

Lab #2:

By the beginning of the next lab (Jan 30), send what you have to afodor@uncc.edu
Send your code and the answers to questions..

Make sure the text “Lab #2” is in the subject line...

Question #1

In a population, there is $1/3$ chance that a given person has a mutation in some gene.

You sample 30 people; what are the odds that exactly 12 of the people have the mutation?

In R plot a probability density function (with `dbinom`) that shows the distribution for observing exactly (0,1,2,...30) people with the mutation .

What is the mean and variance for the expected number of people with the mutation.

(2) The background expected survival rate for a disease is 0.4. You are running a clinical trial. You have 100 patients on a new drug. 47 patients die (and 53 survive)

From the binomial test:

(2A) Plot out the probability density function with the x-axis the number of patients that survive under the null hypothesis.

(2B) What is the p-value for a null hypothesis that the drug has no effect.
(Show the one line of R code that produces this p-value)

(2C) What is the p-value for a null hypothesis that the drug does not improve survival.
(show you can get the same answer with `binom.test(...)` and `sum(dbinom(...))`)

- (3A) Use the rbiom function to simulate 1,000 experiments in which 10,000 patients are sampled with a $1/2$ chance of seeing a mutation.
(You should get 1,000 numbers back with each # the # of patients from the 10,000 that had the mutation...)

```
> head(myVals)
[1] 4936 5088 4977 5009 5020 5007
> length(myVals)
[1] 1000
> |
```

(What is the one line of r-code that would produce myVals?)

- (3B) What is the expected mean and variance of the vector in (3A). Show that the actual mean and variance are close to the expected mean and variance.
- (3C) Take the vector that results from (3A). For each element in that vector, calculate a p-value with `binom.test(...)$p.value` for the null hypothesis that the frequency of the allele in the population for that experiment is $1/2$.

Graph the histogram of all of those p-values.

What distribution would you expect? Is that what you see?

- (3D) Change the expected value of $1/2$ in (3C) to some other value.
What happens to the p-values in the histogram.
Would you expect the same shape of the p-value histogram with expected values of .49 as with .51? Why or why not?