Day 8: Variability in estimates

BSTA 511/611

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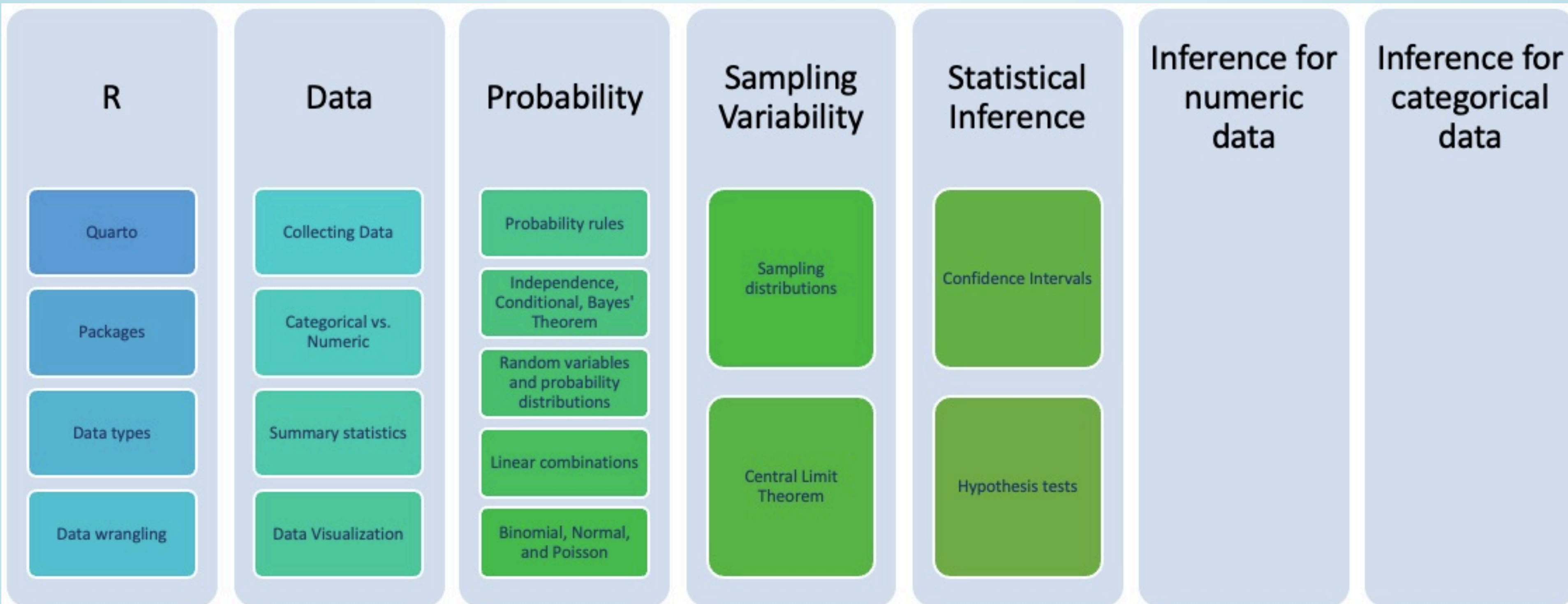
Where are we?


R
Quarto
Packages
Data types
Data wrangling
Data
Collecting Data
Categorical vs. Numeric
Summary statistics
Data Visualization
Probability
Probability rules
Independence, Conditional, Bayes' Theorem
Random variables and probability distributions
Linear combinations
Binomial, Normal, and Poisson
Sampling Variability
Sampling distributions
Central Limit Theorem
Statistical Inference
Confidence Intervals
Hypothesis tests
Inference for numeric data
Inference for categorical data

