

# Lecture 13: One Sample Hypothesis Tests

STAT 324

Ralph Trane  
University of Wisconsin–Madison

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**WISCONSIN**  
UNIVERSITY OF WISCONSIN–MADISON

# One Sample Hypothesis Test: Example IV



- Secondhand smoke is of great health concern, especially for children.
- A sample was taken of 15 children in foster care suspected of being exposed to secondhand smoke, and the amount of cotinine (a metabolite of nicotine) in the urine was measured in ng/mL.
- Cotinine in unexposed children should be below 75 units. The data were as follows:

```
library(tidyverse); theme_set(theme_bw())
secondhand_smoking <- tibble(cotinine = c( 29,  30,  53,  75,  34,
                                           21,  12,  58, 117, 119,
                                           115, 134, 253, 289, 287))
```

Based on this data, does it seem like the mean of cotinine of children exposed to secondhand smoke is greater than 75 ng/mL?

# One Sample Hypothesis Test: Example IV



We would like to test  $H_0 : \mu = 75$  vs.  $H_A : \mu > 75$ .

What significance level would you pick?

Recall,  $\alpha = P(\text{type I error}) = P(\text{reject } H_0 \mid H_0 \text{ true})$ . Also, decreasing  $P(\text{type I error})$  increases  $P(\text{type II error})$  (will see why later). So, picking  $\alpha$  can be done by assessing which is worse: type I or type II error.

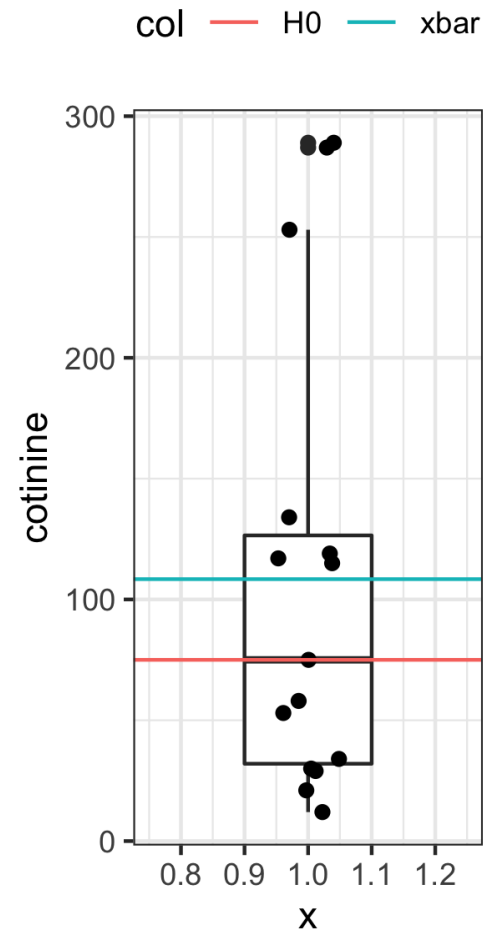
Here, I would say type II error is worse: if we fail to reject the null, but we should have, we conclude that the children are fine, when in reality the levels of cotinine is too high.

So, let's pick  $\alpha = 0.1$ , which is traditionally relatively "large".

# One Sample Hypothesis Test: Example IV



```
hlines <- tibble(  
  y = c(mean(secondhand_smoking$cotinine  
            75),  
  col = c('xbar', 'H0')  
)  
  
ggplot(secondhand_smoking,  
  aes(x = 1, y = cotinine)) +  
  geom_boxplot(width = 0.2) +  
  geom_jitter(height = 0,  
    width = 0.05) +  
  geom_hline(data = hlines,  
    aes(yintercept = y,  
      color = col)) +  
  xlim(c(0.75, 1.25)) +  
  theme_bw() +  
  theme(legend.position = "top")
```



# One Sample Hypothesis Test: Example IV



Since the mean is our parameter of interest, we would like to use  $T = \frac{\bar{X} - 75}{\widehat{SD}(\bar{X})}$  as our metric for being "far from the null".

Here, since  $H_A : \mu > 75$ , we would reject  $H_0$  if  $T$  is much larger than 0.

First, we calculate  $T_{\text{obs}} = \frac{\bar{x}_{\text{obs}} - 75}{\widehat{SD}(\bar{X})}$ . Per usual, we will use  $\widehat{SD}(\bar{X}) = \hat{\sigma} / \sqrt{n} = S / \sqrt{n}$ .

```
sum_stats <- secondhand_smoking %>%  
  summarize(xbar = mean(cotinine),  
            SD = sd(cotinine),  
            n = n(),  
            T_obs = (xbar - 75)/(SD/sqrt(n)))  
sum_stats
```

```
## # A tibble: 1 x 4  
##   xbar    SD    n T_obs  
##   <dbl> <dbl> <int> <dbl>  
## 1  108.  95.6   15  1.35
```

Now the question is: is 1.3531105 much larger than 0?

