

Bootstrapping

Nate Wells

Math 141, 3/7/22

Outline

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- Review how the sampling distribution can be used to assess sampling variability
- Discuss bootstrapping as means of approximating the sampling distribution

Sampling Distribution

Polling Example

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- **Point Estimate/Sample Statistic:** The sample proportion \hat{p} of Americans who plan to vote for Trump/Pence. In this case, $\hat{p} = 0.46$.

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 - For a sample of size $n = 1020$, the standard error is at most $SE = 0.016$.

Sampling Variability

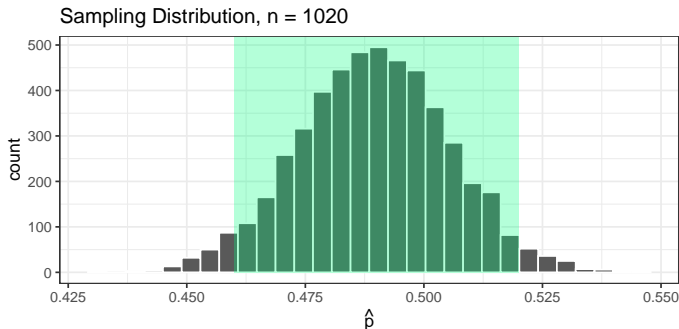
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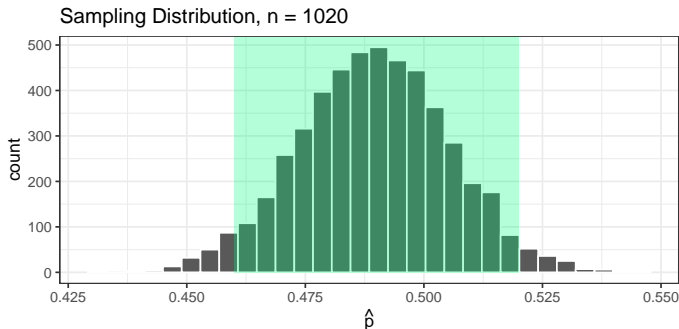
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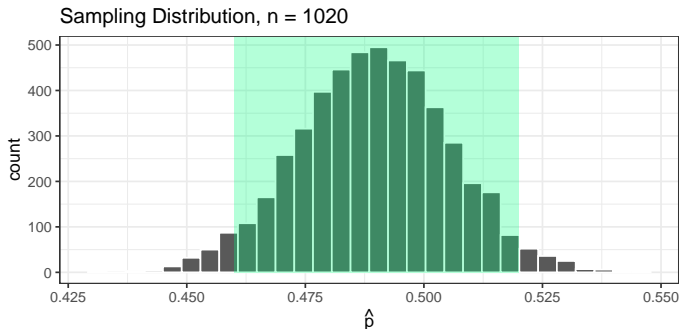
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- Of these, only 6% differed from the true value $p = .49$ by more than .03
- But this also means that for 94% of samples, the true proportion p is within 0.03 of the sample proportion \hat{p} .

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- The fix?

Section 2

Bootstrapping

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 - The phrase originated in the 19th century as reference to a ludicrous or impossible feat
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- Its use in statistics alludes to both interpretations.

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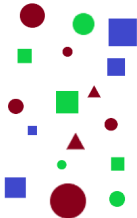
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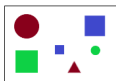
- The original sample approximates the population
- Resampling from the sample approximates sampling many times from the population
- The distribution of statistics from the resamples approximates the sampling distribution