Goals for today

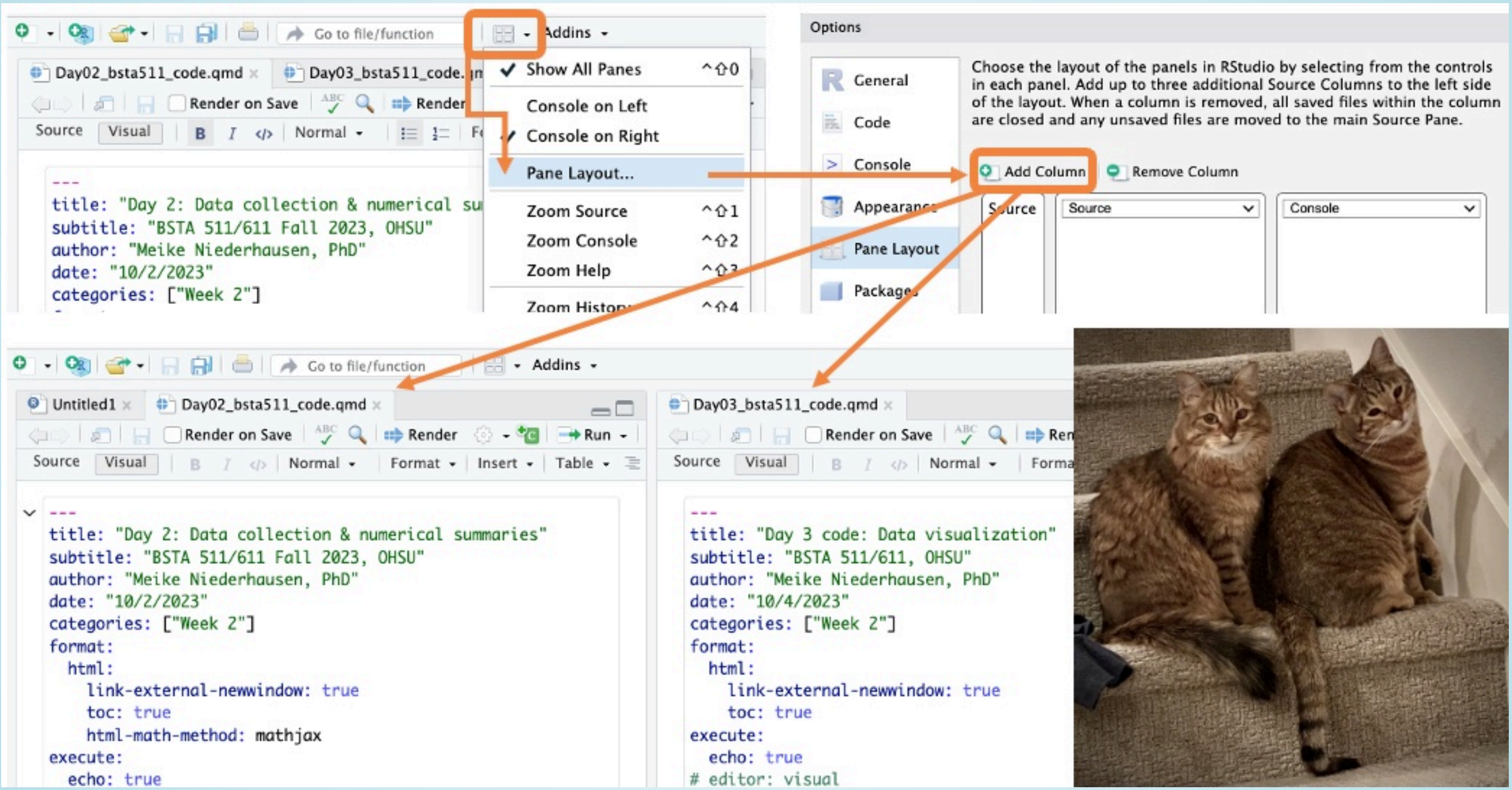
Section 4.1

- Sampling from a population
  - population parameters vs. point estimates
  - sampling variation
- Sampling distribution of the mean
  - Central Limit Theorem

Artwork by @allison_horst

MoRitz's tip of the day: add a code pane in RStudio

Do you want to be able to view two code files side-by-side?
You can do that by adding a column to the RStudio layout.



See https://posit.co/blog/rstudio-1-4-preview-multiple-source-columns/ for more information.

