# STA130H1F

## Class #6

**Prof. Nathan Taback**

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# Today's Class

Answering the question:

**if we see a difference between two groups, is it meaningful? Or could it just be due to chance?**

- Comapring two proportions
- Comapring two means
- Type I and Type II Errors
- Interpretation of P-values

# Comapring two proportions

# Is Tylenol or Aspirin Better for Headache Relief?

- Consider a sample of four people with a headache.
- Two people are randomly assigned to Aspirin and two assigned to Tylenol. This is called **randomization**.
- This randomization could be carried out by shuffling four cards - 2 red suit cards marked and 2 black suit cards, and assigning each person a card.

# Is Tylenol or Aspirin Better for Headache Relief?

- If a person receives a card with a red suit then they receive Tylenol, and if they receive a card with a black suit then they receive an Aspirin.
- After an hour a researcher asked if they still had pain.

| Subject | Drug | Pain |
|---|---|---|
| 1 | T | No |
| 2 | T | No |
| 3 | A | Yes |
| 4 | A | No |

# Is Tylenol or Aspirin Better for Headache Relief?

- The null hypothesis is that changing the treatment for a subject has no effect on pain, in particular, no effect on the proportion that have no pain.
- Assuming this null hypothesis is true Tylenol (T) and Aspirin (A) are mere labels and don't affect the outcome.
- For example, assuming $H_0$ is true, subject 1 would have no pain if they had Tylenol or Aspirin.
- The alternative hypothesis is that the proportion of subjects without pain is different for Tylenol and Aspirin.

# Is Tylenol or Aspirin Better for Headache Relief?

All the possible ways to assign two subject to Aspirin and two subjects to Tylenol.

| Subject | Drug | Pain | R1 | R2 | R3 | R4 | R5 |
|---|---|---|---|---|---|---|---|
| 1 | T | No | T | T | A | A | A |
| 2 | T | No | A | A | T | T | A |
| 3 | A | Yes | T | A | T | A | T |
| 4 | A | No | A | T | A | T | T |
| `$\hat{p}_T - \hat{p}_A$` | | 0.5 | -0.5 | 0.5 | -0.5 | 0.5 | -0.5 |

# Gender Bias in Promotion

- 1972 study on "sex role stereotypes on personnel decisions".
- 48 male managers were asked to rate whether several candidates were suitable for promotion.
- Managers were randomly assigned to review the file of either a male or female candidate. The files were otherwise identical.

B. Rosen and T.H. Jerdee (1974). Influence of sex role stereotypes on personnel decisions. *Journal of Applied Psychology* **59**(1), 9-14.

# What they found

| Observed results | Male | Female | Total |
|---|---|---|---|
| Promoted | 21 | 14 | 35 |
| Not promoted | 3 | 10 | 13 |
| Total | 24 | 24 | 48 |

- 21/24 = 87.5% of males and 14/24 = 58.3% of females were recommended for promotion.
- This suggests that the males were more likely to be recommended for promotion. But the sample size is small. Is the difference 87.5% - 58.3% = 29.2% due to gender or chance?
- If many similar studies were conducted, assuming there is no difference between male and female promotion rates, then how many of these studies would produce a difference as extreme as this study?

# Review: The Logic of Hypothesis Testing

# 1. The hypotheses

Two claims:

1.There is no difference between the two groups. This is the **null hypothesis**, written $H_0$.

For the gender bias in promotion study:

2.There is a difference between the two groups. This is the **alternative hypothesis**, written $H_A$ (or $H_a$ or $H_1$). The alternative is almost always corresponds to the research question.

For the gender bias in promotion study:

# 2. The test statistic

The **test statistic** is a number, calculated from the data, that captures what we're interested in.

For the gender bias promotion example, what would be a useful test statistic?

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The **test statistic** is a number, calculated from the data, that captures what we're interested in.

For the gender bias promotion example, what would be a useful test statistic?

*Is it possible that the value of the test statistic occured just by chance and there was really no difference between genders in being recommended for promotion?*

To answer this, simulate possible values of the test statistic assuming there's no difference (i.e., the null hypothesis is true).

# 3. Simulate what $H_0$ predicts will happen

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- Imagine we have 24 cards labelled with an "F" and 24 cards labelled with an "M".
- Shuffle the cards ...
- Assign the cards to the 48 people then calculate the difference in the proportion of males versus females that were promted. This is one simulated value of the test statistic.