# One Sample Hypothesis Test: Example IV

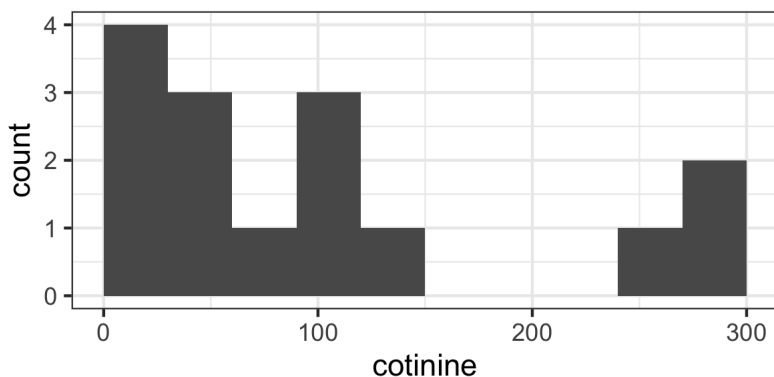


To assess if 1.3531105 is "much larger than 0", we want to calculate  $P(T > 1.3531105 \mid H_0 \text{ true})$ .

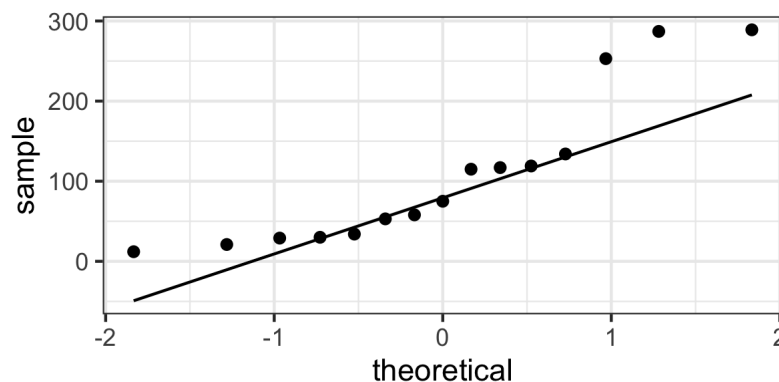
If  $\bar{X} \sim N$ , then  $T \sim t_{n-1}$ . So, need to check if  $\bar{X} \sim N$ .

Small  $n$ , so CLT might be a stretch. Let's consider the data:

```
ggplot(data = secondhand_smoking,  
       aes(x = cotinine)) +  
  geom_histogram(binwidth = 30, boundary
```



```
ggplot(data = secondhand_smoking,  
       aes(sample = cotinine)) +  
  geom_qq() + geom_qq_line()
```



# One Sample Hypothesis Test: Example IV



So it does NOT seem like  $\bar{X} \sim N$ . What else can we do to find the distribution of  $T = \frac{\bar{X} - 75}{\widehat{SD}(\bar{X})}$ ?

