

Chp2 Homework

Wendy Liang

2/10/2021

Process To Get Critical Value

Firstly, let's define the Null Hypothesis and Alternative Hypothesis of this example.

$$H_0 : p = 0.6; H_1 : p > 0.6$$

where p is the probability that the new aspirin is effective. And we assume that the total people $n = 100$ and critical value is m .

Secondly, let's calculate the two types of errors.

The **Type I error** is

$$\alpha(p) = \sum_{60 \leq k \leq 100} b(100, 0.6, k)$$

which means when $p = 0.6$, we think $p > 0.6$. In other words, when the new drug isn't more effective, we regard it as more effective.

```
m1=rep(0,40)
alpha=rep(0,40)

# calculate reject area: P(m1 < X < 100) when H0 is true
for(i in 0:40){
  m1[i]=i+60
  alpha[i]=pbinom(q=100,size=100,prob=0.6)-pbinom(q=m1[i]-1,size=100,prob=0.6)
}
error1=data.frame(cbind(m1,alpha))
```

The **Type II error** is

$$\beta(p) = 1 - \alpha(p) = \sum_{k \leq 80} b(100, 0.8, k)$$

, which means when $p > 0.6$, we think $p = 0.6$. In other words, when the new drug is more effective, we don't regard it as more effective.

```
m2=rep(0,20)
beta=rep(0,20)

# calculate accept area: P(X < m2) when H0 is false
for(i in 0:20){
  m2[i]=80-i
  beta[i]=pbinom(q=m2[i]-1,size=100,prob=0.8)
}
error2=data.frame(cbind(m2,beta))
```

What we hope to do then, for a given test population n , is to choose a value of m , if possible, which makes both these probabilities small. So, assume the two types of errors are both less than 0.05.

```
min(error1[which(error1[,2]<0.05),1])
```

```
## [1] 69
```

```
max(error2[which(error2[,2]<0.05),1])
```

```
## [1] 73
```

Above are the process to get the critical value range [69, 73].

Process To Get Figure 3.7

The left line represents the case where $m = 69$ and the right line represents the case $m = 73$. As m increases, the graph of $\alpha(p)$ moves to the right.

```
# p(the probability of new drug effectiveness) ranges from [0.4,1]
p=seq(from=0.4,to=1,length=100)

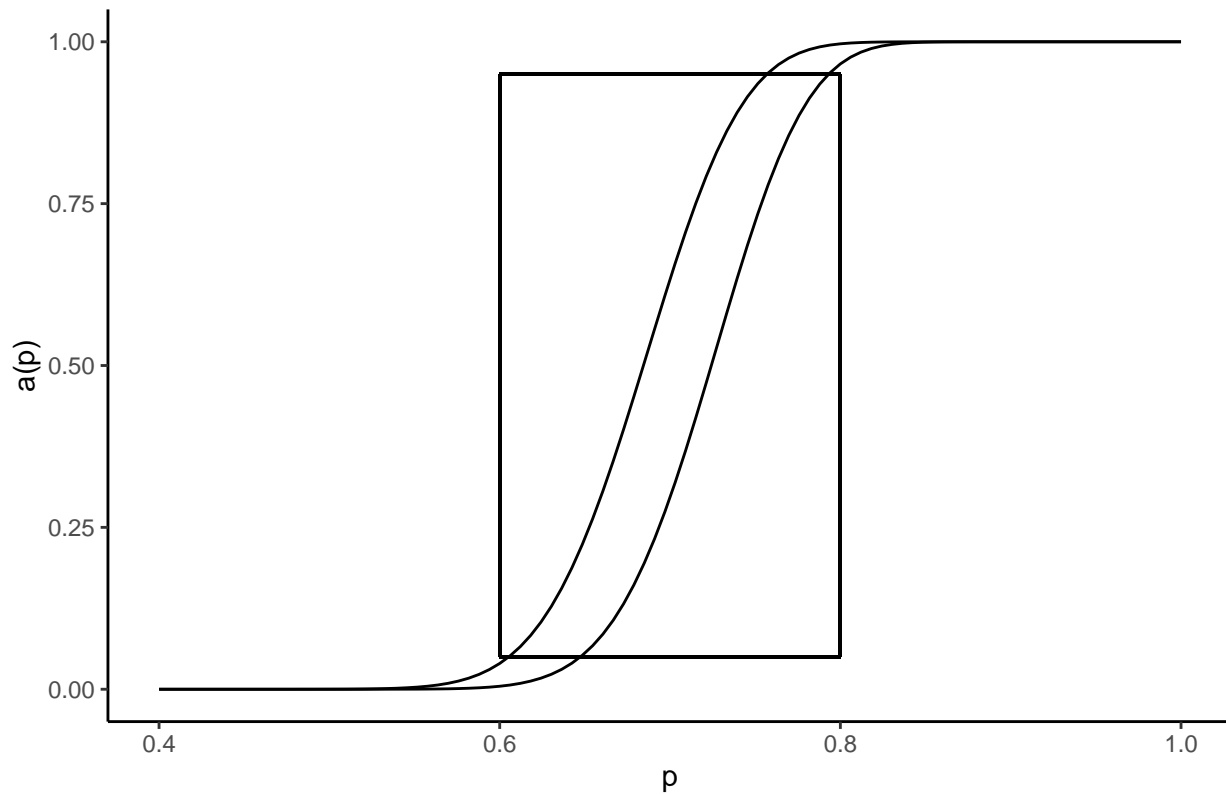
# Type I Error for m1 m2
alpha69=rep(0,100)
for(i in 1:100){
  alpha69[i]=pbinom(q=100,size=100,prob=p[i])-pbinom(q=68,size=100,prob=p[i])
}

alpha73=rep(0,100)
for(i in 1:100){
  alpha73[i]=pbinom(q=100,size=100,prob=p[i])-pbinom(q=72,size=100,prob=p[i])
}

df=data.frame(cbind(p,alpha69,alpha73))

#plot
ggplot(data=df,mapping=aes(x=p))+
  geom_line(mapping=aes(y=alpha69))+
  geom_line(mapping=aes(y=alpha73))+
  labs(x="p",y="a(p)")+
  ggtitle("Figure 3.7: The power curve")+
  geom_segment(mapping=aes(x=0.6,xend=0.8,y=0.05,yend=0.05))+
  geom_segment(mapping=aes(x=0.6,xend=0.8,y=0.95,yend=0.95))+
  geom_segment(mapping=aes(x=0.6,xend=0.6,y=0.05,yend=0.95))+
  geom_segment(mapping=aes(x=0.8,xend=0.8,y=0.05,yend=0.95))+
  theme(panel.grid=element_blank(),
        panel.background = element_blank(),
        panel.border=element_blank(),
        axis.line=element_line(colour="black"),
        plot.title = element_text(hjust=0.5,size=15))
```

Figure 3.7: The power curve



We include in our graph a box (in dotted lines) from 0.6 to 0.8, with bottom and top at heights 0.05 and 0.95. Then a value for m satisfies our requirements if and only if the graph of α enters the box from the bottom, and leaves from the top (left bottom is the type 1 and right top is the type 2 criterion).