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- Shuffle the cards again ...
- Assign the cards to the 48 people then calculate the difference in the proportion of males versus females that were promoted. This is another simulated value of the test statistic.
- Repeat: shuffle, assign cards, calculate difference

# Gender Bias Data

Data are in the dataframe `bias` (which I created)

```
# create datafrome
bias <- data_frame(gender = c(rep("male", 24), rep("female", 24)),
                   promoted = c(rep("yes", 21), rep("no", 3),
                                rep("yes", 14), rep("no", 10)))
```

```
glimpse(bias)
```

```
## Observations: 48
## Variables: 2
## $ gender   <chr> "male", "male", "male", "male", "male", "male", "male...
## $ promoted <chr> "yes", "yes", "yes", "yes", "yes", "yes", "yes", "yes...
```

- How many variables are in the data frame?

- Are the variables numerical or categorical?

# Calculate the proportion of males and females promoted

```
n_female <- bias %>% filter(gender=="female") %>% count()
n_male <- bias %>% filter(gender=="male") %>% count()

yes_female <- bias %>%
  filter(promoted=="yes" & gender=="female") %>% count()
as.numeric(yes_female) # treat as a number (not a dataframe)
```

```
## [1] 14
```

```
yes_male <- bias %>%
  filter(promoted=="yes" & gender=="male") %>% count()
as.numeric(yes_male)
```

```
## [1] 21
```

```
p_diff <- yes_female/n_female - yes_male/n_male
as.numeric(p_diff)
```

```
## [1] -0.2916667
```

# Is the difference between the proportion of males and females promoted meaningful?

- The difference in the proportions of people who were deemed suitable for promotion between the females and males is

$$\hat{p}_{female} - \hat{p}_{male} = 0.583 - 0.875 = -0.292$$

- This suggests that the males were more likely to be recommended for promotion.
- But the sample size is small. Could this difference just be due to chance?
- Repeat the experiment assuming it's just due to chance (using simulation), and see what happens

# How to Shuffle Gender in R

The `sample()` command by default produces a random sample of the same length of the data without replacement

```
# illustration of sample
a_vector <- c(1,1,1,2,2)
a_vector
```

```
## [1] 1 1 1 2 2
```

```
sample(a_vector)
```

```
## [1] 2 1 2 1 1
```

```
sample(a_vector)
```

```
## [1] 2 1 1 2 1
```

```
sample(a_vector)
```

```
## [1] 2 2 1 1 1
```

# Before the shuffle

```
bias$gender # the values of gender in the data
```

```
##  [1] "male"   "male"   "male"   "male"   "male"   "male"   "male"
##  [8] "male"   "male"   "male"   "male"   "male"   "male"   "male"
## [15] "male"   "male"   "male"   "male"   "male"   "male"   "male"
## [22] "male"   "male"   "male"   "female" "female" "female" "female"
## [29] "female" "female" "female" "female" "female" "female" "female"
## [36] "female" "female" "female" "female" "female" "female" "female"
## [43] "female" "female" "female" "female" "female" "female"
```

```
bias$promoted
```

```
##  [1] "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes"
## [12] "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes" "no"
## [23] "no"  "no"  "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes"
## [34] "yes" "yes" "yes" "yes" "yes" "no"  "no"  "no"  "no"  "no"  "no"
## [45] "no"  "no"  "no"  "no"
```

# After the shuffle

```
sim <- bias %>% mutate(gender = sample(gender)) #shuffle gender labels
sim$gender
```

```
##  [1] "female" "male"   "male"   "male"   "female" "female" "male"
##  [8] "female" "male"   "female" "male"   "male"   "female" "male"
## [15] "female" "female" "male"   "female" "male"   "male"   "female"
## [22] "male"   "male"   "female" "male"   "female" "female" "female"
## [29] "male"   "male"   "female" "female" "female" "male"   "male"
## [36] "female" "male"   "male"   "female" "male"   "male"   "female"
## [43] "female" "male"   "male"   "female" "female" "female"
```

```
sim$promoted
```

```
##  [1] "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes"
## [12] "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes" "no"
## [23] "no"  "no"  "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes" "yes"
## [34] "yes" "yes" "yes" "yes" "yes" "no"  "no"  "no"  "no"  "no"  "no"
## [45] "no"  "no"  "no"  "no"
```

# After the shuffle

```
yes_female <- sim %>%
  # only promoted females
  filter(promoted == "yes" & gender == "female") %>%
  count()  # count
  as.numeric(yes_female) #convert to numeric
```

```
## [1] 17
```

```
  yes_male <- sim %>%
  # only promoted males
  filter(promoted == "yes" & gender == "male") %>%
  count()  # count
  as.numeric(yes_male)
```

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

```
  # calculate the difference in the proportion of
  # people promoted by gender
  p_diff <- yes_female / n_female - yes_male / n_male
  as.numeric(p_diff)
```

```
## [1] -0.04166667
```

