

Simulation-based testing

Part 2

Prof. Maria Tackett

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- **Parameter**: a numerical quantity derived from the population (almost always unknown)
- **Statistical inference** is the process of using sample data to make conclusions about the underlying population the sample came from.
- **Testing**: evaluating whether our observed sample provides evidence for or against some claim about the population

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- 2 Choose a (representative) sample, collect data, and analyze the data.
- 3 Figure out how likely it is to see data like what we observed, IF the null hypothesis were in fact true (called a **p-value**)
- 4 If our data would have been extremely unlikely if the null hypothesis were true, then we reject it in favor of the alternative hypothesis.

Otherwise, we cannot reject the null hypothesis

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Suppose we test a certain null hypothesis, which can be either true or false (we never know for sure!). We make one of two decisions given our data: either reject or fail to reject H_0 .

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It is important to weigh the consequences of making each type of error.

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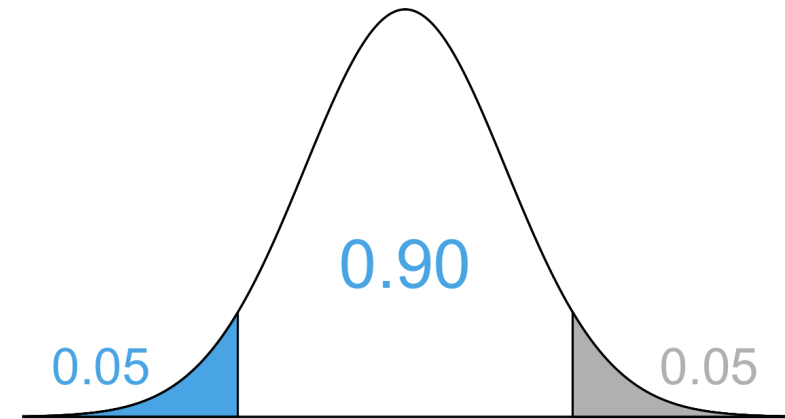
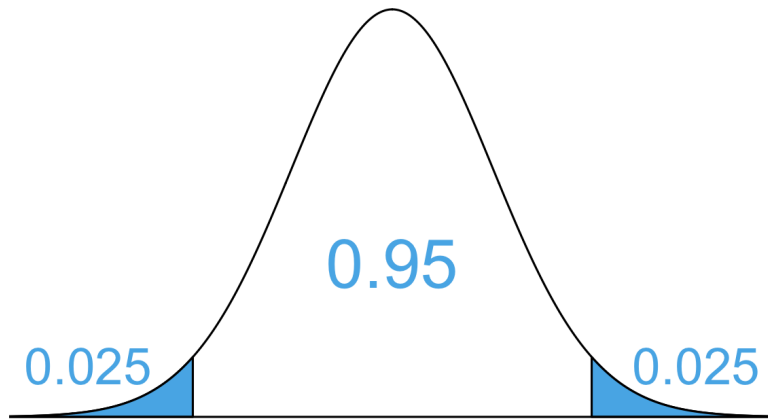
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Though we'd like to know if we're making a correct decision or making a Type I or Type II error, hypothesis testing does **NOT** give us the tools to determine this.

Equivalency of confidence and significance levels

- Two sided alternative hypothesis test with $\alpha \rightarrow CL = 1 - \alpha$
- One sided alternative hypothesis with $\alpha \rightarrow CL = 1 - (2 \times \alpha)$



Back to Asheville!



Your friend claims that the mean price per guest per night for Airbnbs in Asheville is \$100. **What do you make of this statement?**

Let's use hypothesis testing to assess this claim!

1 Defining the hypotheses

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What will our null and alternative hypotheses be for this example?