Theory

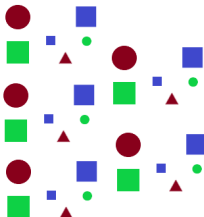
Population



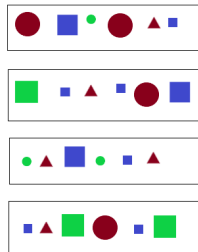
Sample



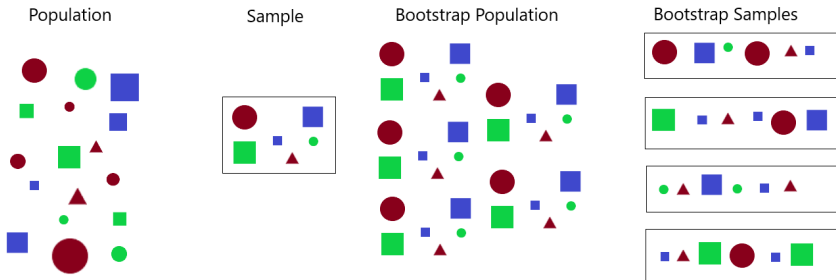
Bootstrap Population



Bootstrap Samples

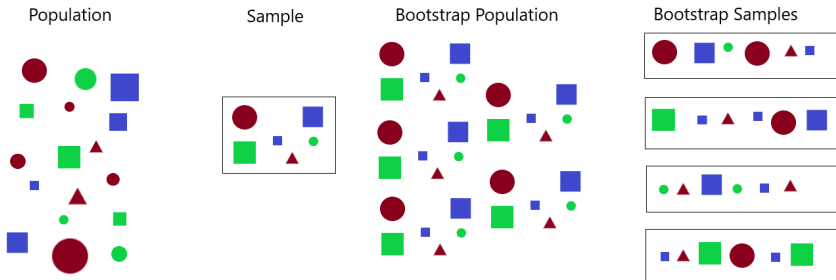


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- We could copy the original sample many times to create a bootstrap population, and then sample *without replacement* to get bootstrap samples
- But this is the same as sampling *with replacement* from the original sample

The Bootstrap Procedure

To generate a **bootstrap distribution**:

- ① Obtain an SRS of size n from the population.
- ② Generate a bootstrap sample of size n by resampling *with* replacement from the original sample
- ③ Repeat (2) a large number of times (with technology, at least 1000 times)
- ④ For each bootstrap sample, calculate the appropriate statistic (called the **bootstrap statistic**)
- ⑤ The collection of the bootstrap statistics form the **bootstrap distribution**

Proof of Concept

- Consider a very large deck of cards (5200 cards) with 100 of each standard card.

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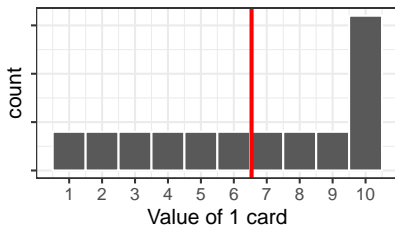
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- Suppose we draw a sample hand of size 25 and calculate the mean value of the hand.

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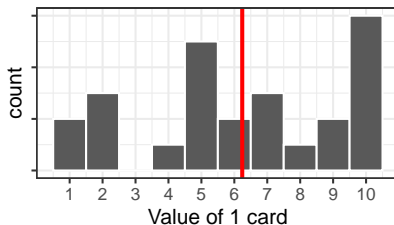
- Consider a very large deck of cards (5200 cards) with 100 of each standard card.
- Suppose we draw a sample hand of size 25 and calculate the mean value of the hand.
- Since we have the deck of cards, we can look at:
 - ① The population distribution
 - ② The single sample's distribution
 - ③ The sampling distribution for sample means
 - ④ The bootstrap distribution for sample means

House of Cards

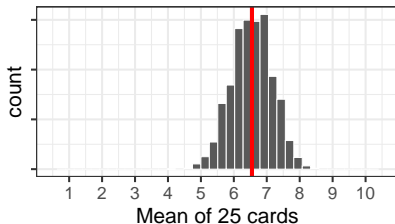
Population Distribution



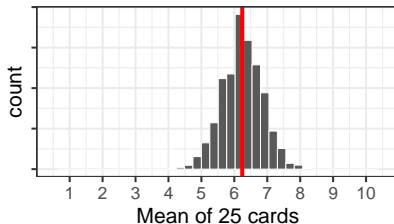
Sample's Distribution



Sampling Distribution



Bootstrap Distribution



House of Cards

We can compute some relevant statistics:

