

Assignment 5

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9.7

Let X_1, \dots, X_n be a sample from a Poisson distribution. Find the likelihood ratio for testing $H_0: \lambda = \lambda_0$ versus $H_A: \lambda = \lambda_1$, where $\lambda_1 > \lambda_0$. Use the fact that the sum of independent Poisson random variables follows a Poisson distribution to explain how to determine a rejection region for a test at level α .

From Rice Page 339,347

$$\Lambda = \frac{\max_{\theta \in w_0} \text{lik}(\lambda_0)}{\max_{\theta \in w_0} \text{lik}(\lambda_1)} = \frac{\prod_{i=1}^n \frac{e^{-\lambda_0} \lambda_0^{X_i}}{X_i!}}{\prod_{i=1}^n \frac{e^{-\lambda_1} \lambda_1^{X_i}}{X_i!}} = \frac{e^{-n\lambda_0} \lambda_0^{\sum_{i=1}^n X_i}}{e^{-n\lambda_1} \lambda_1^{\sum_{i=1}^n X_i}} = e^{n(\lambda_1 - \lambda_0)} \left(\frac{\lambda_0}{\lambda_1}\right)^{\sum_{i=1}^n X_i}$$

Since $\lambda_1 > \lambda_0$, $\frac{\lambda_0}{\lambda_1} < 1$. So, for higher values of $\sum_{i=1}^n X_i$, Λ is small, which is favourable to H_A .

Therefore, we will reject H_0 when $\sum_{i=1}^n X_i > c$, where c is the critical value [Rice Page 330] that determines α , which is our significance level.

Now, we know that the sum of independent Poisson random variables follows a Poisson distribution as well. So, $\sum_{i=1}^n X_i \sim P_0(n\lambda)$ Let $Y = \sum_{i=1}^n X_i$ Then under H_0 , $Y \sim P_0(n\lambda_0)$

Recall, Type I error = $\mathbb{P}(\text{reject } H_0 \mid H_0) = \alpha$

So,

$$\begin{aligned} \alpha &= \mathbb{P}(\text{reject } H_0 \mid H_0) \\ &= \mathbb{P}\left(\sum_{i=1}^n X_i > c \mid \lambda = \lambda_0\right) \\ &= 1 - \mathbb{P}(Y \leq c) \\ &= 1 - F(c) \end{aligned}$$

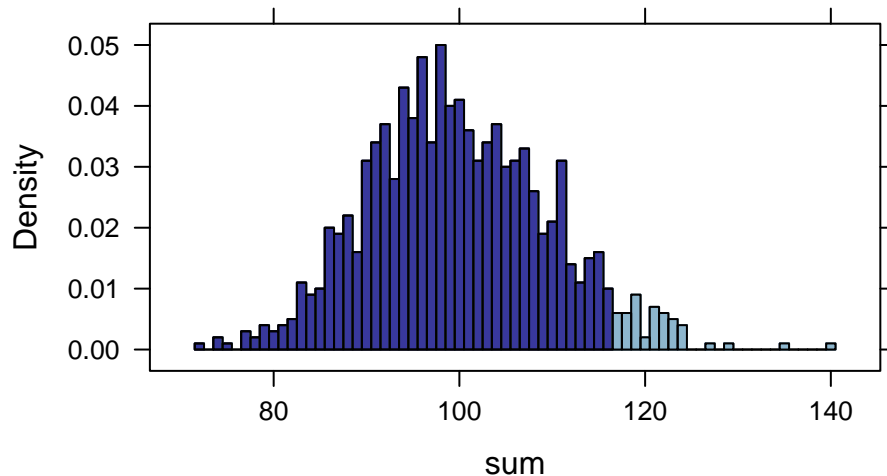
Simulation

Here we're going to have $H_0: \lambda_0 = 1$ and $H_A: \lambda_1 = 3$, and with a sample size of 100, we're going to calculate a critical value, c , based on $\alpha = 5\%$.

```
set.seed(370)
hist1<-do(1000)*sum(rpois(100, lambda = 1)) #generate random numbers from a Poisson distribution.
#take lambda_0 (lambda under null) =1 and lambda_1 (lambda under alternative) = 3 arbitrarily
hist1 <- mutate(hist1, statistic = (1/3)^sum) #test statistic of ((lambda_0)/(lambda_1))^sum
favstats(~ statistic, data=hist1)
```

```
##           min           Q1           median           Q3           max
## 1.595969e-67 2.661626e-51 5.820976e-48 4.243491e-45 4.438842e-35
##           mean           sd      n missing
## 5.668464e-38 1.421479e-36 1000           0
```

```
c <- quantile(hist1$sum, 0.95) #let's say we want alpha = 5%, so we can determine the critical value, c
histogram(~ sum, width=1, group=sum>c, data=hist1) #using the critical value calculated above
```



```
#Tally the sums greater than c and divide by 1000 to check the alpha level
tally(hist1$sum>c)[1]/1000
```

```
## TRUE
## 0.049
```

9.8

Show that the test of Problem 7 is uniformly most powerful for testing $H_0 : \lambda = \lambda_0$ versus $H_A : \lambda > \lambda_0$.

