

Lab Assignment 3

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March 15, 2024

General Instructions

- Put your name in the author section above.
- Write R code in the R chunks provided to answer the questions posed.
- Execute each chunk of code to ensure that your code works properly.
- Sometimes one of your chunks of code will not compile properly, but you must hand your document in. In that case, 'Comment' out the R code that is not working properly using # as the first character in your lines of code.
- Save the Rmd file.
- Knit the Rmd file to pdf.
- Upload the pdf file to the **Lab Assignment 3 activity** on Brightspace.
- **If your file will not knit to pdf, then knit to Word and save the Word document as a pdf.**

Independent Binomials [10 marks]

Four hundred patients took part in a study to compare the effectiveness of three similar drugs versus a placebo. Each drug was given to 100 patients, and the remaining 100 patients received a placebo. It was then observed whether or not there was improvement in the condition of each patient. The results were as follows:

	Drug A	Drug B	Drug C	Placebo	Total
Improvement	24	19	29	10	82
No Improvement	76	81	71	90	318
Total	100	100	100	100	400

Test the null hypothesis that the probability of improvement is the same in all four groups.

- [2 marks] Display/print the estimated probability of improvement under the null hypothesis.
- [2 marks] Display/print the observed value of the Likelihood ratio statistic (dobs).
- [2 marks] Display/print the degrees of freedom (k-q) for the chi-square p-value evaluation.
- [2 marks] Display/print the p-value for the test.
- [2 marks] Write a sentence with your conclusion.

Note: The BASIC model has 4 independent Binomials($n=100$, p_i), $i=1,2,3,4$.

```
y<-c(24, 19, 29, 10)
n<-rep(100, 4)

bin.dat <- y
bin.mle <- bin.dat/n

ell <- function(x, n, p){
  loglike <- 0
```

```

for (i in 1:length(x)){
  loglike <- loglike + dbinom(x[i], n[i], p[i], log=TRUE)
}
return(loglike)
}

phathypoth <- rep(sum(bin.dat)/sum(n), 4)

lhat <- ell(bin.dat,n,bin.mle)
k <- 4

lhypoth <- ell(bin.dat,n,phathypoth)
q <- 1

dobs <- 2*(lhat - lhypoth)

df <- k-q

p_value <- 1 - pchisq(dobs,df)

### Print results
print(paste("Hypothesized prob improvement: ", phathypoth[1]))

## [1] "Hypothesized prob improvement: 0.205"
print(paste("LRS val: ", dobs))

## [1] "LRS val: 12.897491940277"
print(paste("Degrees of freedom: ", df))

## [1] "Degrees of freedom: 3"
print(paste("P-value: ", p_value))

## [1] "P-value: 0.00486361146272807"
#print(paste("Conclusion: ", "with p-value = ", round(p_value, 4), "there is strong evidence against the
# Define the conclusion string
conclusion <- paste("Conclusion: ", "with p-value =", round(p_value, 4), "there is strong evidence again

# Wrap the conclusion string to a specified width (e.g., 80 characters)
wrapped_conclusion <- strwrap(conclusion, width = 80)

# Print the wrapped conclusion using cat()
cat(wrapped_conclusion, sep = "\n")

## Conclusion: with p-value = 0.0049 there is strong evidence against the null
## hypothesis H0 that the improvement is the same for all groups.

```