02 Randomization Distribution

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Learning Objectives

- Understand quantifying uncertainty using the randomization distribution.
- Section 1.3 in *Statistical Sleuth*.

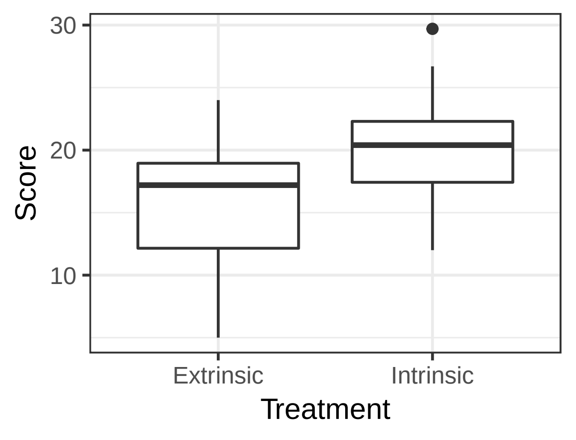
Case Study 1.1.1

```
library(Sleuth3)
data("case0101")
head(case0101)
```

```
##   Score Treatment
## 1   5.0 Extrinsic
## 2   5.4 Extrinsic
## 3   6.1 Extrinsic
## 4  10.9 Extrinsic
## 5  11.8 Extrinsic
## 6  12.0 Extrinsic
```

EDA

```
library(ggplot2)
qplot(x = Treatment, y = Score,
      data = case0101, geom = "boxplot")
```



EDA

```
ext_scores <- case0101$Score[case0101$Treatment == "Extrins
int_scores <- case0101$Score[case0101$Treatment == "Intrins
ext_mean <- mean(ext_scores)
int_mean <- mean(int_scores)
int_mean
```

```
## [1] 19.88
```

```
ext_mean
```

```
## [1] 15.74
```

```
int_mean - ext_mean
```

```
## [1] 4.144
```

Question

Is 4.144 a big difference? A small difference?

Two possibilities

1. H_A: There is actually a difference in creativity scores between the two groups.
2. H_0: There is no difference, and 4.144 happened because, by *chance*, the intrinsic group happened to have more creative people in it.

We can explore how likely a value of 4.144 is if there were no difference.

Hypothesize

- Let's suppose that there is no difference (H_0) and that the people were going to get the same creativity score no matter which treatment they received.
- Would we expect the difference between groups to be exactly 0?

Hypothesize

- Let's suppose that there is no difference (H_0) and that the people were going to get the same creativity score no matter which treatment they received.
- Would we expect the difference between groups to be exactly 0? (hint: NO!)
- Under H_0, each person has the same creativity score no matter what treatment.
- Differences in average creativity between repeated samples is just due to randomly assigning each person to each group.
- We can simulate this random mechanism.

The idea of resampling is to

- use only the observed data
- resample (sample from the sample)
- with or without replacement
- I create different realizations of possible experimental results (if the null hypothesis were actually true).

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- use only the observed data
- resample (sample from the sample)
- with or without replacement
- I create different realizations of possible experimental results (if the null hypothesis were actually true).
- I compare many, many resampled experimental results with the observed experimental results I decide if observed result is common or rare to occur by chance.
- If observed data are rare compared to resampled results: the data may point to something interesting (an effect)
- If observed data are common within resampled results: maybe result just occurred by chance (no evidence of an effect)

