

Discrete Multivariate Analysis - 579 - HW #8

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Problem 1

Consider an experiment on chlorophyll inheritance in maize. A genetic theory predicts the ratio of green to yellow to be 3:1. In a sample of $n = 1103$ seedlings, $n_1 = 854$ were green and $n_2 = 249$ were yellow.

Part (a)

Compute the statistic G^2 for testing the proposed model.

The likelihood ratio statistic is defined as

$$G^2 = -2 \log \Lambda = 2 \sum_{j=1}^c \log \left(\frac{n_j}{n\pi_{j0}} \right).$$

We use the following R code to compute the observed statistic G_0^2 .

```
# below is code for testing a specified multinomial  
# data is entered as a vector of counts  
obs = c(854,249)  
n = sum(obs)  
  
# the null model is entered as a vector of hypothesized probabilities  
# expected counts under the null model are computed as n*prob  
pi.0 = c(.75,.25)  
m = n*pi.0  
  
# log-likelihood ratio test  
G2 = 2*sum(obs*log(obs/m))  
print(G2)
```

```
## [1] 3.539017
```

We see that the observed statistic is given by $G_0^2 = 3.54$.

Part (b)

Compute the p -value for the proposed model.

The reference distribution is the chi-squared distribution with $c - 1 = 1$ degrees of freedom.

The p -value with k degrees of freedom is defined as

$$p\text{-value} = P(\chi^2(k) > G^2),$$

or in this case

$$p\text{-value} = P(\chi^2(1) > 3.54) = 0.06.$$

The following R code computes the p -value.

```
# the p-value, a calculation based on tail probabilities
c = length(obs)
pvalue.G2 = pchisq(G2,c-1,lower.tail=FALSE)
print(pvalue.G2)

## [1] 0.05994099
```

Part (c)

Provide an interpretation of your result, stated in the context of the problem.

According to the Fisher scale for interpreting p -values, p -values of 0.05 and 0.1 denote respectively *moderate* and *boderline* evidence against the null model.

Since we obtained a p -value of 0.06, the data provides *moderate* evidence against the genetic theory positing that the ratio of green to yellow seedlings is 3:1.

Part (d)

What are the shortcomings of using a p -value as a measure of evidence?

The p -value overstates evidence against the null model by comparing the null model to the alternative model that is best supported by the data.

Part (e)

Compute the Bayes Factor B_{01} for medium, wide, and ultrawide prior distributions. According to the Bayes Factors, which model is supported by the data?

Below is code for computing Bayes Factors in a test for a specified probability.

```
library(BayesFactor)
# g denotes number of green seedlings
# y denotes number of yellow seedlings
# n = g+y denotes total number of seedlings
g = 854
y = 249
n = g+y
p0 = 3/4

bf.medium = 1/proportionBF(y=g,N=n,p=p0,rscale="medium")
bf.wide = 1/proportionBF(y=g,N=n,p=p0,rscale="wide")
bf.ultra = 1/proportionBF(y=g,N=n,p=p0,rscale="ultrawide")

bf.medium

## Bayes factor analysis
## -----
## [1] Null, p=0.75 : 1.931436 ±0%
##
## Against denominator:
##   Alternative, p0 = 0.75, r = 0.5, p != p0
## ---
## Bayes factor type: BFproportion, logistic
bf.wide
```

```
## Bayes factor analysis
## -----
## [1] Null, p=0.75 : 2.700316 ±0%
##
## Against denominator:
##   Alternative, p0 = 0.75, r = 0.707106781186548, p != p0
## ---
## Bayes factor type: BFproportion, logistic
bf.ultra
```

```
## Bayes factor analysis
## -----
## [1] Null, p=0.75 : 3.796726 ±0.01%
##
## Against denominator:
##   Alternative, p0 = 0.75, r = 1, p != p0
## ---
## Bayes factor type: BFproportion, logistic
```

If $BF_{01} > 1$, then the data supports the null model over the alternative model.

According to the Bayes Factors, the results for *medium*, *wide* and *ultra* are given respectively by 1.9, 2.7, and 3.8. Thus, the null model is supported by the data in each case.