[Rice Pg 336] We can extend the Neyman-Pearson Lemma so that if the alternative H_1 is composite, a test that is most powerful for *every* simple alternative in H_1 is said to be **uniformly most powerful**. In more detail, we know that $Y \sim \text{Pois}(n\lambda)$. So, $\mathbb{P}(Y > c) = \alpha$. We reject H_0 when $Y > c$. $Y > c$ is the most powerful test at α level for every $\lambda_1 > \lambda_0$ and so consequentially the test that rejects H_0 if $Y \geq c$ is the uniformly most powerful test for $H_0 : \lambda = \lambda_0$ vs $H_1 : \lambda > \lambda_0$.

This problem is very similar to the scenario Rice presents on page 336 with Example A of Section 9.2 where since the most powerful test that for a particular alternative $\mu_1 > \mu_0$ rejects for $\bar{X} > x_0$ is the most powerful and is same for every alternative, it is uniformly most powerful.

9.11

Suppose that X_1, \dots, X_{25} form a random sample from a normal distribution having a variance of 100. Graph the power of the likelihood ratio test of $H_0: \mu = 0$ versus $H_A: \mu \neq 0$ as a function of μ , at significance levels .10 and 0.05. Do the same for a sample size of 100. Compare the graphs and explain what you see.

Rice defines type II error on page 331 as the probability of failing to accept the alternative hypothesis (accepting null) given that the alternative is true $[P(\text{accept}H_0 \mid H_1)]$. In comparison, type I error is defined as the probability of rejecting null given that null is true $[P(\text{reject}H_0 \mid H_0)]$. Power is the probability that the null hypothesis is rejected when it is false and equals 1 minus the probability of a type II error. To calculate the power given an alpha level, one can calculate the type I error probability and use that bound to calculate the probability of failing to accept the alternative (accepting the null hypothesis) given that alternative is true. The bounds can be used as quantiles to find the type II error probabilities and the result can be subtracted from 1 to find the power as illustrated below:

```

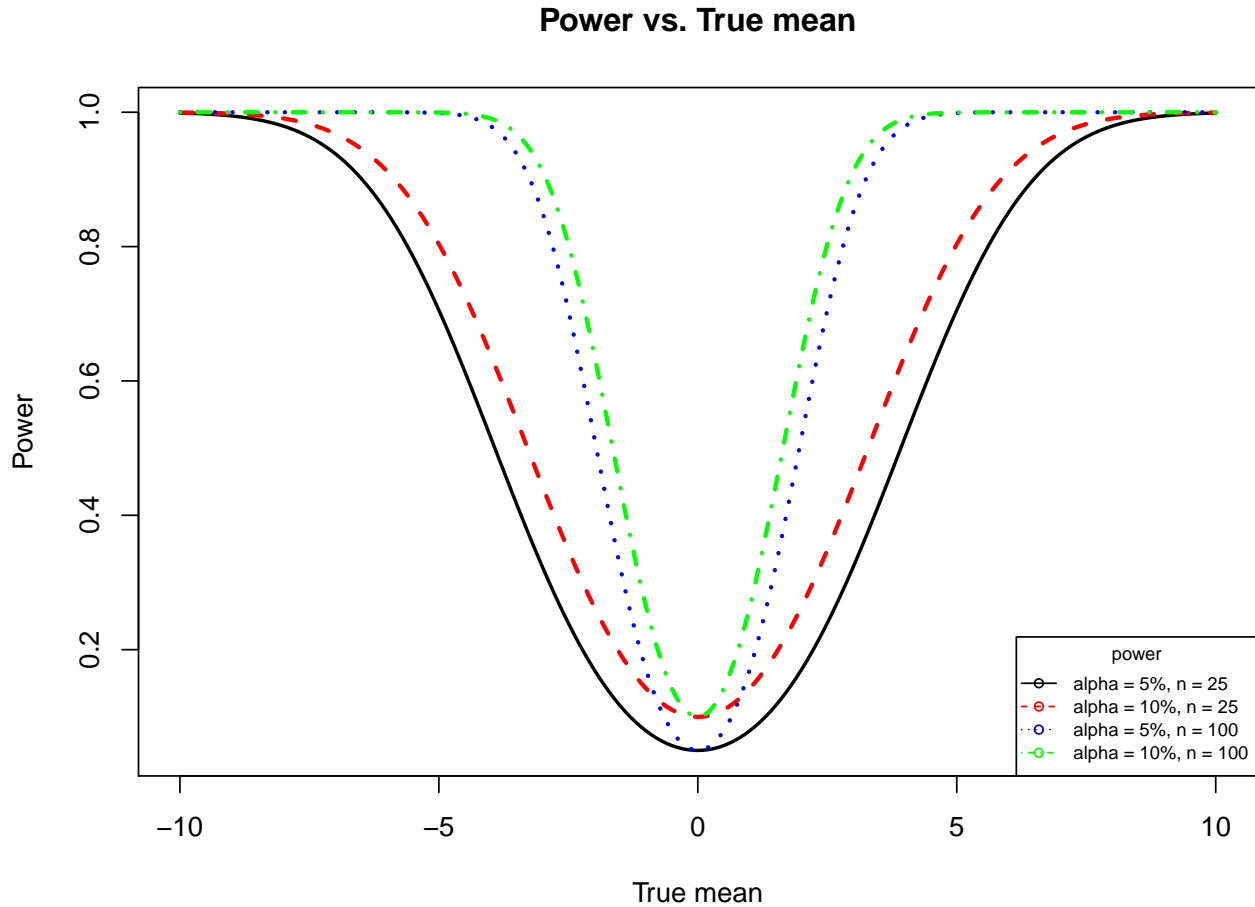
set.seed(370)
var=100
n1=25
n2=100
sd25=sqrt(var)/sqrt(n1) #standard deviation with sample size 25
sd100=sqrt(var)/sqrt(n2) #standard deviation with sample size 100
twotailed_z10 = 1.645 #critical value for two-sided test at alpha 0.10
twotailed_z5 = 1.960 #critical value for two-sided test at alpha 0.05
null_mean = 0
#Bound at significance level 0.10 for n = 25
bound10_25 = c(null_mean - twotailed_z10*sd25, null_mean + twotailed_z10*sd25)
#Bound at significance level 0.05 for n = 25