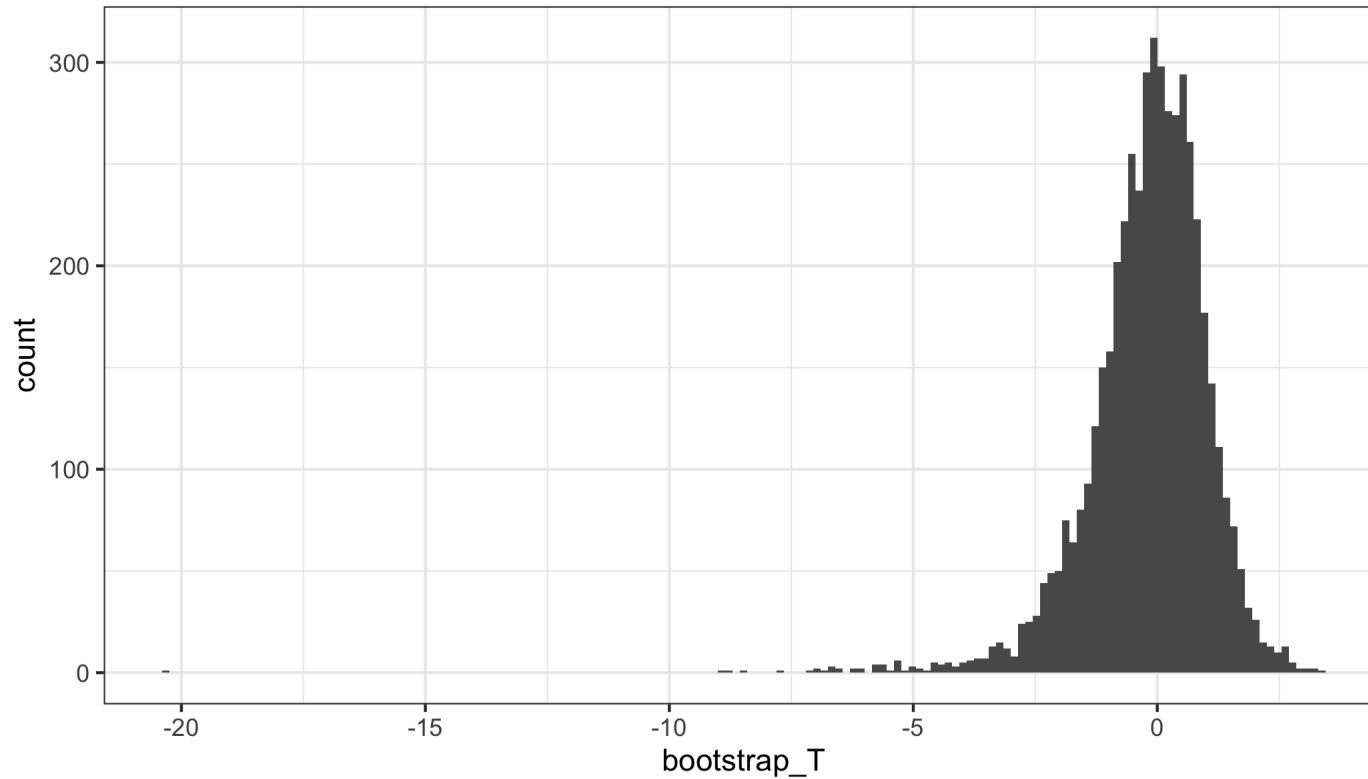
Bootstrap!

```
xbar_orig <- sum_stats$xbar

bootstrap_samples <- tibble(i = 1:5000) %>%
  mutate(bootstrap_sample = map(i,
                                ~sample_n(secondhand_smoking,
                                             size = 15,
                                             replace = TRUE)$cotinine),
         bootstrap_mean = map_dbl(bootstrap_sample, mean),
         bootstrap_sd = map_dbl(bootstrap_sample, sd),
         bootstrap_T = (bootstrap_mean - xbar_orig) /
                       (bootstrap_sd / sqrt(15)))

ggplot(bootstrap_samples,
       aes(x = bootstrap_T)) +
  geom_histogram(binwidth = 0.15, boundary = 0)
```

