

Problem Section 7

Monday Feb 26 2024

Exercises

1. We have our observed value as $x = 3$. Under the null hypothesis we have that:

$$X \sim \text{Binom}(n = 10, \pi = 1/6)$$

Since we are considering a composite alternative hypothesis, we will conduct a 2 tailed test.

First we can examine the null binomial PMF:

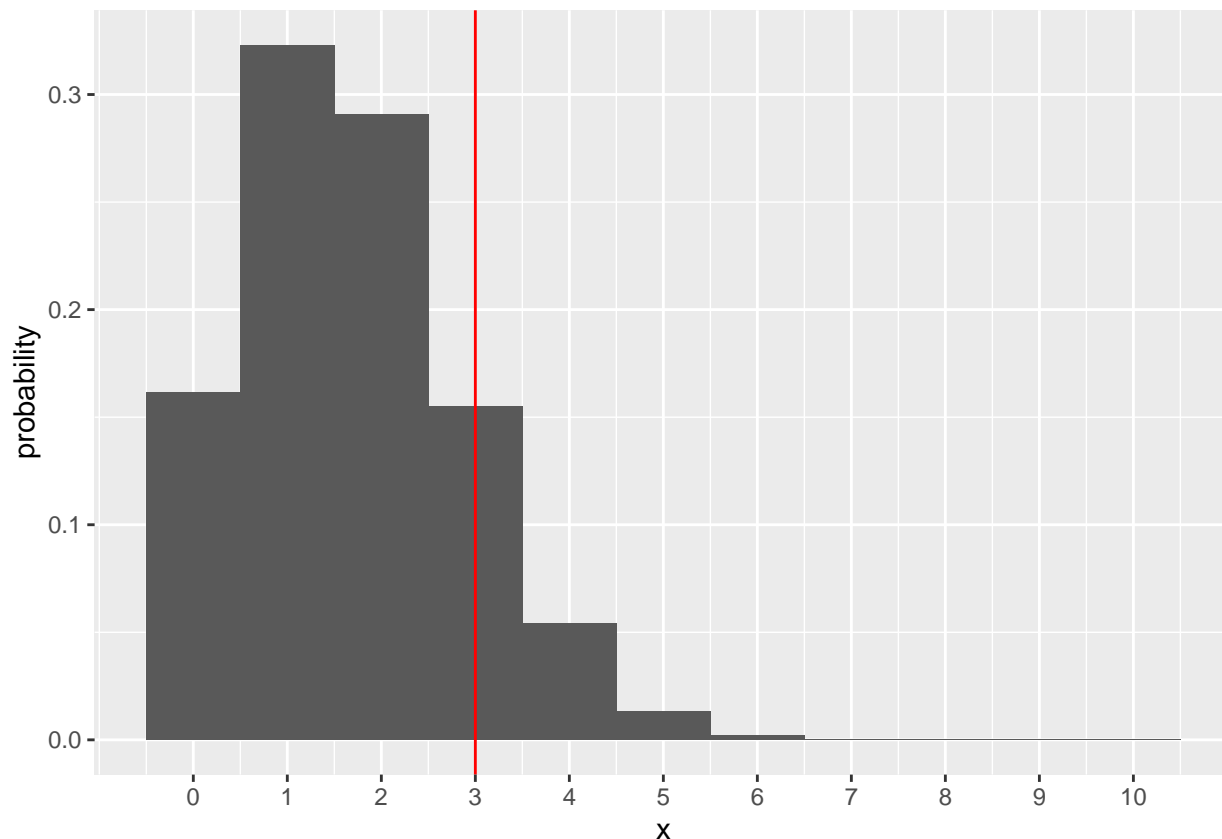
```
binom_tibble <- tibble(  
  x = seq(0,10),  
  binom_pmf = dbinom(x,10,1/6)  
)
```

binom_tibble

```
## # A tibble: 11 x 2  
##       x    binom_pmf  
##   <int>    <dbl>  
## 1     0 0.162  
## 2     1 0.323  
## 3     2 0.291  
## 4     3 0.155  
## 5     4 0.0543  
## 6     5 0.0130  
## 7     6 0.00217  
## 8     7 0.000248  
## 9     8 0.0000186  
## 10    9 0.000000827  
## 11   10 0.0000000165
```