# Set up Simulation in R

```
set.seed(130) # remove in practice

repetitions <- 1000  # "many times" will be 1000
# create a vector of missing values to store results
# rep() is the replicate function
# NA means a missing value
simulated_stats <- rep(NA, repetitions) # 1000 missing values

# initialize some values
n_female <- bias %>% filter(gender == "female") %>% count()
n_male <- bias %>% filter(gender == "male") %>% count()
```

# Calculate Observed Value of Test Statistic

```
# calculate the test statistic
yes_female <- bias %>%
  # only promoted females
  filter(promoted == "yes" & gender == "female") %>%
  count()  # count

yes_male <- bias %>%
  # only promoted males
  filter(promoted == "yes" & gender == "male") %>%
  count()  # count

test_stat <- as.numeric(yes_female / n_female -
                          yes_male / n_male)
```

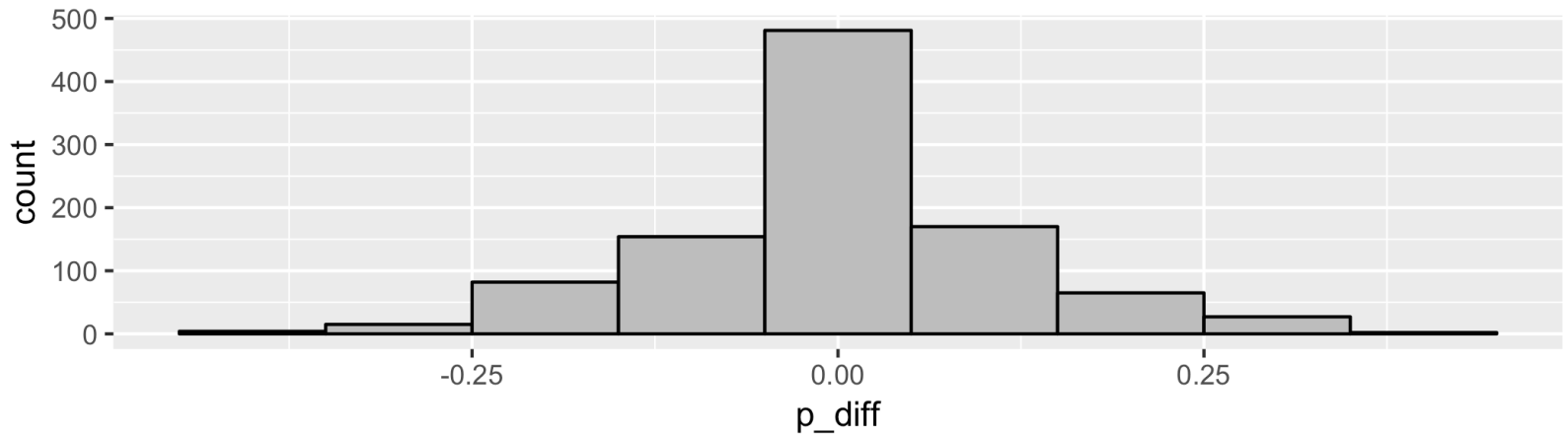
## Shuffle, Assign, Calculate Difference, Repeat ...

```
for (i in 1:repetitions)
{
  sim <- bias %>%
    mutate(gender = sample(gender)) # shuffle gender labels

   yes_female <- sim %>%
     filter(promoted == "yes" & gender == "female") %>%
     count()

   yes_male <- sim %>%
     filter(promoted == "yes" & gender == "male") %>%
     count()

   # calculate the difference in the proportion of people
   # promoted by gender in the simulation

   p_diff <- yes_female / n_female - yes_male / n_male

   # add the new simulated value to the ith entry in the
   # vector of results

   simulated_stats[i] <- as.numeric(p_diff) #treat result as a number
}

# turn results into a data frame for plotting
sim <- data_frame(p_diff = simulated_stats)
```

# Distribution of simulated values of $\hat{p}_{female} - \hat{p}_{male}$ assuming $H_0$ is true

The for loop in the previous slide produced a simulated distribution of differences in proportion of males and females promoted. This can be visualized using a histogram.

```
ggplot(sim, aes(x = p_diff)) + geom_histogram(binwidth = 0.1,
                                              colour = "black",
                                              fill = "grey")
```




Around what value is this distribution centred? Does this make sense?

# 4. The P-value

- Assuming that the null hypothesis is true, the **P-value** gives a measure of the probability of getting data that are at least as unusual as the sample data.

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- What does "at least as unusual" mean?

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- Assuming that the null hypothesis is true, the **P-value** gives a measure of the probability of getting data that are at least as unusual as the sample data.
- What does "at least as unusual" mean?
- Values that are as far away or even farther from the null hypothesis value than the test statistic.