Population vs. sample (from section 1.3)

(Target) Population

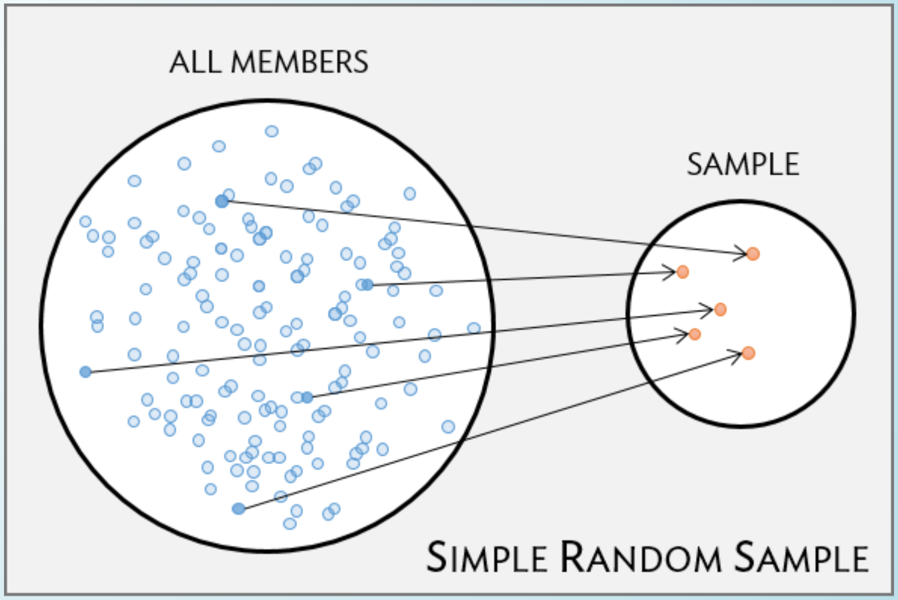
- group of interest being studied
- group from which the sample is selected
  - studies often have *inclusion* and/or *exclusion* criteria

Sample

- group on which data are collected
- often a small subset of the population

Simple random sample (SRS)

- each individual of a population has the *same chance* of being sampled
- randomly sampled
- considered best way to sample



Population parameters vs. sample statistics

Population parameter

Sample statistic (point estimate)

Our hypothetical population: YRBSS

Youth Risk Behavior Surveillance System (YRBSS)

- Yearly survey conducted by the US Centers for Disease Control (CDC)
- "A set of surveys that track behaviors that can lead to poor health in students grades 9 through 12."[1]
- Dataset `yrbss` from `oibiostat` pacakge contains responses from *n* = 13,572 participants in 2013 for a subset of the variables included in the complete survey data

```r
library(oibiostat)
data("yrbss")  #load the data
# ?yrbss
```

```r
dim(yrbss)
```

```
[1] 13583    13
```

```r
names(yrbss)
```

```
 [1] "age"                       "gender"
 [3] "grade"                     "hispanic"
 [5] "race"                      "height"
 [7] "weight"                    "helmet.12m"
 [9] "text.while.driving.30d"    "physically.active.7d"
[11] "hours.tv.per.school.day"   "strength.training.7d"
[13] "school.night.hours.sleep"
```


1. Youth Risk Behavior Surveillance System https://www.cdc.gov/healthyyouth/data/yrbs/index.htm (YRBSS)

Getting to know the dataset: `glimpse()`

```r
glimpse(yrbss)  # from tidyverse package (dplyr)
```