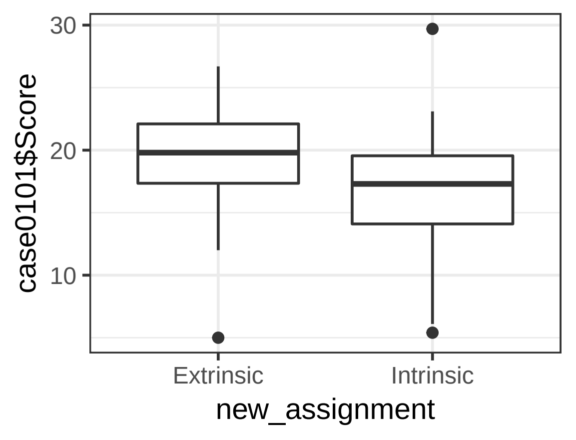
Another Sample

```
new_assignment <- sample(case0101$Treatment)
new_assignment
```

```
##  [1] Extrinsic Intrinsic Intrinsic Intrinsic Intrinsic
##  [8] Intrinsic Intrinsic Intrinsic Intrinsic Intrinsic
## [15] Intrinsic Extrinsic Intrinsic Intrinsic Extrinsic
## [22] Extrinsic Extrinsic Intrinsic Intrinsic Extrinsic
## [29] Extrinsic Extrinsic Extrinsic Intrinsic Intrinsic
## [36] Extrinsic Extrinsic Intrinsic Intrinsic Extrinsic
## [43] Intrinsic Extrinsic Extrinsic Extrinsic Intrinsic
## Levels: Extrinsic Intrinsic
```

EDA of new sample

```
qplot(new_assignment, case0101$Score, geom = "boxplot")
```



Another Sample

```
new_assignment <- sample(case0101$Treatment)
new_assignment
```

```
##  [1] Intrinsic Extrinsic Intrinsic Extrinsic Extrinsic I
##  [8] Intrinsic Intrinsic Intrinsic Extrinsic Intrinsic I
## [15] Extrinsic Intrinsic Intrinsic Intrinsic Intrinsic E
## [22] Extrinsic Extrinsic Extrinsic Extrinsic Intrinsic I
## [29] Extrinsic Extrinsic Extrinsic Extrinsic Extrinsic E
## [36] Extrinsic Intrinsic Intrinsic Intrinsic Extrinsic I
## [43] Extrinsic Intrinsic Intrinsic Extrinsic Intrinsic
## Levels: Extrinsic Intrinsic
```

EDA of new sample

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qplot(new_assignment, case0101$Score, geom = "boxplot")
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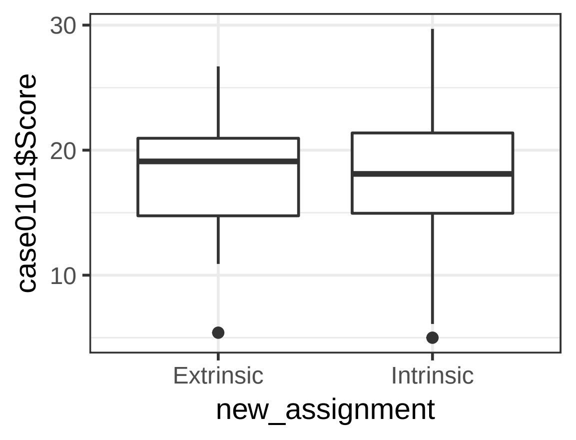
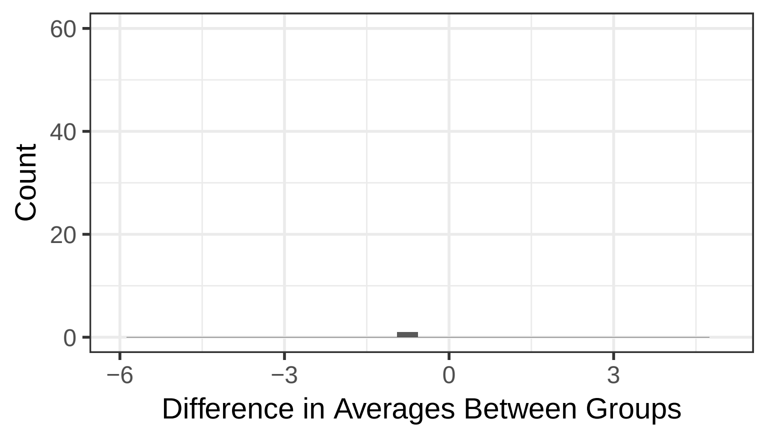