- H_0 : the true mean price per guest is \$100 per night
- H_a : the true mean price per guest is NOT \$100 per night

Expressed in symbols:

- $H_0 : \mu = 100$
- $H_a : \mu \neq 100$

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```
asheville <- read_csv("data/asheville.csv")  
  
asheville %>%  
  summarize(mean_price = mean(ppg))
```

```
## # A tibble: 1 x 1  
##   mean_price  
##   <dbl>  
## 1       76.6
```

3 Assessing the evidence

Next, we calculate the probability of getting data like ours, or more extreme, if H_0 were in fact actually true.

This is a conditional probability:

Given that H_0 is true (i.e., if μ were *actually* 100), what would be the probability of observing $\bar{x} = 76.6$ or more extreme?

This probability is known as the **p-value**.

Simulating the null distribution

Let's return to the Asheville data. We know that our sample mean was 76.6, but we also know that if we were to take another random sample of size 50 from all Airbnb listings, we might get a different sample mean.

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How might we quantify the sampling distribution of the mean using only the data that we have from our original sample?

Bootstrap distribution of the mean

```
set.seed(12345)
```

```
library(infer)
```

```
boot_means <- asheville %>%
```

```
  specify(response = ppg) %>%
```

```
  generate(reps = 5000, type = "bootstrap") %>%
```

```
  calculate(stat = "mean")
```

```
ggplot(data = boot_means, aes(stat)) +
```

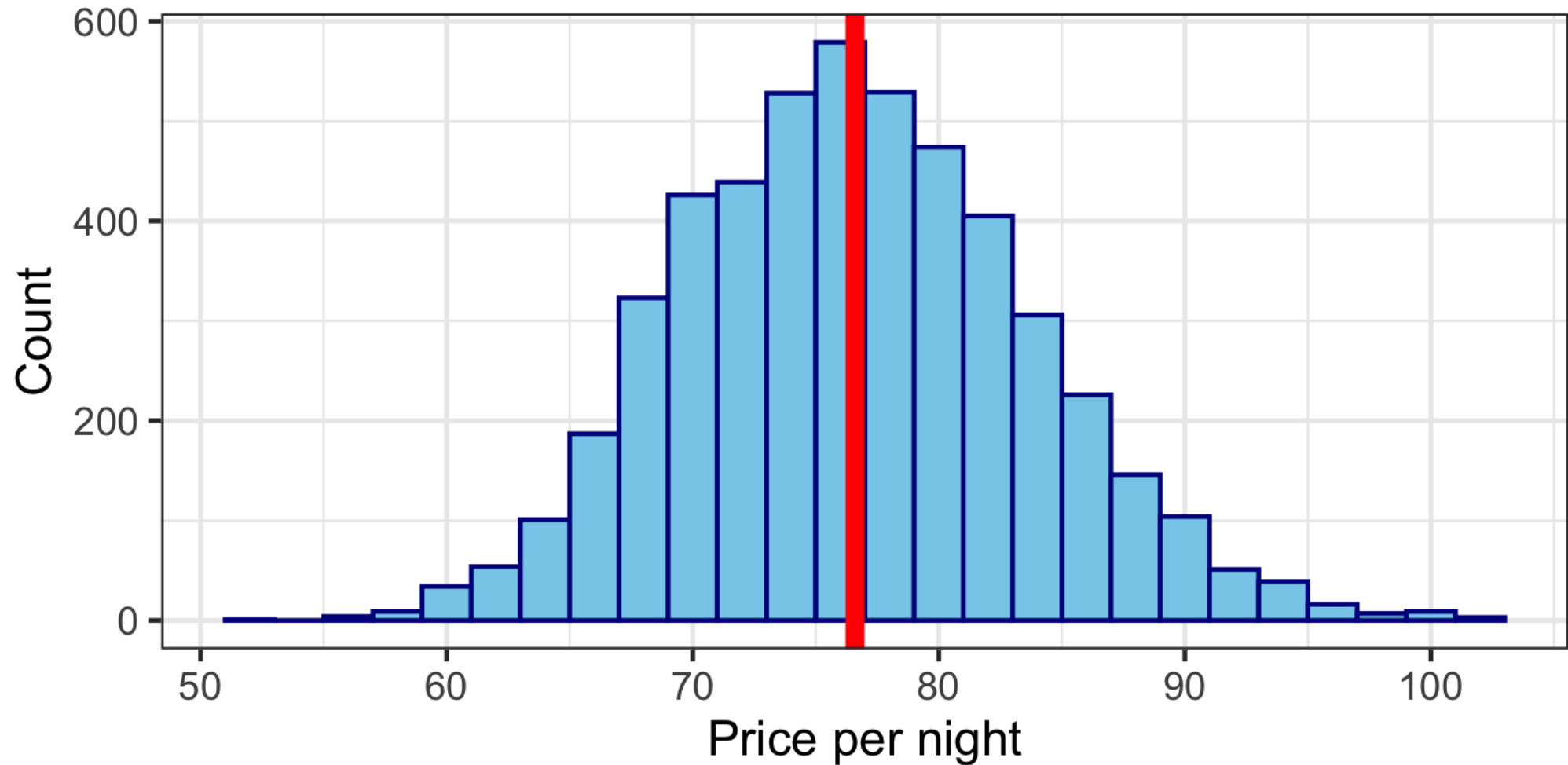
```
  geom_histogram(binwidth = 2, color = "darkblue", fill = "skyblue") +
```