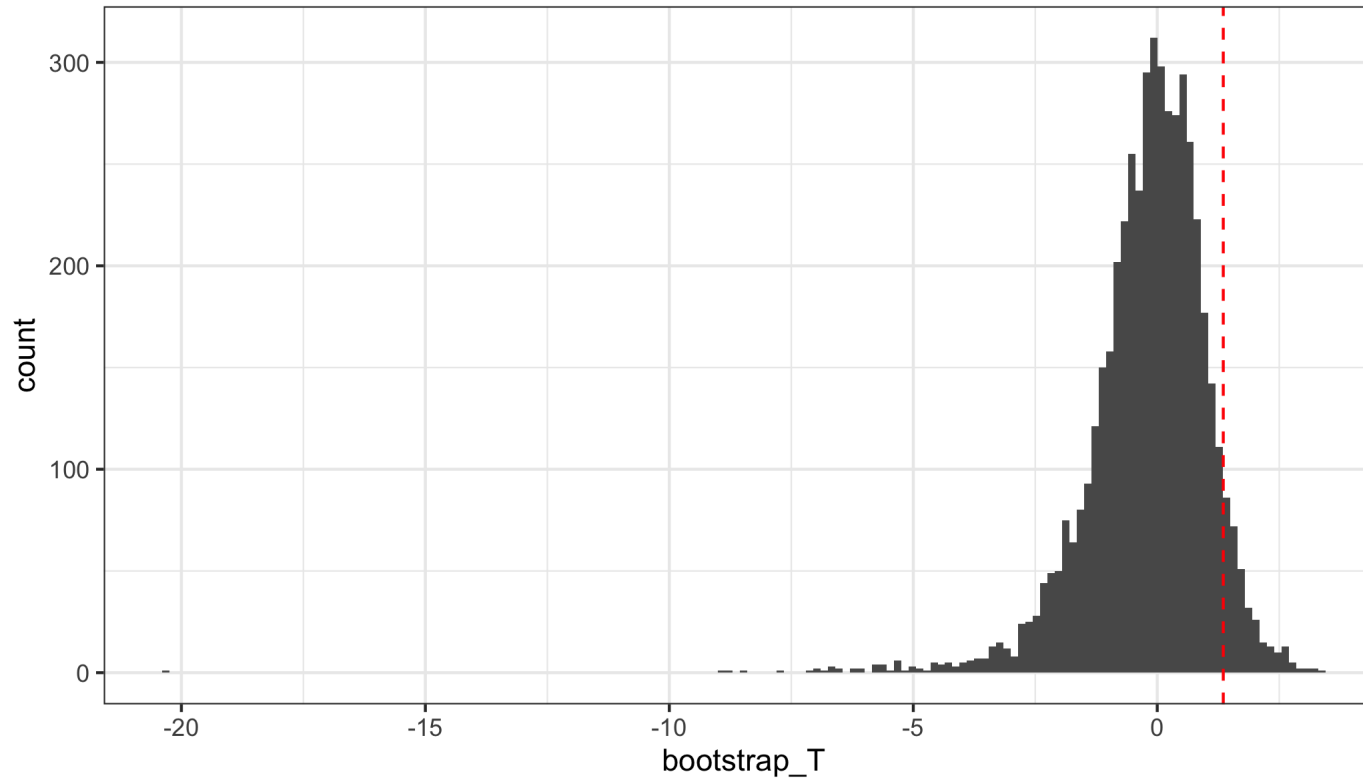
# One Sample Hypothesis Test: Example IV



Now that we know the distribution of  $T$ , we can find  $P(T > 1.3531105)$ . But how?



# One Sample Hypothesis Test: Example IV



Now that we know the distribution of  $T$ , we can find  $P(T > 1.3531105)$ . But how? Proportion of the area under the curve to the right of 1.3531105.

# One Sample Hypothesis Test: Example IV



The proportion of the area under the curve to the right of 1.3531105 is the same as the proportion of bootstrap  $T$ 's that are greater than 1.3531105. So

$$\text{p-value} = P(T > 1.3531105) = \frac{\#T_{\text{boots}} > 1.3531105}{5000}.$$

```
n_larger <- sum(bootstrap_samples$bootstrap_T > 1.3531105)
n_larger
```

```
## [1] 326
```

```
p_value <- n_larger/5000
p_value
```

```
## [1] 0.0652
```

Since the p-value is smaller than our significance level  $\alpha = 0.1$ , we reject the null hypothesis: these data suggest that the true mean amount of cotinine in the urine is greater than 75 ng/mL.

# One Sample Hypothesis Tests: summary



## One Sample T-test

If  $\bar{X} \sim N$ , the hypothesis  $H_0 : \mu = \mu_0$  can be tested using the *test-statistic*  $T = \frac{\bar{X} - \mu_0}{\widehat{SD}(\bar{X})}$ .

Under the null hypothesis,  $T \sim t_{n-1}$ , and we reject  $H_0$  if the p-value =  $P(T \text{ more extreme than } T_{\text{obs}} | H_0) < \alpha$ .

- Here,  $\widehat{SD}(\bar{X}) = s/\sqrt{n}$

## One Sample Test for Proportion

If  $P \sim N$  (approximately), the hypothesis  $H_0 : \pi = \pi_0$  can be tested using the *test-statistic*  $Z = \frac{P - \pi_0}{SD_0(P)}$ .

Under the null hypothesis,  $Z \sim N(0, 1)$ , and we reject  $H_0$  if the p-value =  $P(Z \text{ more extreme than } Z_{\text{obs}} | H_0) < \alpha$ .

- Here,  $SD_0(P) = \sqrt{\pi_0(1 - \pi_0)/n}$  is the standard deviation of  $P$  **IF** the null hypothesis is true.

## One Sample Bootstrap Test

If  $\bar{X}$  is NOT normally distributed, but the observations are independent, we can test  $H_0 : \mu = \mu_0$  using the *test-statistic*  $T = \frac{\bar{X} - \mu_0}{\widehat{\text{SD}}(\bar{X})}$ .

We estimate the distribution of  $T$  under the null by the distribution of  $T_{\text{boot}}$ , and reject  $H_0$  if the p-value =  $P(T_{\text{boot}} \text{ more extreme than } T_{\text{obs}}) < \alpha$ .