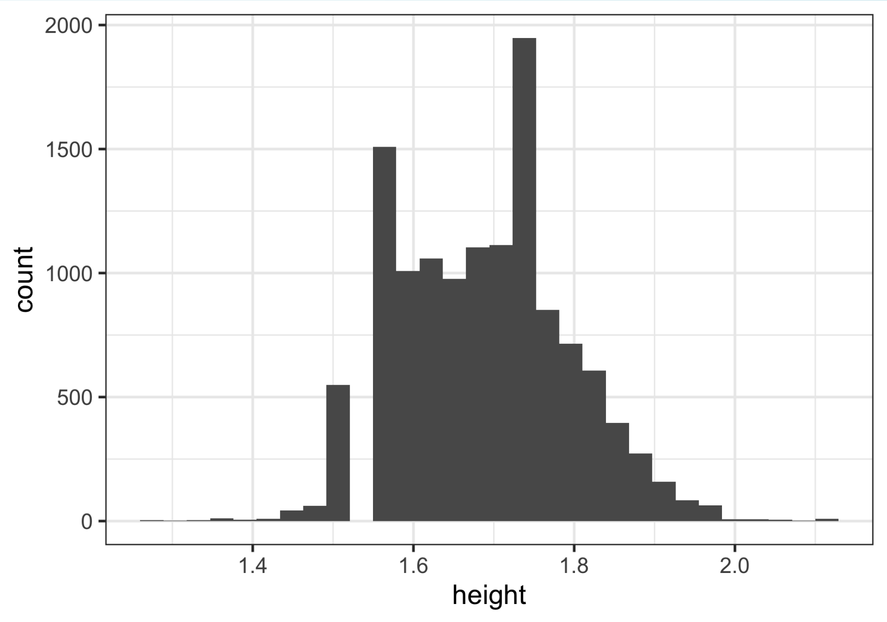
```
Rows: 13,583
Columns: 13
$ age                      <int> 14, 14, 15, 15, 15, 15, 15, 14, 15, 15, 15, 1…
$ gender                   <chr> "female", "female", "female", "female", "fema…
$ grade                    <chr> "9", "9", "9", "9", "9", "9", "9", "9", "9", …
$ hispanic                 <chr> "not", "not", "hispanic", "not", "not", "not"…
$ race                     <chr> "Black or African American", "Black or Africa…
$ height                   <dbl> NA, NA, 1.73, 1.60, 1.50, 1.57, 1.65, 1.88, 1…
$ weight                   <dbl> NA, NA, 84.37, 55.79, 46.72, 67.13, 131.54, 7…
$ helmet.12m               <chr> "never", "never", "never", "never", "did not …
$ text.while.driving.30d   <chr> "0", NA, "30", "0", "did not drive", "did not…
$ physically.active.7d     <int> 4, 2, 7, 0, 2, 1, 4, 4, 5, 0, 0, 0, 4, 7, 7, …
$ hours.tv.per.school.day  <chr> "5+", "5+", "5+", "2", "3", "5+", "5+", "5+",…
$ strength.training.7d     <int> 0, 0, 0, 0, 1, 0, 2, 0, 3, 0, 3, 0, 0, 7, 7, …
$ school.night.hours.sleep <chr> "8", "6", "<5", "6", "9", "8", "9", "6", "<5"…
```

Height & weight variables

```r
yrbss %>%
  select(height, weight) %>%
  summary()
```

```
    height          weight      
 Min.   :1.270   Min.   : 29.94  
 1st Qu.:1.600   1st Qu.: 56.25  
 Median :1.680   Median : 64.41  
 Mean   :1.691   Mean   : 67.91  
 3rd Qu.:1.780   3rd Qu.: 76.20  
 Max.   :2.110   Max.   :180.99  
 NA's   :1004    NA's   :1004    
```

```r
ggplot(data = yrbss,
       aes(x = height)) +
  geom_histogram()
```



Transform height & weight from metric to to standard

Also, drop missing values and add a column of id values

```
yrbss2 <- yrbss %>%                       # save new dataset with new name
  mutate(                                 # add variables for
    height.ft = 3.28084*height,           #     height in feet
    weight.lb = 2.20462*weight            #     weight in pounds
  ) %>%
  drop_na(height.ft, weight.lb) %>% # drop rows w/ missing height/weight values
  mutate(id = 1:nrow(.)) %>%             # add id column
  select(id, height.ft, weight.lb)  # restrict dataset to columns of interest

head(yrbss2)
```

```
  id height.ft weight.lb
1  1  5.675853  186.0038
2  2  5.249344  122.9957
3  3  4.921260  102.9998
4  4  5.150919  147.9961
5  5  5.413386  289.9957
6  6  6.167979  157.0130
```

```
dim(yrbss2)
```

```
[1] 12579     3
```

```
# number of rows deleted that had missing values for height and/or weight:
nrow(yrbss) - nrow(yrbss2)
```

```
[1] 1004
```