```
  labs(x = "Price per night", y = "Count") +
```

```
  geom_vline(xintercept = mean(boot_means$stat),
```

```
            lwd = 2, color = "red")
```

Bootstrap distribution of the mean



Shifting the distribution

We've captured the variability in the sample mean among samples of size 50 from Asheville area Airbnbs, but remember that in the hypothesis testing paradigm, we must assess our observed evidence under the assumption that the null hypothesis is true.

```
boot_means %>%  
  summarize(mean(stat))
```

```
## # A tibble: 1 x 1  
##   `mean(stat)`  
##           <dbl>  
## 1           76.6
```

Remember,

$$H_0 : \mu = 100$$

$$H_a : \mu \neq 100$$

Where should the bootstrap distribution of means be centered if in fact H_0 were actually true?

Shifting the distribution

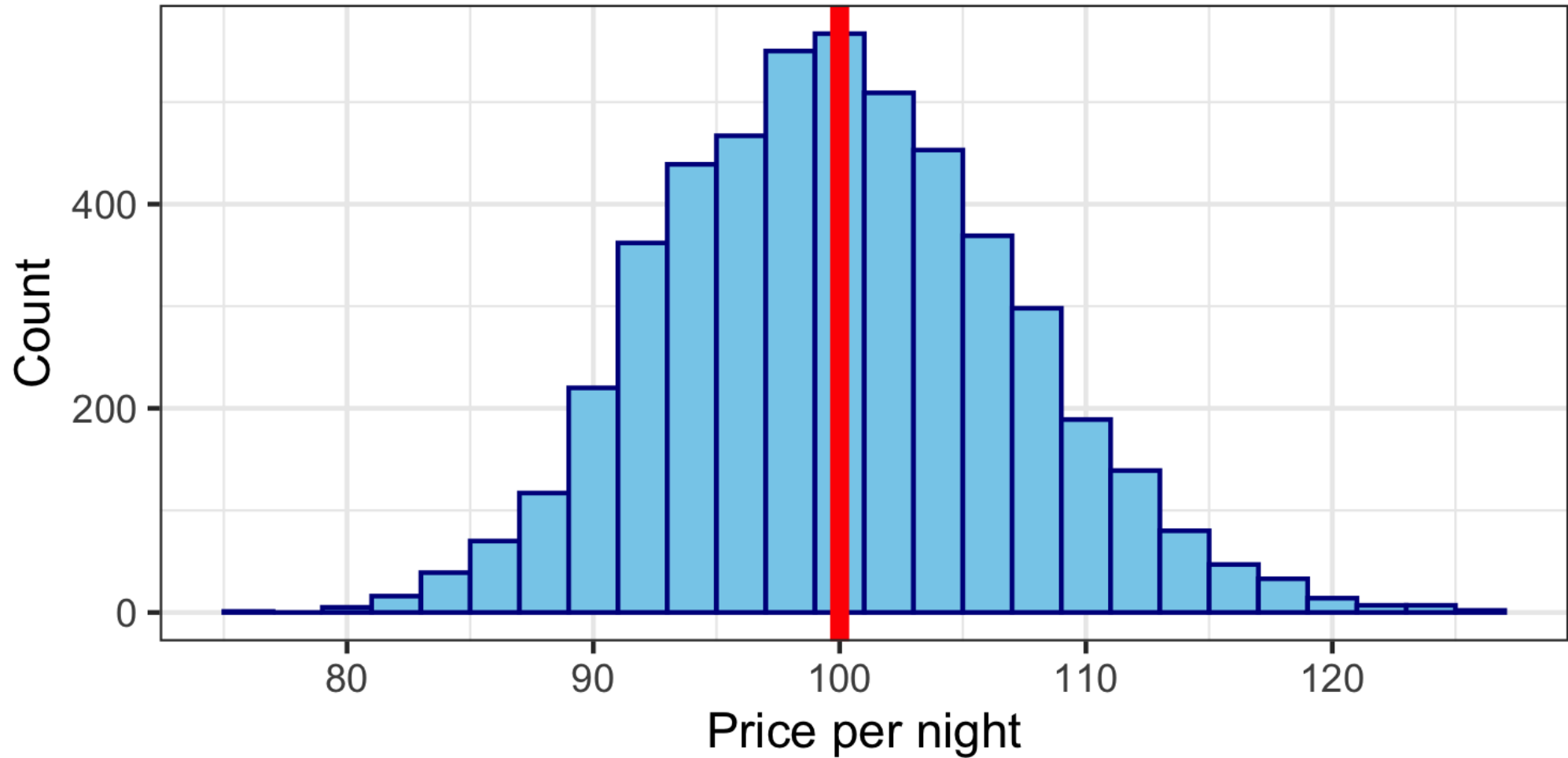
```
ash_boot_mean <- boot_means %>%  
  summarize(mean = mean(stat)) %>%  
  pull()
```