Here,

- $B$  = number of bootstrap samples created.
- $T_{\text{boot}} = \frac{\bar{x}_{\text{boot}} - \bar{x}_{\text{obs}}}{s_{\text{boot}}/\sqrt{n}}$  is calculated for each of the bootstrap samples.

# One Sample Hypothesis Tests: summary



## "More extreme"

What it means to be more extreme is determined by the alternative hypothesis:

- if  $H_A : \mu > \mu_0$ , then "more extreme" = "greater than", and p-value =  $P(T > T_{\text{obs}})$
- if  $H_A : \mu < \mu_0$ , then "more extreme" = "smaller than", and p-value =  $P(T < T_{\text{obs}})$
- if  $H_A : \mu \neq \mu_0$ , then "more extreme" = "further from 0", and p-value =  $P(T < -|T_{\text{obs}}|) + P(T > |T_{\text{obs}}|)$

For test of proportion, replace  $\mu$  with  $\pi$ , and  $T$  with  $Z$ .

# One Sample Hypothesis Test: Power



Recall: for every hypothesis test, there is a conclusion. For every conclusion, one of three things will happen:

- we make the right decision
  - i.e. reject when  $H_0$  is false, do not reject when  $H_0$  is true
- we make a type I error
  - i.e. reject when  $H_0$  is actually true
- we make a type II error
  - i.e. fail to reject when  $H_0$  is actually false

# One Sample Hypothesis Test: Power



We have full control over the type I error rate - it is exactly  $\alpha$ . To see this, say we are testing  $H_0 : \mu = \mu_0$  against  $H_A : \mu \neq \mu_0$ .

$$\begin{aligned} P(\text{reject } H_0 \mid H_0 \text{ true}) &= P(T \text{ very far from } 0 \mid H_0 \text{ true}) \\ &= P(T > t_{n-1, \alpha/2} \mid H_0 \text{ true}) + P(T < -t_{n-1, \alpha/2} \mid H_0 \text{ true}) \\ &= \alpha \end{aligned}$$

Similarly can be done for the two other alternative hypotheses.

# One Sample Hypothesis Test: Power



The Type II error rate is a bit more tricky:  $P(\text{type II}) = P(\text{fail to reject } H_0 \mid H_A \text{ true})$ .

To get a better sense of how this works, we will consider a simple case that we haven't talked about yet: one sample hypothesis test with known variance  $\sigma^2$ .

Remember: good old paint thickness data.

```
paint_thickness <- tibble(  
  thickness = c(1.29, 1.12, 0.88, 1.65, 1.48, 1.59, 1.04, 0.83,  
                1.76, 1.31, 0.88, 1.71, 1.83, 1.09, 1.62, 1.49)  
)
```

Let us assume that  $\bar{X} \sim N$ , and that we know the true variance  $\sigma^2 = 0.115$ .