yrbss2 summary

```
summary(yrbss2)
```

```
       id          height.ft       weight.lb
 Min.   :    1   Min.   :4.167   Min.   : 66.01
 1st Qu.: 3146   1st Qu.:5.249   1st Qu.:124.01
 Median : 6290   Median :5.512   Median :142.00
 Mean   : 6290   Mean   :5.549   Mean   :149.71
 3rd Qu.: 9434   3rd Qu.:5.840   3rd Qu.:167.99
 Max.   :12579   Max.   :6.923   Max.   :399.01
```

Another summary:

```
yrbss2 %>%
  get_summary_stats(type = "mean_sd") %>%
  kable()
```

variable	n	mean	sd
id	12579	6290.000	3631.389
height.ft	12579	5.549	0.343
weight.lb	12579	149.708	37.254

Random sample of size n = 5 from `yrbss2`

Take a random sample of size n = 5 from `yrbss2`:

```r
library(moderndive)
samp_n5_rep1 <- yrbss2 %>%
  rep_sample_n(size = 5,
               reps = 1,
               replace = FALSE)
samp_n5_rep1
```

```
# A tibble: 5 × 4
# Groups:   replicate [1]
  replicate    id height.ft weight.lb
      <int> <int>     <dbl>     <dbl>
1         1  5869      5.15      145.
2         1  6694      5.41      127.
3         1  2517      5.74      130.
4         1  5372      6.07      180.
5         1  5403      6.07      163.
```

Calculate the mean of the random sample:

```r
means_hght_samp_n5_rep1 <-
  samp_n5_rep1 %>%
  summarise(
    mean_height = mean(height.ft))

means_hght_samp_n5_rep1
```

```
# A tibble: 1 × 2
  replicate mean_height
      <int>       <dbl>
1         1        5.69
```

Would we get the same mean height if we took another sample?

Sampling variation

- If a different random sample is taken, the mean height (point estimate) will likely be different
  - this is a result of **sampling variation**

Take a 2nd random sample of size n = 5 from `yrbss2`:

```
samp_n5_rep1 <- yrbss2 %>%
  rep_sample_n(size = 5,
               reps = 1,
               replace = FALSE)
samp_n5_rep1
```

```
# A tibble: 5 × 4
# Groups:   replicate [1]
  replicate    id height.ft weight.lb
      <int> <int>     <dbl>     <dbl>
1         1  2329      6.07      182.
2         1  8863      5.25      125.
3         1  8058      5.84      135.
4         1   335      6.17      235.
5         1  4698      5.58      124.
```

Calculate the mean of the 2nd random sample:

```
means_hght_samp_n5_rep1 <-
  samp_n5_rep1 %>%
  summarise(
    mean_height = mean(height.ft))

means_hght_samp_n5_rep1
```

```
# A tibble: 1 × 2
  replicate mean_height
      <int>       <dbl>
1         1        5.78
```

Did we get the same mean height with our 2nd sample?

100 random samples of size n = 5 from `yrbss2`

Take 100 random samples of size n = 5 from `yrbss2`:

```
samp_n5_rep100 <- yrbss2 %>%
  rep_sample_n(size = 5,
               reps = 100,
               replace = FALSE)
samp_n5_rep100
```

```
# A tibble: 500 × 4
# Groups:   replicate [100]
   replicate    id height.ft weight.lb
       <int> <int>     <dbl>     <dbl>
 1         1  6483      5.51     145. 
 2         1  9899      4.92      90.0
 3         1  6103      5.68     118. 
 4         1  2702      5.68     150. 
 5         1 11789      5.35     115. 
 6         2 10164      5.51     140. 
 7         2  5807      5.41     215. 
 8         2  9382      5.15      98.0
 9         2  4904      6.00     196. 
10         2   229      6.07     101. 
# ℹ 490 more rows
```

Calculate the mean for each of the 100 random samples:

```
means_hght_samp_n5_rep100 <-
  samp_n5_rep100 %>%
  group_by(replicate) %>%
  summarise(
    mean_height = mean(height.ft))

means_hght_samp_n5_rep100
```