```
boot_means <- boot_means %>%  
  mutate(null_dist_stat = stat - (ash_boot_mean - 100))
```

If we shifted the bootstrap distribution by **offset**, then it will be centered at μ_0 : the null-hypothesized value for the mean.

```
ggplot(data = boot_means, aes(x = null_dist_stat)) +  
  geom_histogram(binwidth = 2, color = "darkblue", fill = "skyblue") +  
  labs(x = "Price per night", y = "Count") +  
  geom_vline(xintercept = mean(boot_means$null_dist_stat), lwd = 2,
```

Distribution of $\bar{x}$ under H_0



Simulating the null distribution with infer

```
null_dist <- asheville %>%  
  specify(response = ppg) %>%  
  hypothesize(null = "point", mu = 100) %>%  
  generate(reps = 5000, type = "bootstrap") %>%  
  calculate(stat = "mean")
```

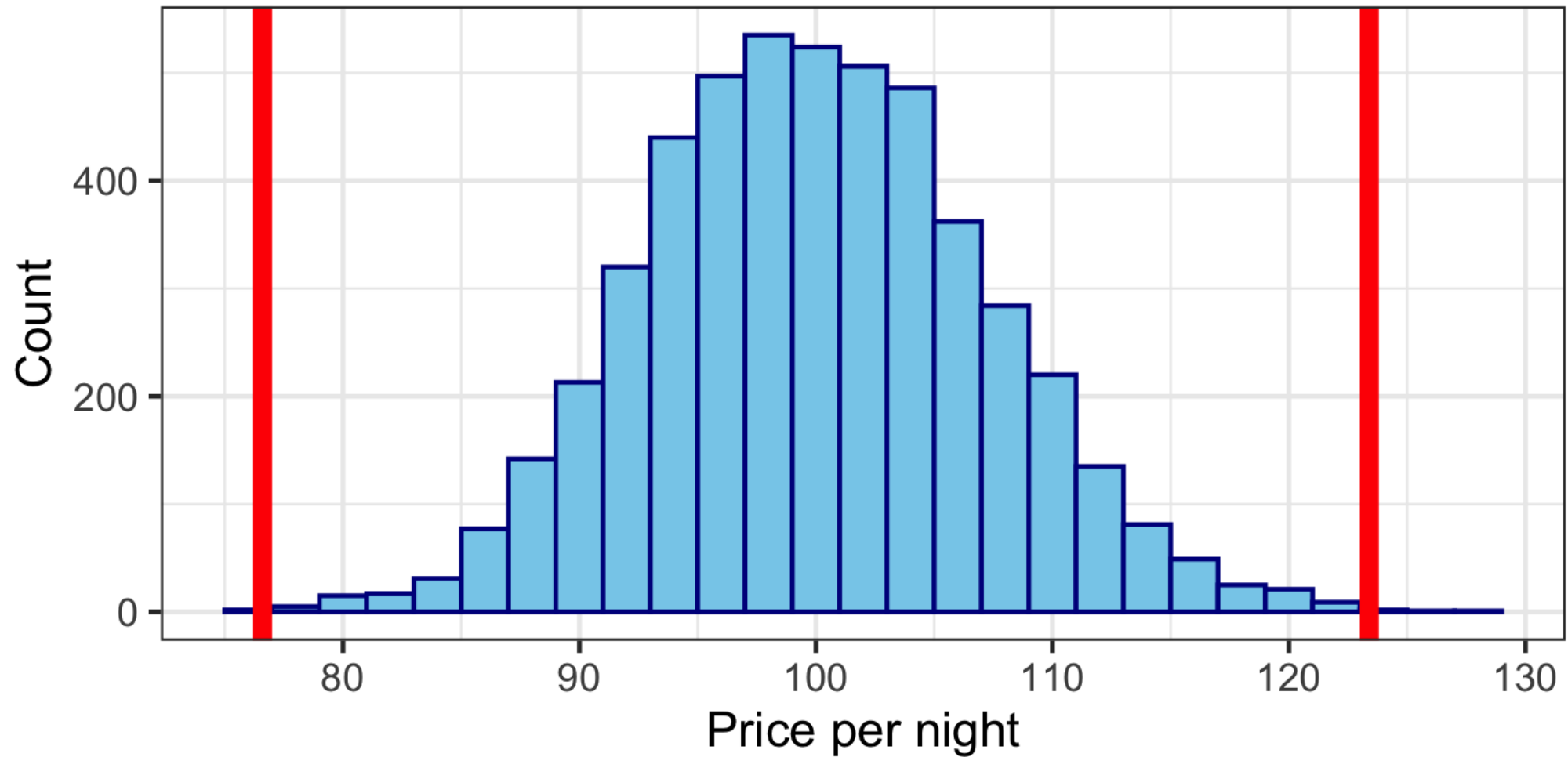
```
null_dist
```

```
## # A tibble: 5,000 x 2  
##   replicate  stat  
##   <int> <dbl>  
## 1         1 104.  
## 2         2 112.  
## 3         3  92.7  
## 4         4 102.
```

```
null_dist %>%  
  summarise(mean = mean(stat))
```

```
## # A tibble: 1 x 1  
##   mean  
##   <dbl>  
## 1 100.
```

3 Assessing the evidence



3 Assessing the evidence

```
null_dist %>%  
  filter(stat <= 76.6 | stat >= (100 + (100 - 76.6))) %>%  
  summarise(p_value = n()/nrow(null_dist))
```

```
## # A tibble: 1 x 1  
##   p_value  
##   <dbl>  
## 1 0.0008
```

4 Make conclusion

What might we conclude at the $\alpha = 0.05$ level?

The p-value, 0.0008 is less than 0.05, so we **reject (H_0)**. The data provide sufficient evidence that the mean price per guest per night for Airbnbs in Asheville is not equal to \$100.

Discussion questions

- H_a here was a **two-sided** hypothesis ($H_a : \mu \neq 100$). How does this compare to the **one-sided** hypothesis from last time ($H_a : p < 0.1$)?

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- H_a here was a **two-sided** hypothesis ($H_a : \mu \neq 100$). How does this compare to the **one-sided** hypothesis from last time ($H_a : p < 0.1$)?
- How might the p-value change depending on what type of alternative hypothesis is specified?
- Why did we need to "shift" the bootstrap distribution when we generated the null distribution in this example, but we didn't need shift the distribution last time when we generated the null distribution for inference on the population proportion?