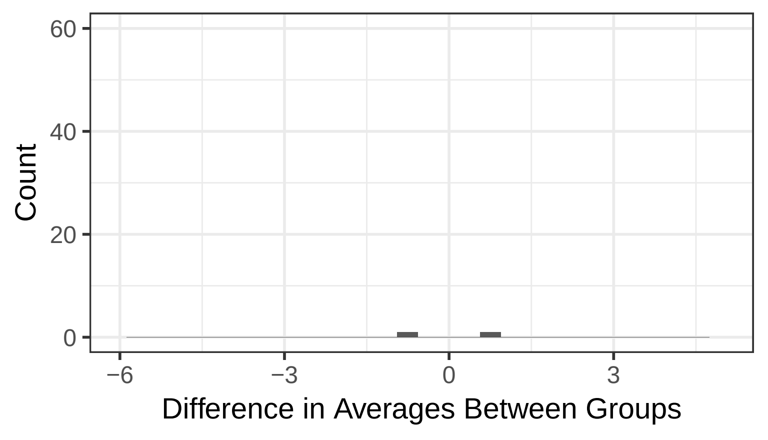
Many Samples i

```r
set.seed(1)
itermax <- 5000
diffvec <- rep(NA, length = itermax)
for (index in seq_len(itermax)) {
  new_assignment <- sample(case0101$Treatment)
  diffvec[index] <-
    mean(case0101$Score[new_assignment == "Intrinsic"]) -
    mean(case0101$Score[new_assignment == "Extrinsic"])
}
```

