

HW1-3.11

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Explanation of the example showing how the authors reached their conclusion that the critical value should be between 69 and 73 people cured

The ordinary aspirin was found effective against headache 60%. Now a drug company has a new aspirin and claims it to be more effective. We take a test for that. The null hypothesis is that $p=0.6$, the alternate hypothesis is that $p>0.6$. p is the probability that the new drug is effective. m is the least number of cured people when we reject the null hypothesis. So we want to have type 1 and type 2 error as small as possible.

The function *alpha* is the probability that we reject the null hypothesis, that is under the circumstances that the null hypothesis is true.

$$\alpha(p) = \sum_{m < k < n} b(n, p, k)$$

p in this case is 0.6, we count the values of $\alpha(0.6)$ for different m values ($m > 60$).

```
a<-rep(0,100)
b<-rep(0,100)
p<-rep(0,100)
m1<-rep(0,100)

n=100
for (i in 0:40){
  m1[i]=60+i
  a[i]=pbinom(n,n,0.6)-pbinom(m1[i]-1,n,0.6)
}
y1=data.frame(cbind(m1,a))
head(y1)
```

```
##   m1      a
## 1 61 0.4620753
## 2 62 0.3821877
## 3 63 0.3068098
## 4 64 0.2386107
## 5 65 0.1794694
## 6 66 0.1303365
```

$\alpha(0.6)$ is the probability of a type 1 error. We want to choose m to make $\alpha(0.6)$ small. The list above shows that as m increase, $\alpha(0.6)$ becomes smaller. So we take out the smallest m that makes $\alpha(0.6)$ smaller than 0.05, which is 69.

```
ma<-y1[which(y1$a<0.05),1]
ma[1]
```

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

$\beta(p)$ is the probability of a type 2 error, is to accept the null hypothesis when it is wrong.

$$\beta(p) = 1 - \alpha(p) = 1 - \sum_{m < k < n} b(n, p, k)$$

Now suppose that the additive is effective then p is greater than 0.6, which is 0.8. We want to choose m to make $\beta(0.8) = 1 - \alpha(0.8)$ small.

The list below shows that as m increases, $\beta(0.8)$ becomes larger. So we take out the maximum m that makes $\beta(0.8)$ smaller than 0.05, which is 73.

```
n=100
m2<-rep(0,100)
for (i in 1:20){
  m2[i]=80-i
  b[i]=1-(pbinom(n,n,0.8)-pbinom(m2[i]-1,n,0.8))
}
y2=data.frame(cbind(m2,b))
head(y2)
```

```
##      m2      b
## 1 79 0.34596678
## 2 78 0.26106725
## 3 77 0.18908721
## 4 76 0.13135322
## 5 75 0.08747538
## 6 74 0.05583272
```

```
mb<-y2[which(y2$b<0.05),1]
mb[1]
```

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

Conclusion: So we choose m between 69 and 73 to make the sum of probabilities of type 1 error and type 2 error small. If we want to make type1 error smaller, m could be set close to 73. If we want to make type2 error smaller, m could be set close to 69.

Power Curve

Here we will replicate and explain how the power curve of the Figure 3.7 is produced. Two lines are drawn with $m=69, 73$.

```
n=100
a1<-rep(0,100)
a2<-rep(0,100)
p<-seq(from=0.4,to=1,length=n)
for (i in 0:100){
  a1[i]=pbinom(n,n,p[i])-pbinom(69-1,n,p[i])
}
for (i in 0:100){
  a2[i]=pbinom(n,n,p[i])-pbinom(73-1,n,p[i])
}
data.all=data.frame(cbind(p,a1,a2))

plot<-ggplot(data=data.all,mapping=aes(x=p))+ geom_line(mapping=aes(y=a1))+ geom_line(mapping=aes(y=a2))
plot+
```

```

annotate("segment", x = 0.6, xend = 0.8, y = 0.05, yend = 0.05)+
annotate("segment", x = 0.6, xend = 0.8, y = 0.95, yend = 0.95)+
annotate("segment", x = 0.6, xend = 0.6, y = 0.05, yend = 0.95)+
annotate("segment", x = 0.8, xend = 0.8, y = 0.05, yend = 0.95)

```

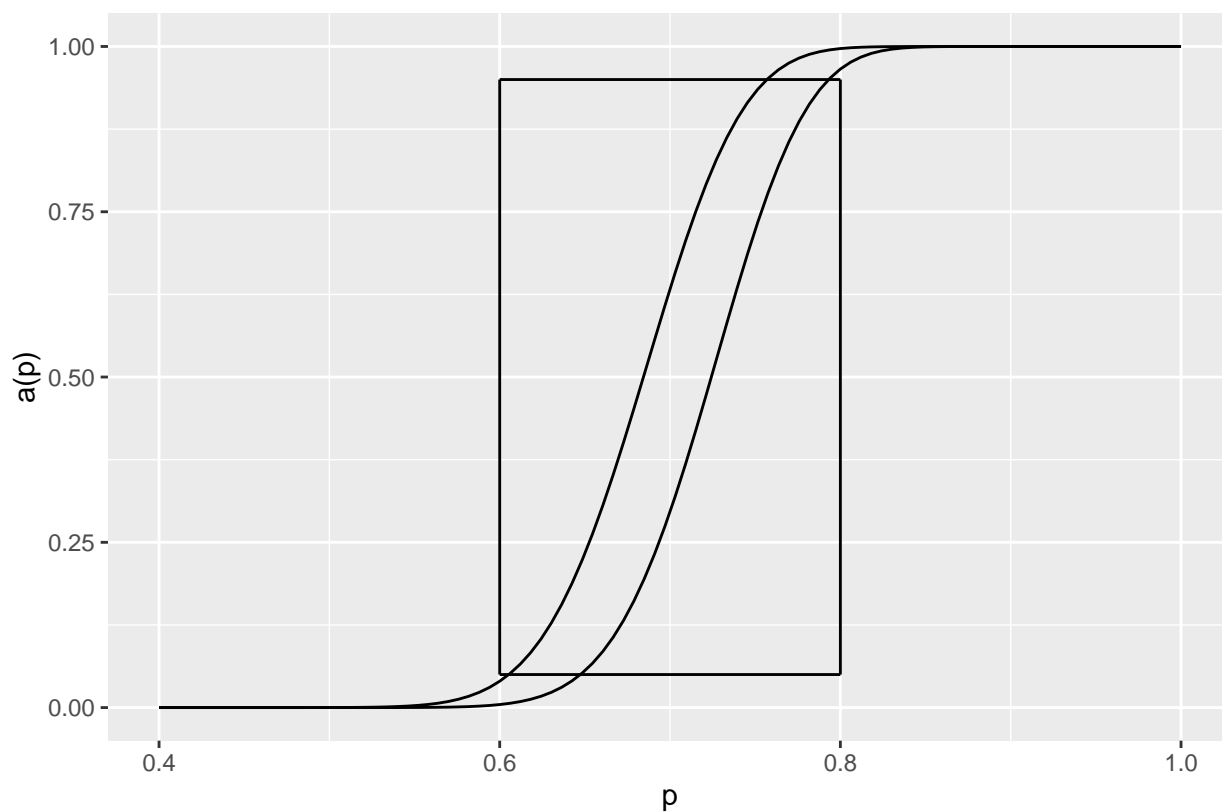


Figure 3.7: The power curve.

Thankfulness

Thanks to my friend Runqi Zhao that she gives me the idea of how the plot is made. Also I feel an immense gratitude to Xijia Luo for how m is chosen.