Population:

mean_value	sd_value
6.538462	3.153211

Sample:

mean_value	sd_value
6.24	3.072458

Sampling Distribution:

mean_xbar	sd_xbar
6.55047	0.6162582

Bootstrap Distribution:

mean_xbar	sd_xbar
6.24119	0.604233

Reproduction Rate for Covid-19

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## 4      3 12
## 5      4  5
## 6      6  1

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- Is the true reproduction rate exactly 2.06?
 - Surely not! This is just one sample of size 50
- But how much does the reproduction rate vary from sample to sample?

Bootstrap Reproduction Rate

Create the bootstrap samples:

```
bootstrap_samples <- covid %>%  
  rep_sample_n(size = 50, replace = TRUE, reps = 2000)  
  
head(bootstrap_samples)
```

```
## # A tibble: 100,000 x 2  
## # Groups:   replicate [2,000]  
##   replicate infected  
##   <int> <int>  
## 1      1      2  
## 2      1      1  
## 3      1      1  
## 4      1      0  
## 5      1      1  
## 6      1      0  
## 7      1      2  
## 8      1      3  
## 9      1      3  
## 10     1      3  
## # ... with 99,990 more rows
```

Bootstrap Reproduction Rate

Compute bootstrap statistics:

```
bootstrap_stats <- bootstrap_samples %>%  
  group_by(replicate) %>%  
  summarize(x_bar = mean(infected))
```

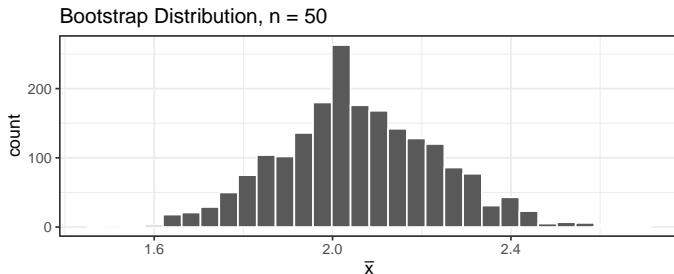
```
bootstrap_stats
```

```
## # A tibble: 2,000 x 2  
##   replicate x_bar  
##       <int> <dbl>  
## 1         1  1.86  
## 2         2  2.36  
## 3         3  2.22  
## 4         4  1.86  
## 5         5  1.88  
## 6         6  1.6  
## 7         7  2.02  
## 8         8  2.16  
## 9         9  2.2  
## 10        10  1.8  
## # ... with 1,990 more rows
```

Bootstrap Reproduction Rate

Graph the bootstrap distribution:

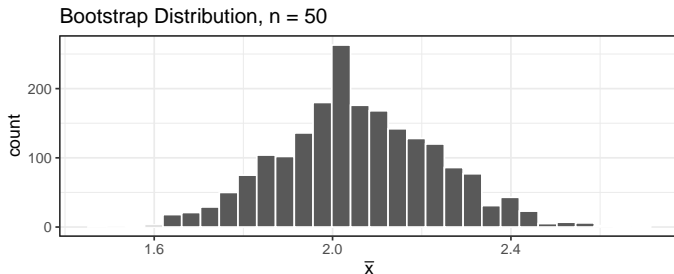
```
ggplot(bootstrap_stats, aes(x = x_bar))+  
  geom_histogram(bins = 30, color = "white")+  
  labs(title = "Bootstrap Distribution, n = 50", x = expression(bar(x)))
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Use the bootstrap distribution to estimate the standard error:

```
bootstrap_stats %>% summarize(SE = sd(x_bar))
```

```
## # A tibble: 1 x 1  
##       SE  
##   <dbl>  
## 1 0.177
```