){
  #generate table
  a <- multGenerate(size1, size2, prob)
  #compute chisq and compare to theoretical cutoff
  #here theoretical alpha = 0.05, but can easily update function to pick alpha
  #df = (I-1)(J-1) = (3-1)(2-1) = 2
  b <- chisq.test(a)
  c <- isTRUE(b$statistic > qchisq(0.95, 2))
  #return T/F value
  return(c)
}

##test wrapper; replicate many many times and store as vector
#alph <- replicate(5000, wrapAlpha(n1[2], n2[2],p1))
##take the mean of the vector to approximate alpha level
#mean(alph)

#set up vectors to store approximated alpha levels
p1Alphas <- c()
p2Alphas <- c()
p3Alphas <- c()

#for each combination of sample sizes, approximate alpha with each set of probabilities
for (i in 1:4) {
  for(j in 1:4){
    p1Alphas <- append(p1Alphas, mean(replicate(N,wrapAlpha(n1[i], n2[j], p1))))
    p2Alphas <- append(p2Alphas, mean(replicate(N,wrapAlpha(n1[i], n2[j], p2))))
    p3Alphas <- append(p3Alphas, mean(replicate(N,wrapAlpha(n1[i], n2[j], p3))))
  }
}


#combine all into data frame
n_1 <- c(20,20,20,20,30,30,30,30,50,50,50,50,100,100,100,100)
n_2 <- c(20,30,50,100,20,30,50,100,20,30,50,100,20,30,50,100)
alP1 <- replicate(16, "equal")
alP2 <- replicate(16, "mixed1")
alP3 <- replicate(16, "mixed2")
d1<-data.frame(alpha=p1Alphas, n1=n_1, n2=n_2, p=alP1)
d2<-data.frame(alpha=p2Alphas, n1=n_1, n2=n_2, p=alP2)
d3<-data.frame(alpha=p3Alphas, n1=n_1, n2=n_2, p=alP3)
alphaDat <- rbind(d1,d2,d3)

#plot
ggplot(alphaDat, aes(x=n2,y=alpha, group=p))+geom_line(aes(color=p))+facet_grid(.~n1)
```




```
#Power inspection
#compare 1-2, 1-3, 2-3

#Similar to multGenerate, but allows for 2 different probabilities
pwrCompare <- function(size1, size2, prob1, prob2) {
  #generate multinomials
  mult1 <- rmultinom(1, size1, prob1)
  mult2 <- rmultinom(1, size2, prob2)
  #combine multinomials into matrix
  multTab <- cbind(mult1, mult2)
  #transpose matrix
  multTrans = t(multTab)
  return(multTrans)
}

wrapPWR <- function(size1, size2, prob1, prob2){
  #generate table
  a <- pwrCompare(size1, size2, prob1, prob2)
  #compute chisq and compare to theoretical cutoff
  #here theoretical alpha = 0.05, but can easily update function to pick alpha
  #df = (I-1)(J-1) = (3-1)(2-1) = 2
  b <- chisq.test(a)
  c <- isTRUE(b$statistic > qchisq(0.95, 2))
  #return T/F value
  return(c)
}
```

```
##test wrapper; replicate many many times and store as vector
#pwr <- replicate(5000, wrapPWR(n1[3], n2[3],p1,p2))
##take the mean of the vector to approximate alpha level
#mean(pwr)

#set up vectors to store approximated power
pwrp1p2 <- c()
pwrp1p3 <- c()
pwrp2p3 <- c()

#for each combination of sample sizes, approximate power with each pair of probabilities
for (i in 1:4) {
  for(j in 1:4){
    pwrp1p2 <- append(pwrp1p2, mean(replicate(N,wrapPWR(n1[i], n2[j], p1,p2))))
    pwrp1p3 <- append(pwrp1p3, mean(replicate(N,wrapPWR(n1[i], n2[j], p1,p3))))
    pwrp2p3 <- append(pwrp2p3, mean(replicate(N,wrapPWR(n1[i], n2[j], p2,p3))))
  }
}


#combine all into data frame
be12 <- replicate(16, "1v2")
be13 <- replicate(16, "1v3")
be23 <- replicate(16, "2v3")
b1<-data.frame(power=pwrp1p2, n1=n_1, n2=n_2, p=be12)
b2<-data.frame(power=pwrp1p3, n1=n_1, n2=n_2, p=be13)
b3<-data.frame(power=pwrp2p3, n1=n_1, n2=n_2, p=be23)
powerDat <- rbind(b1,b2,b3)

#create graphs
ggplot(powerDat, aes(x=n2,y=power, group=p))+geom_line(aes(color=p))+facet_grid(.~n1)
```



Discussion

The results of this simulation indicate for the mixed probability distributions, the simulated alpha is quite good. The alpha values all fall below the $alpha$=0.05 threshold. For the equal probability case, the alpha level tends to be higher than the typical $alpha$=0.05. This might suggest that the test for homogeneity is improved when the true distribution is not equal, but further simulations would be helpful to consider multinomials with different numbers of classes.

As would naturally be expected, the power level of the simulations increases with sample size. There is a particularly high power associated with comparing the first hypothesis to the third - likely due to the fact that the true probabilities being simulated are distinct for each class. In the power calculations for multinomials simulated with at least one class having the same probability, the increase from twenty to fifty replications is particularly steep. This suggests that when comparing populations with overlapping class probabilities, conducting experiments with replicated samples is particularly helpful for making analysis with high power levels.