# One Sample Hypothesis Test: Power



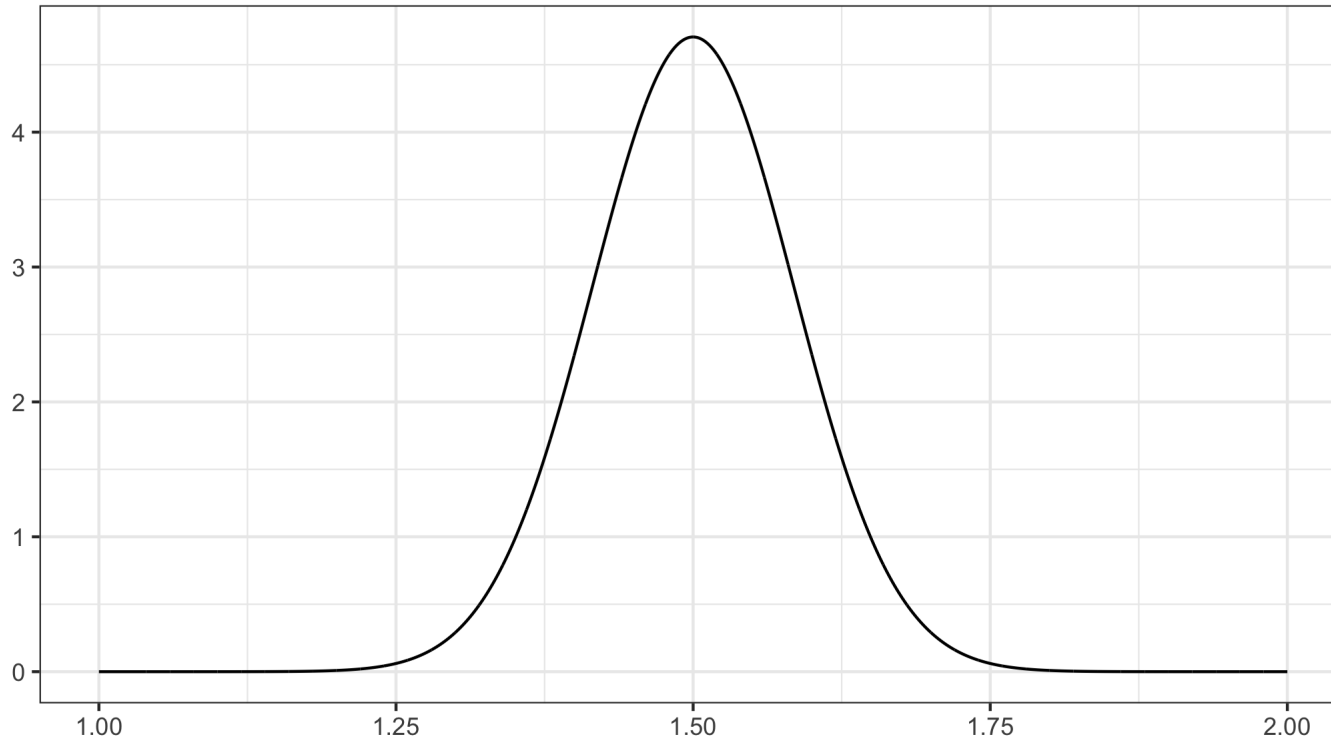
When testing  $H_0 : \mu = 1.5$  against  $H_A : \mu \neq 1.5$  using  $\alpha = 0.05$ , we would reject when  $\bar{x}_{\text{obs}}$  is very, very far from 1.5.

Actually, we reject when  $\bar{x}_{\text{obs}}$  is so far from 1.5 that the probability of  $\bar{X}$  being even further from 1.5 is less than 0.05:  $2 \cdot P(\bar{X} > |\bar{x}_{\text{obs}}| \mid H_0 \text{ true}) < 0.05$ .

# One Sample Hypothesis Test: Power



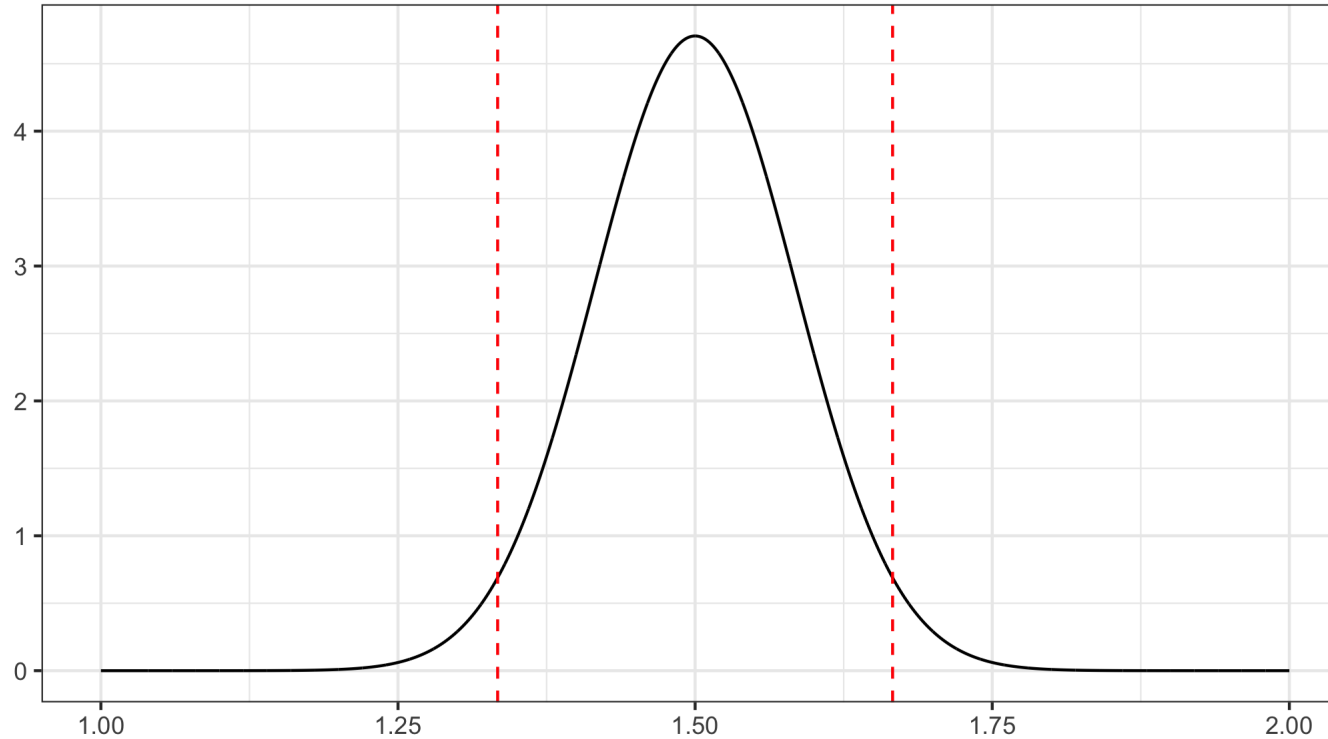
When  $H_0$  is true,  $\bar{X} \sim N(1.5, 0.115/16)$ . So, when  $H_0$  is true,  $\bar{X}$  follows this distribution:



# One Sample Hypothesis Test: Power



Will reject when  $\bar{X}$  outside red dotted lines.



But to talk about type II error rate (or power), we need to find  
 $P(\text{fail to reject } H_0 \mid H_0 \text{ not true}) = P(\text{fail to reject } H_0 \mid H_A \text{ true})$  (or  
 $P(\text{reject } H_0 \mid H_0 \text{ not true})$ ).

# One Sample Hypothesis Test: Power



Assuming we know the true  $\sigma^2 = 0.115$ , and that the null hypothesis is true, then  $\bar{X} \sim N(1.5, 0.115/16)$ .

So, we reject when  $\bar{X}$  outside red dotted lines. I.e. if  $0.025 > P(\bar{X} > |\bar{x}_{\text{obs}}|)$ .

```
X_H0 <- Normal(mu = 1.5, sigma = sqrt(0.115/16))  
quantile(X_H0, c(0.025, 0.975))
```

```
## [1] 1.333836 1.666164
```

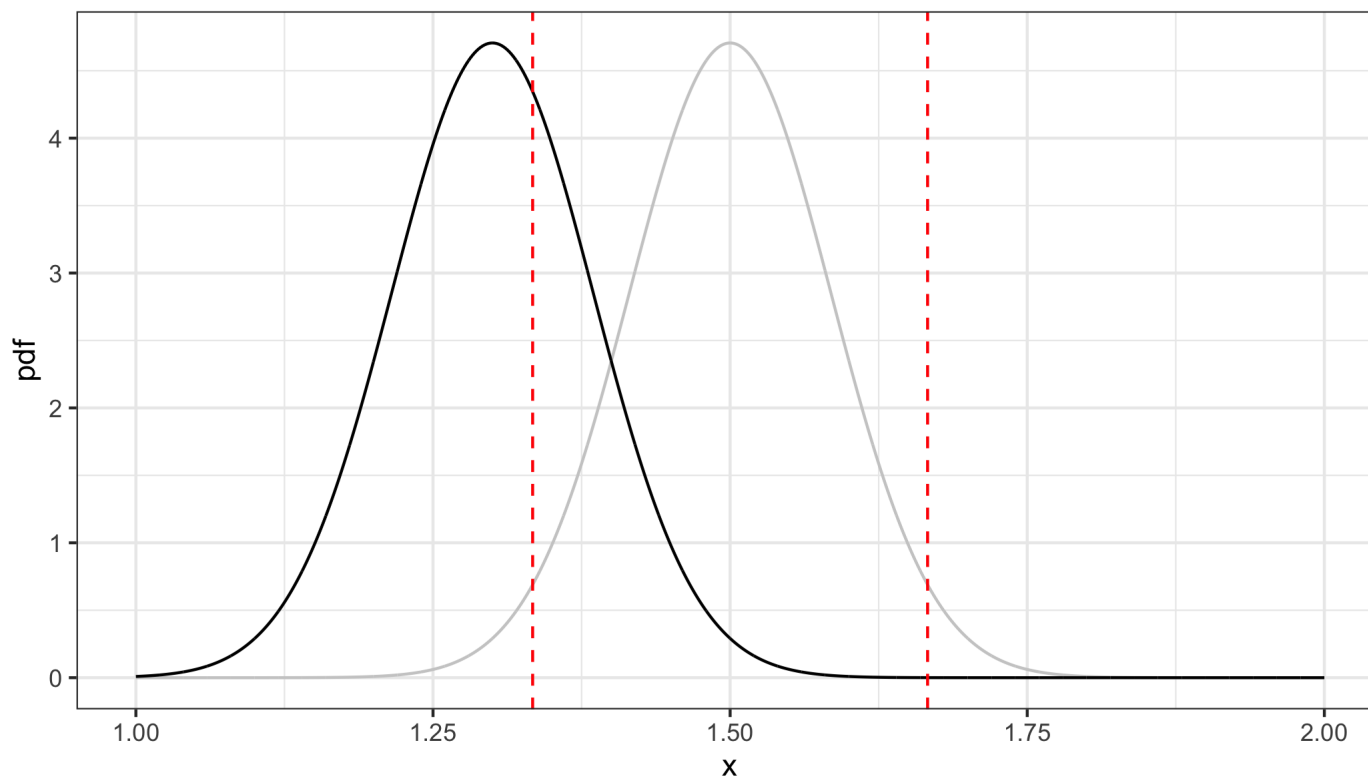
So, we reject when  $\bar{x} < 1.33$  or  $\bar{x} > 1.66$ .