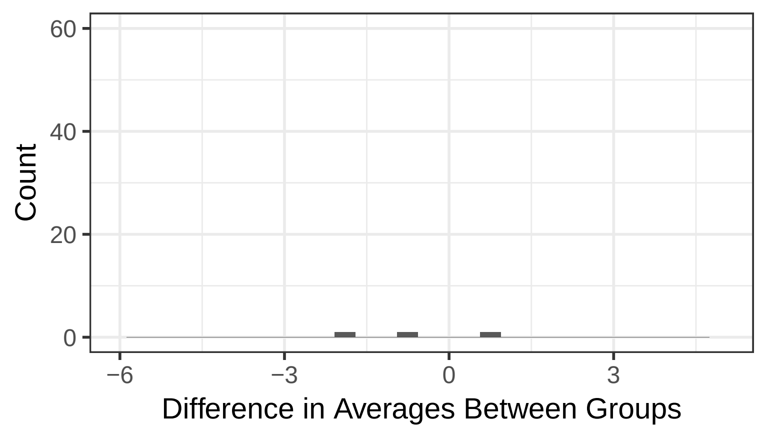
Many Samples ii



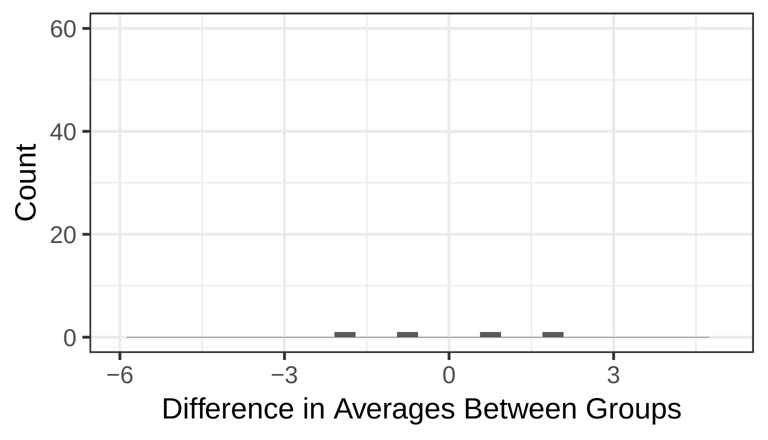
Many Samples iii



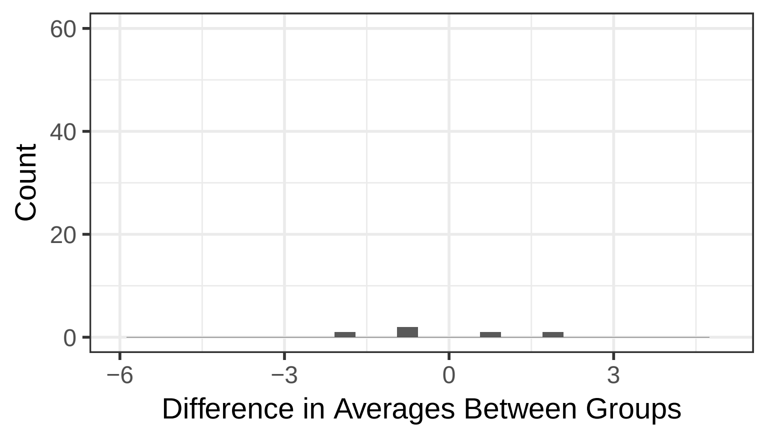
Many Samples iv



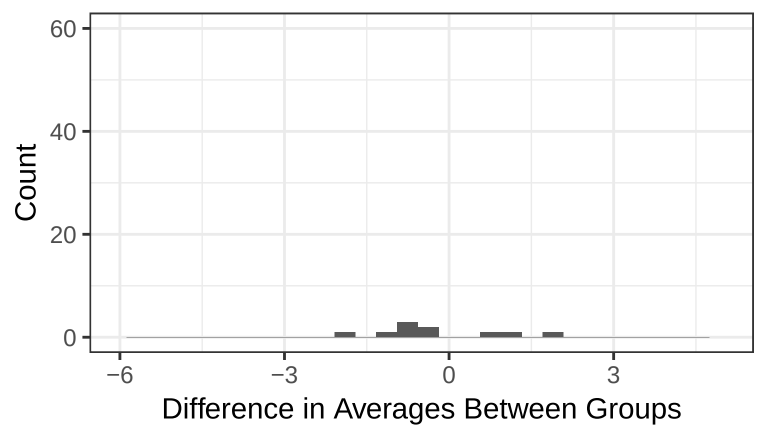
Many Samples v



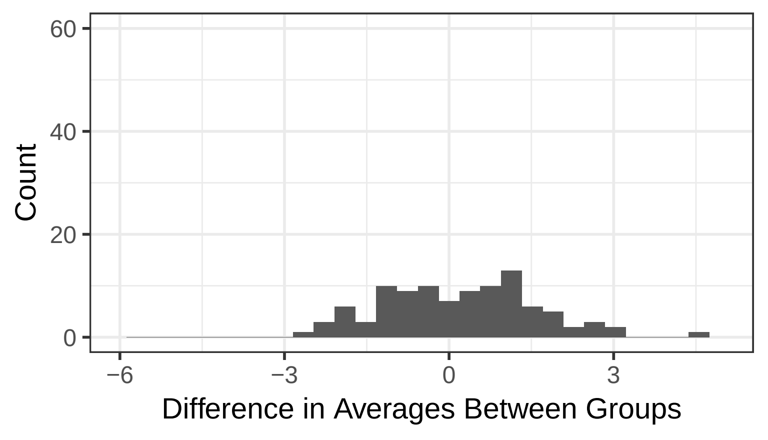
Many Samples vi



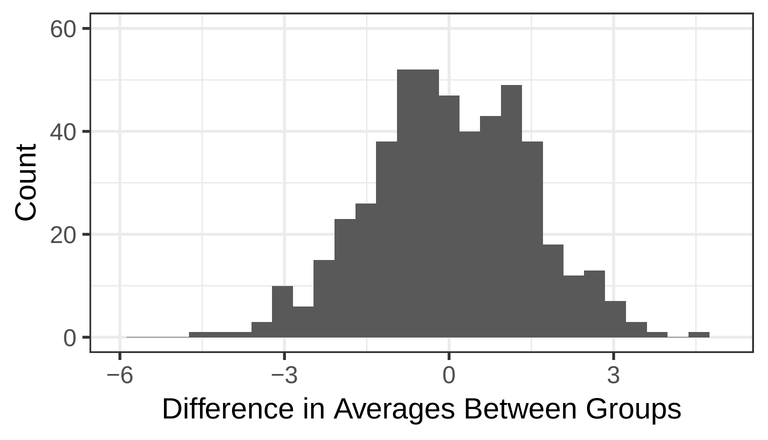
Many Samples vii



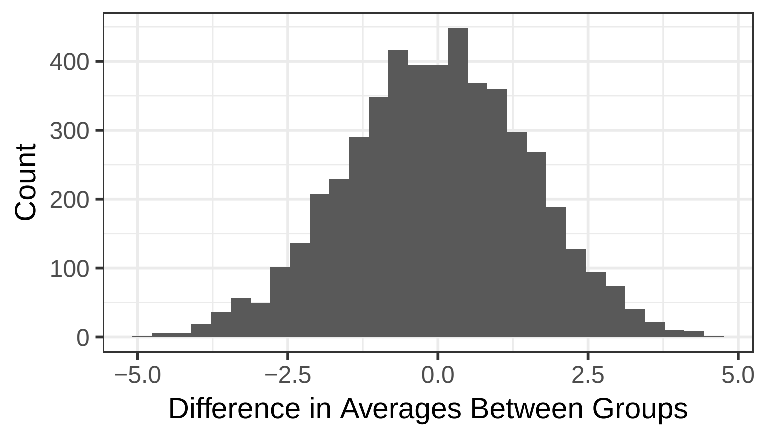
Many Samples viii



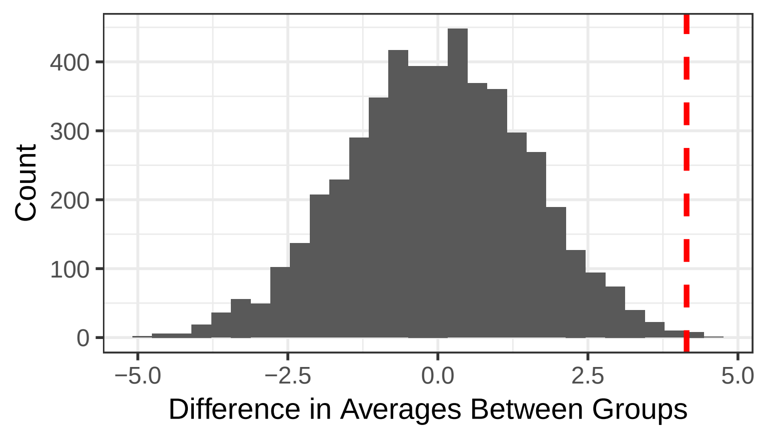
Many Samples ix



Many Samples x