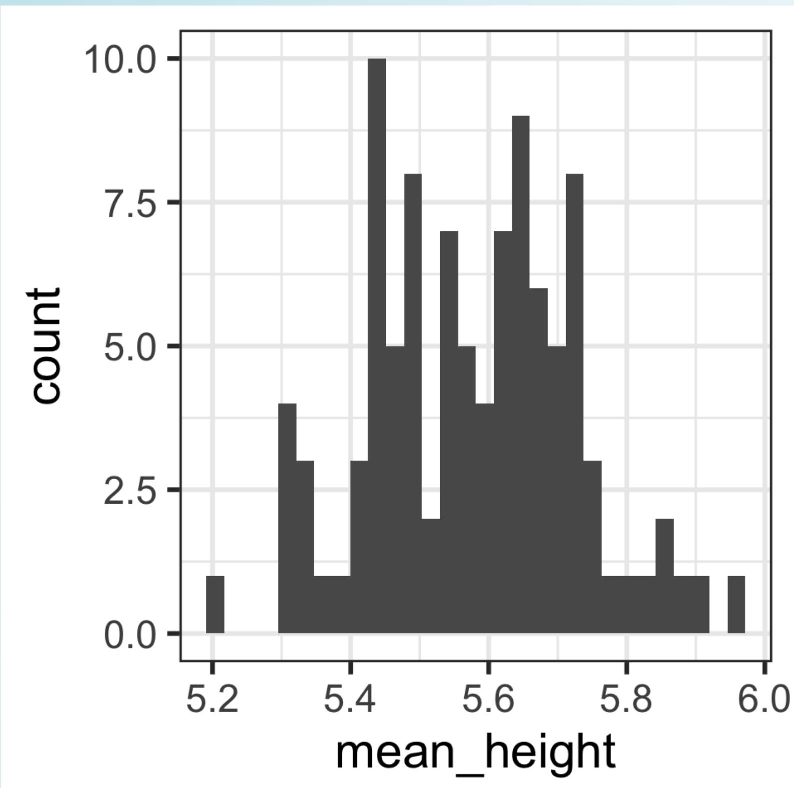
```
# A tibble: 100 × 2
   replicate mean_height
       <int>       <dbl>
 1         1        5.43
 2         2        5.63
 3         3        5.34
 4         4        5.70
 5         5        5.90
 6         6        5.37
 7         7        5.49
 8         8        5.60
 9         9        5.50
10        10        5.68
# ℹ 90 more rows
```

How close are the mean heights for each of the 100 random samples?

Distribution of 100 sample mean heights (n = 5)

Describe the distribution shape.

```r
ggplot(
  means_hght_samp_n5_rep100,
  aes(x = mean_height)) +
  geom_histogram()
```



Calculate the mean and SD of the 100 mean heights from the 100 samples:

```r
stats_means_hght_samp_n5_rep100 <-
  means_hght_samp_n5_rep100 %>%
  summarise(
   mean_mean_height = mean(mean_height),
   sd_mean_height = sd(mean_height)
   )
stats_means_hght_samp_n5_rep100
```

```
# A tibble: 1 × 2
  mean_mean_height sd_mean_height
             <dbl>          <dbl>
1             5.58          0.150
```

Is the mean of the means close to the "center" of the distribution?

10,000 random samples of size n = 5 from yrbss2

Take 10,000 random samples of size n = 5 from yrbss2:

```
samp_n5_rep10000 <- yrbss2 %>%
  rep_sample_n(size = 5,
               reps = 10000,
               replace = FALSE)
samp_n5_rep10000
```

```
# A tibble: 50,000 × 4
# Groups:   replicate [10,000]
   replicate    id height.ft weight.lb
       <int> <int>     <dbl>     <dbl>
 1         1  6383      5.35      126.
 2         1  4019      5.41      107.
 3         1  4856      5.25      135.
 4         1  9988      5.58      120.
 5         1  2245      6.17      270.
 6         2 10580      5.68      155.
 7         2  2254      5.84      159.
 8         2  8081      5.09      110.
 9         2 10194      5.35      115.
10         2  7689      5.35      135.
# ℹ 49,990 more rows
```