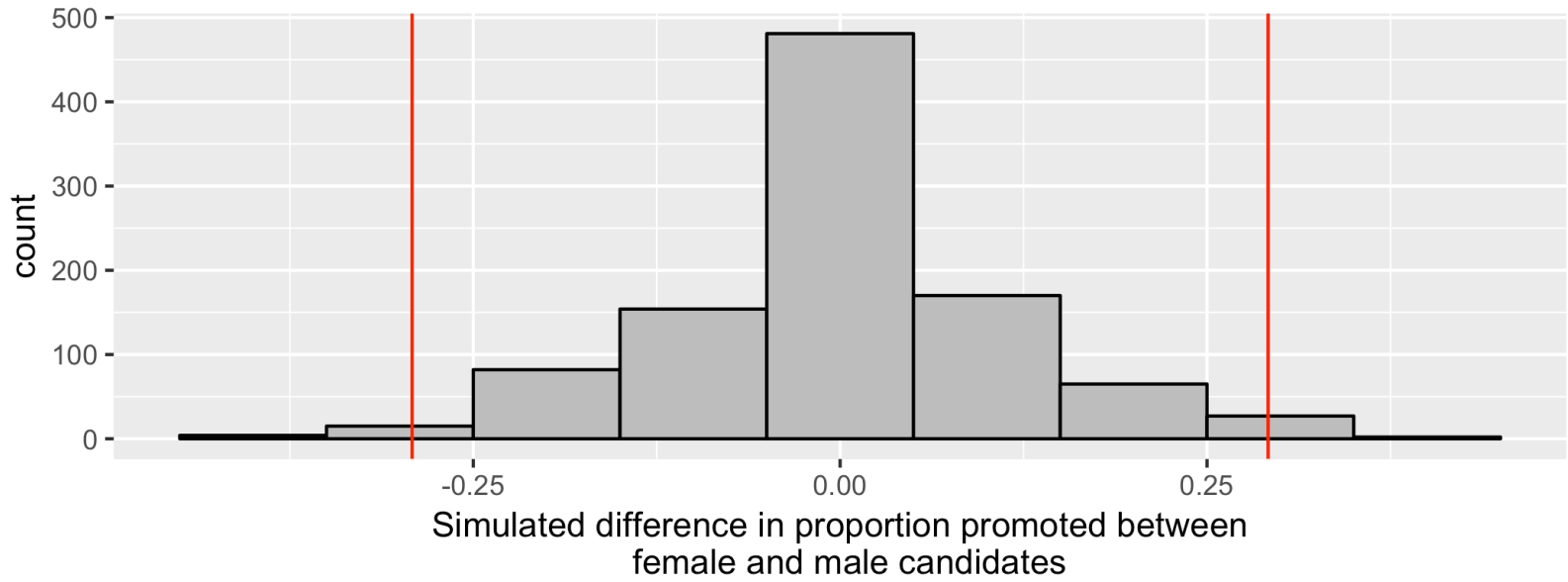
# 4. The P-value - Gender Bias Example

For the gender bias example:

- the null hypothesis value is $p_1 - p_2 = 0$
- the observed estimate from the data (the test statistic) is $\hat{p}_1 - \hat{p}_2 = -0.292$
- values at least as unusual as the data values includes all values *greater than or equal to 0.292* and all values *less than or equal to -0.292*
- This is a **two-sided test** because it considers differences from the null hypothesis that are both larger and smaller than what you observed.

# Values more extreme than the test statistic

```
## [1] -0.2916667
```



# Calculate P-value

```
test_stat
```

```
## [1] -0.2916667
```

```
extreme_count <- sim %>%
  filter(p_diff >= abs(test_stat) | p_diff <= -1*abs(test_stat)) %>%
  count()

as.numeric(extreme_count)
```

```
## [1] 48
```

```
p_value <- as.numeric(extreme_count)/repetitions
as.numeric(p_value)
```

```
## [1] 0.048
```