Compare to our Observed Difference



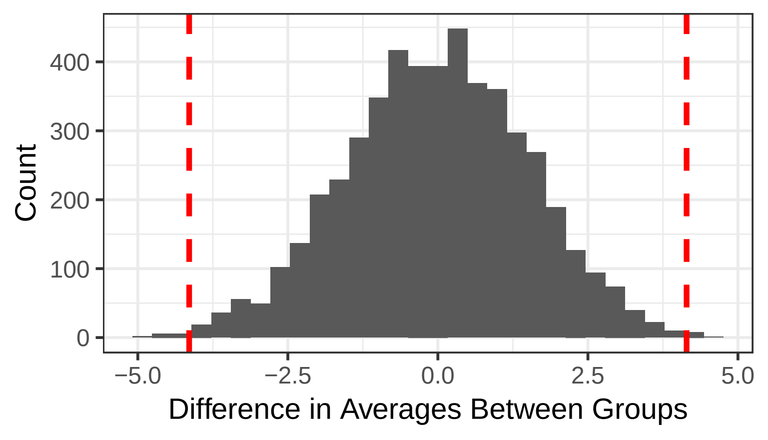
One sided hypothesis

What proportion of random assignments have a score greater than or equal to the observed score?

```
mean(diffvec > int_mean - ext_mean)
```

```
## [1] 0.0016
```

Compare to magnitude of difference



Two sided p-value

What proportion of random assignments have a score as favorable or more favorable to the alternative than our observed score?

```
mean(abs(diffvec) > int_mean - ext_mean)
```

```
## [1] 0.0044
```