BIOS 6611 Homework 4

Due Tuesday, October 1, 2019 by 11:59 pm to Canvas Assignment Basket

1. Summarize briefly (one to two paragraphs, half page max) Sections 1 and 2 of the paper by, Hoenig and Heisey, "*The Abuse of Power: The Pervasive Fallacy of Power Calculations for Data Analysis*", which can be found on Canvas in the Paper Repository.

2. A clinical trial is planned to examine the bioavailability of twice per day betacarotene supplementation. Measurements are to be taken at baseline and 12 weeks later. Below, write out results by hand (i.e., show equations and work) for known s.d. and use R for unknown s.d. For R, you can refer to examples and code in Lecture 8. **Turn in your hand calculations/derivations, R code, and relevant output.**

   a. For the null hypothesis that the mean change in beta carotene is 0 mcg/dL and the alternative hypothesis that the mean change in beta carotene is 100 mcg/dL, with σ_{change} = 75 mcg/dL and n=5, what is the *power* to detect that difference, using α = 0.05 (two-sided)? Assume two cases: known s.d. and unknown s.d.
   b. *How many subjects* would be needed in (a) above if 90% power were desired? Assume two cases: known s.d. and unknown s.d.
   c. What is the *smallest mean change* in betacarotene that could be detected as significantly different from a change of 0 mcg/dL, if σ_{change} = 75 mcg/dL, n = 5, and power is 90%? What is the *smallest mean change* for 80% power? Assume two cases: known s.d. and unknown s.d.

3. In some cases the test statistic you need to apply to a set of data is not of a standard form and so is not included as an option in R (or other sample size and power analysis software), or perhaps an exact formula does not exist for doing the power calculation. In these cases, simulation in R (or other software) can be used to estimate the power, as described below. As an example, consider using simulation in question 2 above. There, formulas exist so simulation would not be necessary, but simulation allows you to check your results. Assume normally distributed data for the change in betacarotene with σ_{change} = 75 mcg/dL, n=5, and significance level = 0.05, with a one-sample two-sided t-test. Answer questions i-iii based on two different motivating scenarios (a) and (b):

   a. Use simulation to show that the one-sample t-test has the correct significance level, that is that under the null hypothesis the test rejects about 5% of the time. Use 10,000 iterations and the seed value 2345.

   b. Use simulation to obtain a power estimate for the situation in 2a for the alternative hypothesis that the mean change is 100 mcg/dL. Use 10,000 iterations and the seed value 1796. Which of your answers in question 2 matches most closely with your answer here? Explain briefly why.

Questions:

i. Using a loop in R, carry out (a) and (b) above. *Summarize your results in a brief paragraph.*

ii. EXTRA CREDIT: Using the same scenario and parameters as in (a) and (b), simulate power under the null and alternative hypotheses by writing a function in R. Provide your function and the results for applying your function for (a) and (b).

iii. It is not so easy to use simulation to estimate sample size or detectable difference directly. Explain in a sentence or two how you could use trial and error to estimate sample size as in 2b above. Do not do any further simulations or calculations (though they are not difficult to do).

Possible approaches

As you have seen over the last few weeks in the R lab documents and R code in the lectures, there are (at least) a couple of ways to carry out a series of repeated calculations - loops and functions. Loops are relatively easy to write, but for complex algorithms can be slow to execute. Functions require more care to write but are generally very efficient in execution. Both of them are useful for simulation studies.

The following are two examples for "generically" simulating power, one using a loop and one using a function.

```
#### Using a loop in R ####
set.seed(2345)
# Set input values
n <- # insert sample size value
mean <- # null or alternative hypothesis value
sd <- # for s.d.
numTrials <- # insert number
alpha <- # chosen significance level

# Set a counter to determine the number of rejected hypothesis tests
count<- 0
for( i in 1:numTrials){
  # Generate data
  y <- # generate sample from desired distribution
  # Perform test
  t <- #insert specific test as function of data, y
  count <- count + (#insert the part of test object containing the
test's p-value < alpha)
}

# Power = proportion of rejections
power <- count/numTrials
power
#power value will show here
```

Using a function in R

```
# The Function below will use sample size, mean, SD, number of trials
# and alpha as inputs

compute_power = function(n, mean, sigma, numTrials, alpha){

  # Generate a matrix with the data
  sample = matrix(#rdist(n*numTrials, mean, sigma), ncol=numTrials)
  # rdist is shorthand for the specific distribution from which random
  # variates are generated

  # Now, write out elements of the test statistic, e.g.
  # xbar <- apply(sample, 2, mean)#find mean of each column of matrix
  # variance <- apply(sample, 2, var)#find variance each column of
matrix
  # df.num = n-1 #e.g. degrees of freedom might be needed

  # …
  # combine elements of test statistic, e.g. numerator, denominator
  # …

  test.stat = #test statistic formula based on elements above


  # Result of the function is the proportion of rejected hypothesis
  # tests over all of the trials

  return (mean(abs(test.stat) >= #qdist((1-(alpha/2)), parameter of
dist)))
# qdist is shorthand for the specific quantile function for the
# sampling distribution of the test statistic
}

# Now, call the function with the arguments it needs – e.g. n, mean,
# sd, number of trials, alpha

set.seed(2345)
compute_power(#n, #mean, #sd, #trials, #alpha)
#power value will show here
```