

# MA677\_hw1

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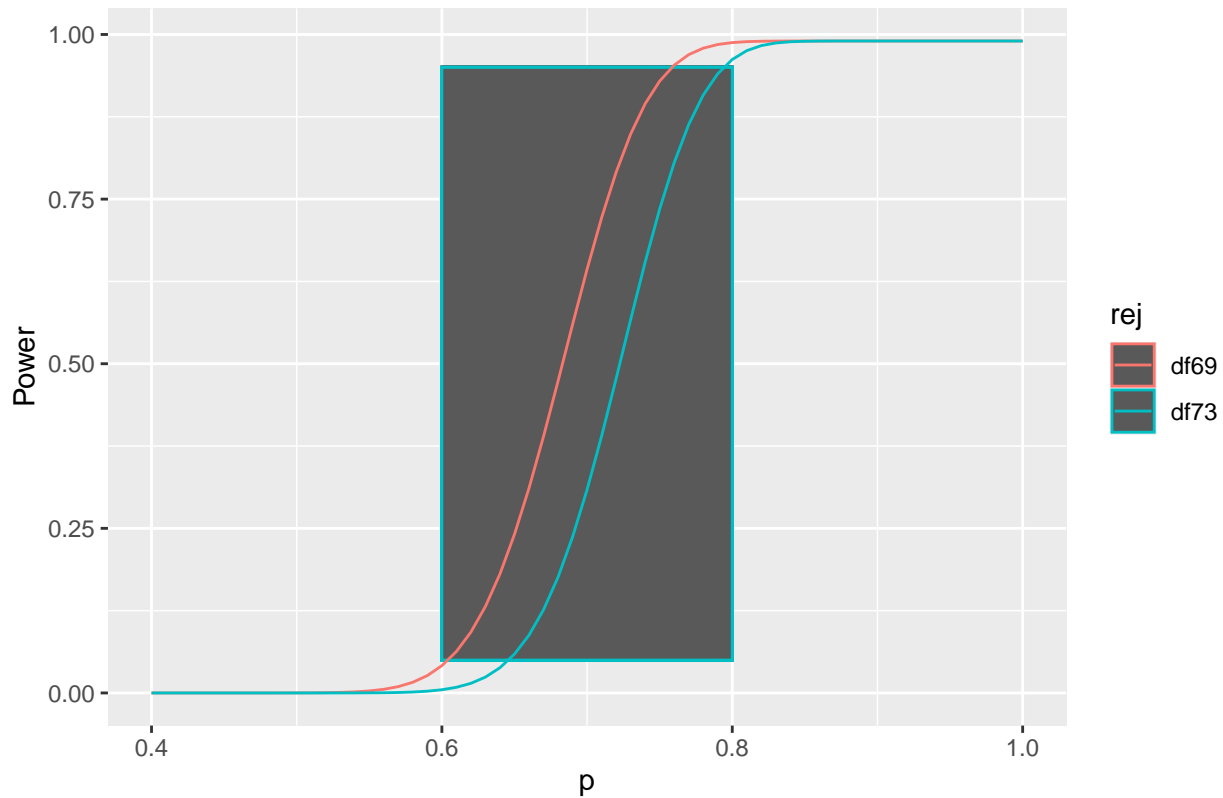
## The explanation of Figure 3.7

```
n = 100
m = c(69, 73)
p = seq(0.4, 1, 1 / n)

for (i in m) {
  if (i == m[1]) {
    df = data.frame(p,
                    rej = paste('df', i, sep = ''),
                    Power = cumsum(dbinom(i, n, p)))
  }
  else {
    df = rbind(df, data.frame(
      p,
      rej = paste('df', i, sep = ''),
      Power = cumsum(dbinom(i, n, p))
    ))
  }
}

ggplot(data = df, aes(x = p, y = Power, color = rej)) +
  geom_rect(aes(xmin = 0.6, xmax = 0.8, ymin = 0.05, ymax = 0.95)) +
  geom_line() +
  labs(title = 'Figure 3.7: The power curve')
```

Figure 3.7: The power curve



From the plot above, we can see a box from 0.6 to 0.8, which means the  $p$  for the old drug is 0.6, and the  $p$  for the new drug is 0.8. The height of bottom and top of the box is 0.05 and 0.95 respectively which indicate the 5% type 1 error and (1-95%) type 2 error respectively. As  $m$  increases, the graph moves to the right. In this case, the line of  $m = 69$  intersect with type 1 error and the line of  $m = 73$  intersect with the type 2 error. Thus, we may choose our critical value between 69 and 73.