Homework 6

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library(tidyverse)

## Question 1

### Part A

How much power would there be to detect the clinically relevant difference at the 0.05 significance level, if 20 individuals who spike in PF4 and 20 individuals who do not spike in PF4 are enrolled? Show some methodology for full credit.

MyPwrFun <- function(alpha, m1, m2, s1, s2, n1, n2){  
 z1a2 <- qnorm(1 - alpha / 2)  
 za2 <- qnorm(alpha / 2)  
 quant <- (m1-m2) / sqrt( (s1^2/n1) + (s2^2/n2) )  
 beta <- pnorm(z1a2 - quant) - pnorm(za2 - quant)  
 power <- 1- beta  
 return(power)  
}  
  
power1 <- MyPwrFun(alpha = .05, m1 = 1, m2 = .8, s1 = .32, s2 = .04, n1 = 20, n= 20)

**The power for this scenario would be** 0.79.

### Part B

Power is the probability of rejecting the null hypothesis when the alternative hypothesis is true. It is affected by variability, and as variability increases, power decreases.If we enroll more individuals in the population with more variability, that normalizes the variance of that group by a larger value, reducing variability, given that we have assumed normally distributed source populations.

### Part C

pwrdf <- data.frame()  
for (x in 0:40){  
 powers <- MyPwrFun(alpha = .05, m1 = 1, m2 = .8, s1= .32, s2 = .04, n1 = x, n2 = 40-x)  
 pwrdf <- rbind(pwrdf, c(x, powers))  
}

**A sample split of 36-4 observations per group would yield us the highest power, with power being calculated as 0.9396 for that split.**

## Question 2

Investigators hope to determine if a large dose of vitamin E will prevent cancer. The investigators will first conduct a feasibility study to determine the dosage of vitamin E. The investigators believe that 80% of participants on a high dose regimen will achieve adequate serum levels while 64% of those on a medium dose regimen will achieve adequate intake.

### Part A

How large of a sample is needed to have 90% power of a two-sided test of proportions at a 0.05 significance level of .05? Assume equal allocation to the two arms.

SampSizePropsFun <- function(alpha, k, beta, p1, p2){  
 z1a2 <- qnorm(1-alpha/2)  
 z1b <- qnorm(1-beta)  
 pstar <- (p1 + k \* p2) / (1 + k)  
 firstquantnum <- z1a2 \* sqrt( pstar \* (1- pstar) \* (1 + (1/k)))  
 secondquantnum <- z1b \* sqrt( p1 \* (1 - p1) + ((p2 \* (1-p2))/k))  
 numerator <- (firstquantnum + secondquantnum)^2  
 denom <- (p1 - p2)^2  
 n <- numerator / denom  
 n  
}  
#k = n2/n1 and is only used for unequal allocation of observations  
  
ans2a <- ceiling(SampSizePropsFun(alpha = .05, beta = .1, k = 1, p1 = .8, p2 = .64))  
ans2a

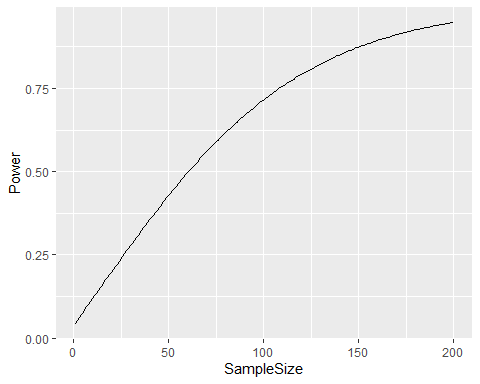
## [1] 164

**A sample size of** 328 **is needed to have a power of 90% using equal allocation.**

### Part B

Create a smooth plot of power as a function of sample size per group assuming equal allocation. Use a dense grid of sample sizes, i.e., nn <- 1:200. How much power does a sample size of 180 per group yield?

MyPwrFun2 <- function(p1, p2, alpha, p.bar, n1, n2){  
 z1a2 <- qnorm(1- alpha/2)  
 d <- abs(p1-p2)  
 quant <- (d - (z1a2 \* sqrt(p.bar \* (1 - p.bar) \* ( (1/n1) + (1/n2) ) ) ) ) / (sqrt(((p1 \* (1-p1) ) / n1) + (p2 \* (1-p2) / n2)))  
 pnorm(quant)  
}  
  
powerdf2 <- data.frame()  
for (x in 1:200){  
 outputs <- MyPwrFun2(p1 = .8, p2 = .64, alpha = .05, p.bar = .72, n1 = x, n2 = x)  
 powerdf2 <- rbind(powerdf2, c(x, outputs))  
}  
  
colnames(powerdf2) <- c("SampleSize", "Power")  
  
ggplot(powerdf2, aes(x = SampleSize, y = Power))+  
 geom\_line()



**The power for a sample size of 180 per group is 0.926.**

## Question 3

One sign of early chronic kidney disease (CKD) is preserved kidney function with excess albumin in the urine, measured as the ratio of albumin to creatinine (ACR) in mg/g. An ACR ≥ 30 mg/g is evidence of CKD. Below are ACR measurements from a small sample of Black Americans with preserved kidney function:

dat <- c(8, 46, 95, 21, 6, 2168, 1056, 19, 15, 55)

### Part A

What is the sample mean of the data? If a researcher wants to determine if the population mean of ACR among Black Americans is greater than 30, why would a one-sample t-test be inappropriate?

**The sample mean for this data is** 348.9. **A one-sample t-test would not be appropriate for this scenario because the data are clearly not normally distributed**

### Part B

Report the p-value and inference at the 0.1 level from a one-sample t-test to determine if mean ACR is greater than 30 in this population (i.e., just give Step 4 and 5).

mytest <- t.test(dat, mu = 30, alternative = "greater", conf.level = .1)

**The p-value is** 0.0962842 **. We fail to reject the null hypothesis based on this result that the mean ACR among Black Americans is less than 30**

### Part C

##### Step 1: Center your data around the hypothesized median

A WSR to determine if the sample median is greater than 30 would be more appropriate for this problem. Perform this test BY HAND for full credit listing all steps of the hypothesis test. (Of course, you may check your answer with software.)

newdat <- dat - 30  
newdf <- newdat %>% as.data.frame()

##### Step 2: Discard any 0 values

There are no values of 0 to discard.

##### Step 3: Rank the data in order of magnitude

colnames(newdf) <- c("obs")  
new2 <- newdf %>% arrange(abs(obs)) %>%   
 mutate(rank = 1:10)

##### Step 4: Define W+ and W-

wplus <- new2 %>% filter(obs > 0) %>%   
 summarise(wp = sum(rank))  
  
wminus <- new2 %>% filter(obs < 0) %>%   
 summarise(wm = sum(rank))

### Hypothesis Test

#### Part 1: Know the data

We assume that the distribution of weight differences is continuous.

#### Part 2: Hypotheses

#### Part 3: Test Statistic and Distribution

We will use as our test statistic, which is a distribution-less statistic.

#### Part 4: P-value

wilcox.test(new2$obs, alternative="greater", mu=0, paired=FALSE,  
 exact=TRUE, correct=FALSE)

##   
## Wilcoxon signed rank exact test  
##   
## data: new2$obs  
## V = 38, p-value = 0.1611  
## alternative hypothesis: true location is greater than 0

The p-value for this test is 0.1611, and the test statistic is 38.

#### Part 5: Conclusions

We fail to reject the null hypothesis at the level that the median ACR is greater than 30.