#plot PMF

```
ggplot(data=binom_tibble, aes(x=x,  
                              y=binom_pmf))+  
  geom_col(width = 1)+  
  geom_vline(xintercept=3,col='red')+  
  scale_x_continuous(breaks = 0:10)+  
  labs(y='probability')
```



Thus for our 2-sided P-value we would consider the probability of observing data as extreme as ours, or more. We see in the above PMF, that the values that are more extreme (have lower probability) than $x=3$, are all values greater than 3. Thus for our p-value we are considering:

$$p = P(X \geq 3) = 0.2247732$$

```
1-pbinom(2,10,1/6)
```

```
## [1] 0.2247732
```

Thus when the null is true, there is a 22% chance of observing $x=3$, or more extreme data. This is a relatively high p-value so in general we would not consider it enough information to reject the null hypothesis. Note: you can also automate the two-sided P-value calculation as shown below.

```
probs <- dbinom(0:10, size = 10, prob = 1/6)
```

```
sum(probs[probs <= dbinom(x = 3, size = 10, prob = 1/6)] )
```

```
## [1] 0.2247732
```

2.

- a. In this setting we would want to see if the observed mean from the 25 basket sample, \$149.75, is large enough to reject the hypothesized mean of \$145.75. Naturally we would form our null and alternative as follows:

$$H_0 : \mu_0 = 145.75 \quad H_1 : \mu_0 \neq 145.75$$

- b. If we assume that the CLT will apply that means that we will have that:

$$\bar{X} \sim N(\mu = \mu_0, \sigma = \frac{9.5}{\sqrt{25}} = 1.9)$$

c. Since this is a two-sided alternative, the P-value is

$$2 \min\{P_{\mu_0=145.75}(\bar{X} \leq 149.75), P_{\mu_0=145.75}(\bar{X} \geq 149.75)\}.$$

Since 149.75 is to the right of 145.75 - the mean of the normal distribution when the null hypothesis is true, it is clear that the P-value = $2 \times P_{\mu_0=145.75}(\bar{X} \geq 149.75)$ as this will be the minimum.

```
2*pnorm(q = 149.75, mean = 145.75, sd = 9.5/sqrt(25), lower.tail=F)
```

```
## [1] 0.03526841
```

Thus when the null is true we see data this unusual or more about 3% of the time.

3.

a. Since small values of S lie in the direction predicted by H_1 (why?), the P-value is

$$\text{P-value} = P_{\lambda_0=6}(S \leq s_{obs})$$

with $S \sim \text{Pois}(4\lambda_0)$.

This is calculated below.

```
ppois(q = 15, lambda = 4*6)
```

```
## [1] 0.03440009
```

b. We will reject for any s_{obs} that satisfies that $P_{\lambda_0=6}(S \leq s_{obs}) \leq 0.1$. Since the Poisson PMF is monotonically decreasing, for large values, we can create the table of Poisson probabilities to find the smallest s_{obs} for which we will reject H_0 . A more succinct alternative to target the search is to find the 10th percentile of the distribution first.

```
qpois(p = 0.1, lambda = 4*6) #18 has at least 10% probability below it
```

```
## [1] 18
```

```
ppois(18, lambda = 24) #let's see how much exactly
```

```
## [1] 0.1282787
```

```
ppois(17, lambda = 24)
```

```
## [1] 0.08712644
```

Therefore we would reject H_0 for any $s_{obs} \leq 17$ since these values would give a P-value smaller than 0.1.

c. A Type 1 error occurs when we mistakenly reject H_0 . That is, we reject H_0 even though H_0 is true. The probability of a Type I error in this example is $P_{\lambda_0=6}(S \leq 17)$.

```
ppois(17, lambda = 4*6)
```

```
## [1] 0.08712644
```

d. A Type II error occurs when we mistakenly fail to reject H_0 . That is, we do not reject H_0 even though H_1 is true. The probability of a Type II error is $P_{\lambda_0=4}(S > 17)$.

```
ppois(16, lambda = 4*4, lower.tail = FALSE)
```

```
## [1] 0.4340376
```

4.