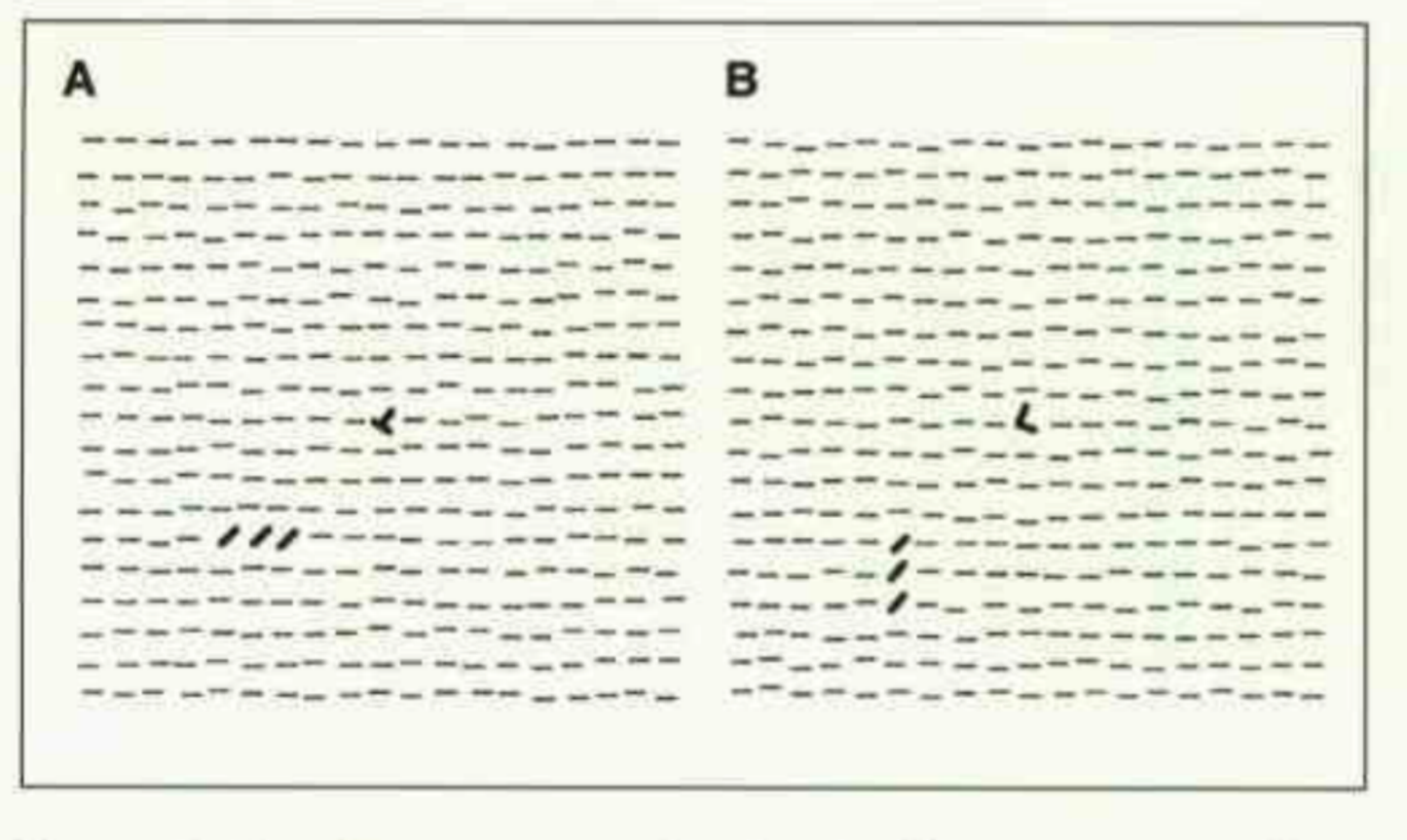
# 5. Make a conclusion

- A large P-value means the data are consistent with the null hypothesis.
- A small P-value means the data are inconsistent with the null hypothesis.
- The P-value is 0.048 for our test that the proportion of people promoted is the same for females and males.
- We conclude that there is moderate evidence of a difference between genders in being chosen for promotion.

# Hypothesis testing for comparing a characteristic of a numerical variable between two groups

# Example: Sleep and performance on a visual discrimination task

Stickgold, James and Hobson (2000). Visual discrimination learning requires sleep after training. *Nature Neuroscience* **3**(12), 1237-8



# Can you recover from an all-nighter after a couple of days of good sleep?

- Subjects: 21 student volunteers (ages 18 to 25)
- Subjects were trained on a visual discrimination task
- Subjects were then randomly assigned into two groups:
  - *sleep deprived*: kept up all night after the training and then not allowed to sleep until 9pm the next day (11 people)
  - *unrestricted sleep*: no restrictions on their sleep (10 people) --
- Subjects then were allowed unrestricted sleep for the next two nights
- Subjects were then retested on the visual discrimination task

# The visual discrimination task

- Subjects shown "target screen"" A or B for 17 milliseonds
- Then shown blank screen for a variable length of time, the "interstimulus interval" (ISI)
- Then shown "mask screen" with random pattern for 17 milliseconds
- Asked if target screen included an L or a T and whether the slashes were vertical or horizontal
- Score on the task for a subject was the minimum interstimulus interval (ISI) required for the subject to achieve accurate results