# One Sample Hypothesis Test: Power



But what if the true mean is NOT 1.5? What if, instead, it is 1.3? What is  $P(\text{type II error})$ ?

To find the probability of rejecting, we need to look at a different curve, because if  $\mu = 1.3$ , then  $\bar{X} \sim N(1.3, 0.115/16)$ .



# One Sample Hypothesis Test: Power



But what if the true mean is NOT 1.5? What if, instead, it is 1.3? What is  $P(\text{type II error})$ ?

To find the probability of rejecting, we need to look at a different curve, because if  $\mu = 1.3$ , then  $\bar{X} \sim N(1.3, 0.115/16)$ .

$$\begin{aligned} P(\text{type II error}) &= P(\text{fail to reject} \mid \mu = 1.3) \\ &= P(1.33 < \bar{X} < 1.66 \mid \mu = 1.3) \\ &= P(\bar{X} < 1.66 \mid \mu = 1.3) - P(\bar{X} < 1.33 \mid \mu = 1.3) \end{aligned}$$

```
X_HA <- Normal(1.3, sqrt(0.115/16))  
cdf(X_HA, 1.66) - cdf(X_HA, 1.33)
```

```
## [1] 0.3617108
```

That is, **IF** the true mean is 1.3, we would fail to reject the idea that  $\mu = 1.5$  about 37% of the time.

Or, similarly, we would only reject  $\mu = 1.5$  about 63% of the time.

What can we do to do better? Increase sample size!

# One Sample Hypothesis Test: Power



What sample size do we need to be able to distinguish between  $\mu = 1.5$  and  $\mu = 1.3$  most of the time? Say, 80% of the time?

That is, what should  $n$  be such that  $P(\text{reject } H_0 : \mu = 1.5 \mid \mu = 1.3) = 0.8$ ?

More general, if we are testing  $H_0 : \mu = \mu_0$  against  $H_A : \mu \neq \mu_0$  at significance level  $\alpha$ , what sample size is needed to make sure that  $P(\text{reject } H_0 \mid \mu = \mu_A) = 1 - \beta$ ?

Turns out, this is approximately

$$n \approx \left( \frac{\sigma(z_{\alpha/2} + z_{\beta})}{\mu_0 - \mu_A} \right)^2$$

In our specific example,  $\sigma = 0.34$ ,  $\alpha = 0.05$ ,  $\beta = 0.2$ ,  $\mu_0 = 1.5$ , and  $\mu_A = 1.3$ .

# One Sample Hypothesis Test: Power



We can find  $z_{0.025}$  and  $z_{\beta}$ :

```
Z <- Normal()
quantile(Z, c(1-0.025, 1-0.2))
```

```
## [1] 1.9599640 0.8416212
```

$$\text{So, } n \approx \left( \frac{0.34(1.96+0.84)}{1.5-1.3} \right)^2 = 22.6576.$$

To have 80% power to reject 1.5 as the true mean if the true mean is in fact 1.3, we would need 23 samples.



# One Sample Hypothesis Test: Power



- sample size depends only on standard deviation,  $\alpha$ ,  $\beta$ , and *difference* between true and hypothesized means.
- in practice, it goes as follows:
  - researchers pick desired  $\alpha$  and  $\beta$
  - from previous, well-done experiments, a solid estimate of  $\sigma$  is obtained
  - from expert knowledge, a "minimal interesting difference" is chosen (i.e.  $\mu_0 - \mu_A$ )
  - based on this, needed sample size is determined.