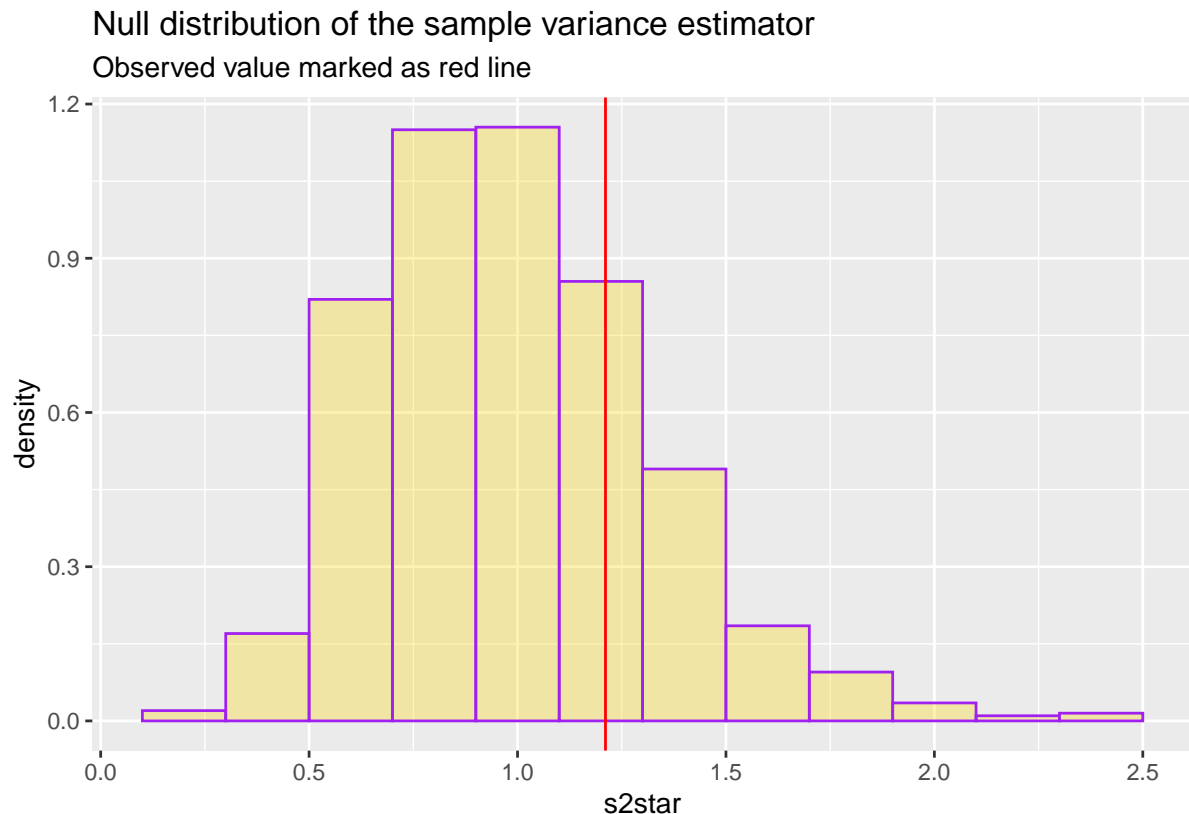
```
a. obs_s2 <- sample_df %>% summarise(s2 = var(x)) %>% pull()
```

The value of s_{obs}^2 is 1.211

```
b. set.seed(2626)                                #random number seed
   B <- 1000                                       # number of replications
   nsamp <- nrow(sample_df)                       # sample size n
   sigma2_null <- 1                              #null value

   null_sim_df <- tibble(
     s2star = replicate(n = B,
       expr = var(rnorm(n = nsamp, 0,sigma2_null))))
```

```
c. ggplot(data = null_sim_df,
  mapping = aes(x = s2star,
    y = after_stat(density))) +
  geom_histogram(binwidth = 0.2,
    alpha=0.3,
    fill="gold",
    color="purple")+
  geom_vline(xintercept = obs_s2,
    color="red")+
  labs(title = "Null distribution of the sample variance estimator",
    subtitle = "Observed value marked as red line")
```



d. Since S^2 is unbiased for the true value of σ_0^2 , we should see around 1 when H_0 is true and values above 1 when H_1 is true. Therefore, the P-value is the probability of seeing a result which is at least as large

as our observed result.

```
#calculate empirical P-value
```

```
pvalue <- null_sim_df %>%  
  summarise( pvalue = mean(s2star >= obs_s2)) %>% pull()
```

The P-value is 0.226