# The data

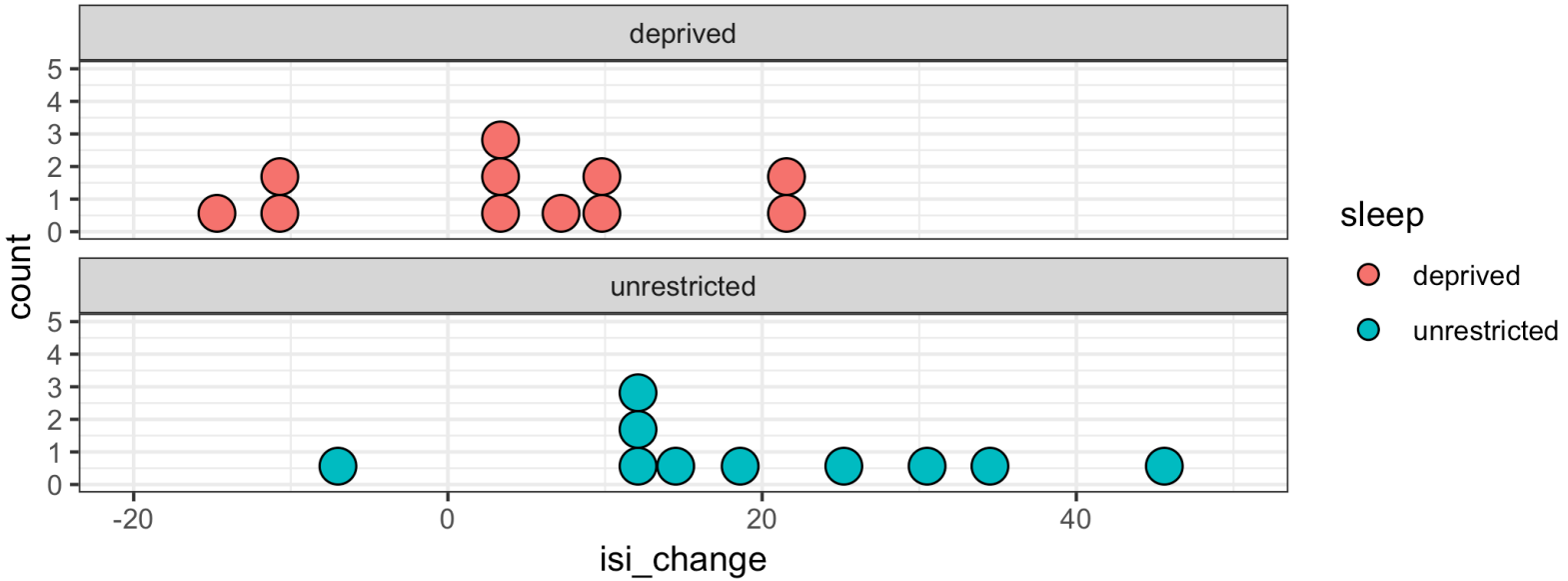
```
sleep <- c(rep("unrestricted",10),rep("deprived",11))
isi_change <- c(25.2,14.5,-7.0,12.6,34.5,45.6,11.6,18.6,12.1,30.5,
                -10.7,4.5,2.2,21.3,-14.7,-10.7,9.6,2.4,21.8,7.2,10.0)
sleep_data <- data_frame(sleep, isi_change)

sleep_data %>% head()
```

```
## # A tibble: 6 x 2
##   sleep        isi_change
##   <chr>             <dbl>
## 1 unrestricted       25.2
## 2 unrestricted       14.5
## 3 unrestricted       -7
## 4 unrestricted       12.6
## 5 unrestricted       34.5
## 6 unrestricted       45.6
```

# The data

```
ggplot(sleep_data, aes(x = isi_change, fill = sleep)) +
  geom_dotplot() +
  xlim(-20, 50) + ylim(0, 5) + facet_wrap( ~ sleep, ncol = 1)  +
  theme_bw()
```




How is the sleep deprivation study similar to the gender discrimination in promotion study?

# Hypotheses

- What is an appropriate statistic to capture the difference in `isi_change` between the sleep deprived and unrestricted sleep group?
- Test whether the mean of the change in ISI is the same for students who are sleep deprived and students who had unrestricted sleep

$$H_0 : \mu_1 = \mu_2 \text{ vs. } H_A : \mu_1 \neq \mu_2$$

- $\mu_1$ is the parameter representing what the mean of the change in ISI would be for all students if they were given this task and had unrestricted sleep.
- $\mu_2$ is the parameter representing what the mean of the change in ISI would be for all students if they were given this task and underwent sleep deprivation.