bound5_25 = c(null_mean - twotailed_z5*sd25, null_mean + twotailed_z5*sd25)
#Bound at significance level 0.10 for n = 100
bound10_100 = c(null_mean - twotailed_z10*sd100, null_mean + twotailed_z10*sd100)
#Bound at significance level 0.05 for n = 100
bound5_100 = c(null_mean - twotailed_z5*sd100, null_mean + twotailed_z5*sd100)

mu <- seq(-10,10,0.1)

#Power calculated by subtracting the type II error probability from 1
power5_25 <- 1-(pnorm(bound5_25[2],mean = mu, sd =sd25) -
  pnorm(bound5_25[1],mean = mu, sd =sd25))
power10_25 <- 1-(pnorm(bound10_25[2],mean = mu, sd =sd25) -
  pnorm(bound10_25[1],mean = mu, sd =sd25))
power5_100 <- 1-(pnorm(bound5_100[2],mean = mu, sd =sd100) -
  pnorm(bound5_100[1],mean = mu, sd =sd100))
power10_100 <- 1-(pnorm(bound10_100[2],mean = mu, sd =sd100) -
  pnorm(bound10_100[1],mean = mu, sd =sd100))

plot(power5_25~mu, type = "l",xlab = "True mean", ylab = "Power",lty = 1,lwd = 2)
title("Power vs. True mean")
lines(power10_25~mu, col = "red",lty = 2,lwd = 2.5)
lines(power5_100~mu,col = "blue",lty = 3,lwd = 2.5)
lines(power10_100~mu,col = "green",lty = 4,lwd = 2.5)
legend("bottomright", c("alpha = 5%, n = 25","alpha = 10%, n = 25","alpha = 5%, n = 100","alpha = 10%, n = 100"),
  pch = 1, col = c("black","red","blue","green"),
  title = "power",lty=c(1,2,3,4),cex=0.7)

```



Looking at the graph above, where power is plotted against the true mean parameter μ for different values of μ , we can note a few things.

1. The power is lowest at $\mu = 0$, reaching a minimum of $\alpha = 5\%$ (black and blue) or $\alpha = 10\%$ (red and green), that is when the alternative hypothesis is the same as the null hypothesis. Which makes sense, because if both our hypotheses are the same then $P(\text{reject } H_0 \mid H_0 \text{ is False})$ is the same as our chosen α .
2. At the same alpha level, we can compare the shapes of the graphs to discern the difference that sample size has on power as a function of varying μ . At $\alpha = 5\%$, we are looking at the black and blue lines, we see that increasing the sample size from 25 to 100 narrows the curve, suggesting that more data increases the power more quickly for small changes in μ . We can see that the same is true when we look at the red and green lines, with the green curve being narrower than the red, but having the same minimum.
3. We see that all the curves eventually reach power = 1 as we get further away from $\mu = 0$ (True mean = 0), but that those with smaller alphas and larger sample sizes do so faster. So the trade-off here is between power, an acceptable confidence level, and the amount of resources we have to collect data for a particular sample size.