# Test statistic

Difference in the means of change in ISI between the sleep deprived and unrestricted sleep groups for the 21 students in our sample of students

$$\text{Test statistic} = \hat{\mu}_1 - \hat{\mu}_2$$

```
mean_data <- sleep_data %>% group_by(sleep) %>%
  summarise(means = mean(isi_change))
  mean_data
```

```
## # A tibble: 2 x 2
##   sleep        means
##   <chr>        <dbl>
## 1 deprived       3.9
## 2 unrestricted  19.8
```

$$\text{Test statistic} = \hat{\mu}_1 - \hat{\mu}_2 = 19.82 - 3.90 = 15.92$$

```
test_stat <- as.numeric(mean_data %>%
                          summarise(test_stat = diff(means)))
test_stat
```

```
## [1] 15.92
```

# Simulate what $H_0$ predicts will happen

**Assume $H_0$ is true:** The value of a subject's ISI is same if they are in the sleep deprived or unrestricted sleep groups.

# Simulate what $H_0$ predicts will happen

**Assume $H_0$ is true:** The value of a subject's ISI is same if they are in the sleep deprived or unrestricted sleep groups. Shuffle, Assign, Calculate Test Statistic, Repeat:

- **Shuffle:** shuffle the categorical variable that says to which sleep group each observation belongs.
- **Assign:** the shuffled labels to the subjects.
- **Calculate the test statistic:** the difference in the means of change in ISI for the observations in each of these new groups
- **Repeat**: lots of times giving an empirical distribution for the test statistic if the null hypothesis were true

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- **Shuffle:** shuffle the categorical variable that says to which sleep group each observation belongs.
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- **Calculate the test statistic:** the difference in the means of change in ISI for the observations in each of these new groups
- **Repeat**: lots of times giving an empirical distribution for the test statistic if the null hypothesis were true

After the distribution of simulated values is obtained compare the test statistic observed from the data to the empirical distribution.

# One value of what the test statistic could be if the null hypothesis were true

```
sim <- sleep_data %>%
  mutate(sleep = sample(sleep)) # shuffle sleep group labels

one_sim <- sim %>%
  group_by(sleep) %>%
  summarise(means = mean(isi_change))
one_sim
```

```
## # A tibble: 2 x 2
##   sleep        means
##   <chr>        <dbl>
## 1 deprived     13.0
## 2 unrestricted  9.86
```

```
one_sim$means[2] - one_sim$means[1]
```

```
## [1] -3.094545
```

# Many values of what the test statistic could be if the null hypothesis were true

```
set.seed(130) # remove in practice

repetitions <- 1000  # "many times" will be 1000
# create a vector of missing values to store results
simulated_stats <- rep(NA, repetitions) # 1000 missing values

for (i in 1:repetitions)
{
  sim <- sleep_data %>%
    mutate(sleep = sample(sleep))  # shuffle sleep group labels

  # calculate test statistic for new data
  sim_test_stat <- sim %>% group_by(sleep) %>%
    summarise(means = mean(isi_change)) %>%
    summarise(sim_test_stat = diff(means))

  # add result to vector of values of test statistics
  # assuming null hypothesis
  simulated_stats[i] <- as.numeric(sim_test_stat)
}
```

# Distribution of simulated values of $\hat{\mu}_1 - \hat{\mu}_2$ assuming $H_0$ is true

```
sim <- data_frame(mean_diff=simulated_stats) # turn results
# into a data frame for plotting

ggplot(sim, aes(x=mean_diff)) +
  geom_histogram(binwidth=5, colour = "black", fill = "grey")
```

# The P-value

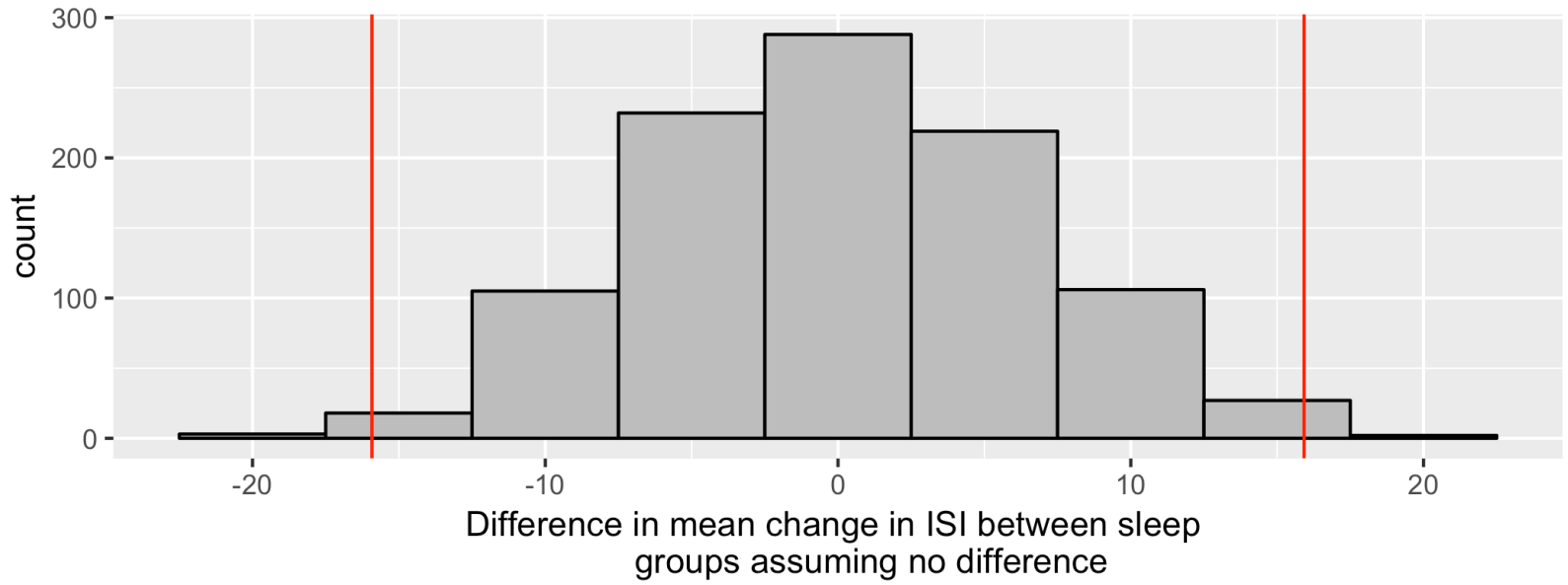
P-value is the proportion of observations in the empirical distribution that are greater than or equal to

$$|\hat{\mu}_1 - \hat{\mu}_2|$$

```
test_stat
```

```
## [1] 15.92
```

```
ggplot(sim, aes(mean_diff)) +
  geom_histogram(binwidth=5, colour = "black",fill = "grey") +
  geom_vline(xintercept = test_stat, color="red") +
  geom_vline(xintercept = -1*test_stat, color="red") +
  labs(x = "Difference in mean change in ISI between sleep
       groups assuming no difference")
```



# Calculate P-value

```
sim %>%
  filter(mean_diff >= abs(test_stat) |
           mean_diff <= -1*abs(test_stat)) %>%
  summarise(p_value = n() / repetitions)
```

```
## # A tibble: 1 x 1
##   p_value
##     <dbl>
## 1    0.01
```

- Assuming that there is no difference in change in ISI between the sleep deprived and unrestricted sleep groups, the chance of seeing as large a difference in the means of change in ISI or even larger than what we observed is 0.01.
- We have strong evidence that the mean of change in ISI is different between the two sleep groups.

# How many simulations is enough?

- In our examples, we've looked at 1000 simulated values assuming the null hypothesis is true, to compare to the value of our test statistic.
- In practice, the number of simulations is more typically on the order of 10,000.
- But that takes a long time to run.
- (Last set of practice problems asked for 100,000. That would take a very long time with all the shuffles, so it's not recommended!)

# Type 1 and Type 2 Errors

- The P-value gives us the probability of getting the data we got (as summarized by the test statistic) or data that are even less likely if the null hypothesis is true.

# Type 1 and Type 2 Errors

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- So it's possible to get data that are not consistent with the null hypothesis just by chance and we conclude that the data give evidence against the null hypothesis, but the null hypothesis is actually true. This is called a **Type 1 error**.

# Type 1 and Type 2 Errors

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- So it's possible to get data that are not consistent with the null hypothesis just by chance and we conclude that the data give evidence against the null hypothesis, but the null hypothesis is actually true. This is called a **Type 1 error**.
- It's also possible that, by chance, the data appear to be consistent with the null hypothesis, but the null hypothesis is actually not true. This is called a **Type 2 error**.

| What we observed / What is the truth | $H_0$ is true | $H_0$ is false |
|---|---|---|
| Test shows data are consistent with $H_0$ | | Type 2 error |
| Test shows evidence against $H_0$ | Type 1 error | |

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|---|---|---|
| Test shows data are consistent with $H_0$ | | Type 2 error |
| Test shows evidence against $H_0$ | Type 1 error | |

- Unfortunately, in practice we don't know if we've committed one of these types of errors.
- The more tests you do, the more likely you'll find a Type 1 error. But you won't know which test(s) resulted in Type 1 errors.
- In future statistics courses, you'll learn about ways to control the chance of making of making one of these types of errors.