Calculate the mean for each of the 10,000 random samples:

```
means_hght_samp_n5_rep10000 <-
  samp_n5_rep10000 %>%
  group_by(replicate) %>%
  summarise(
    mean_height = mean(height.ft))

means_hght_samp_n5_rep10000
```

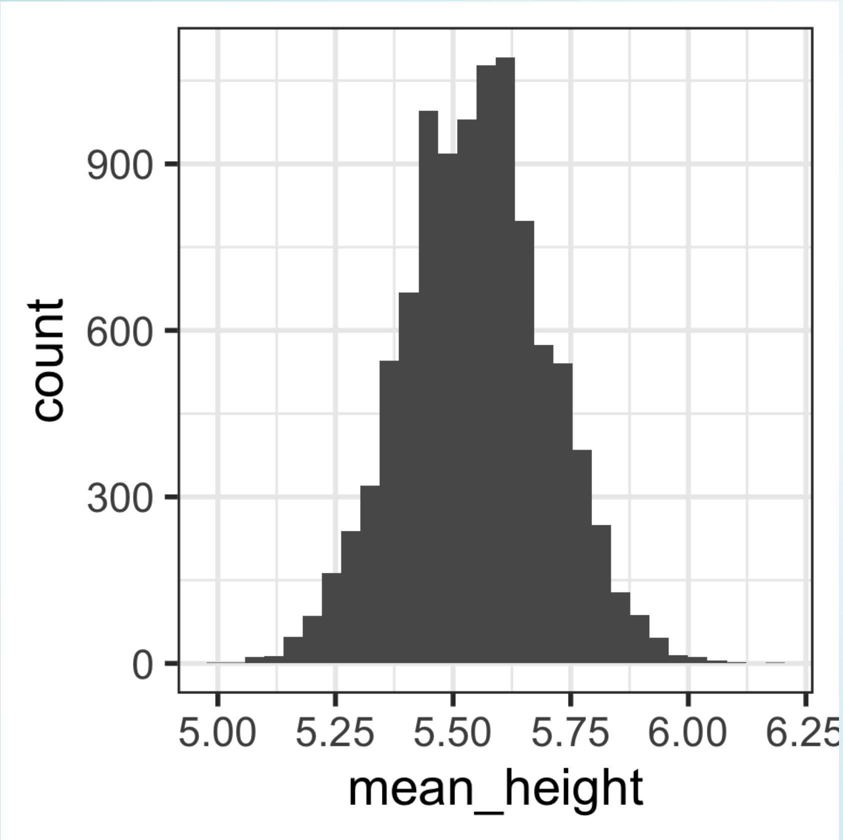
```
# A tibble: 10,000 × 2
   replicate mean_height
       <int>       <dbl>
 1         1        5.55
 2         2        5.46
 3         3        5.49
 4         4        5.60
 5         5        5.47
 6         6        5.83
 7         7        5.68
 8         8        5.47
 9         9        5.37
10        10        5.15
# ℹ 9,990 more rows
```

How close are the mean heights for each of the 10,000 random samples?

Distribution of 10,000 sample mean heights (n = 5)

Describe the distribution shape.

```
ggplot(
  means_hght_samp_n5_rep10000,
  aes(x = mean_height)) +
  geom_histogram()
```



Calculate the mean and SD of the 10,000 mean heights from the 10,000 samples:

```
stats_means_hght_samp_n5_rep10000 <-
  means_hght_samp_n5_rep10000 %>%
  summarise(
   mean_mean_height=mean(mean_height),
   sd_mean_height = sd(mean_height)
   )
stats_means_hght_samp_n5_rep10000
```

```
# A tibble: 1 × 2
  mean_mean_height sd_mean_height
             <dbl>          <dbl>
1             5.55          0.153
```

Is the mean of the means close to the "center" of the distribution?

10,000 samples of size n = 30 from `yrbss2`

Take 10,000 random samples of size n = 30 from `yrbss2`:

```
samp_n30_rep10000 <- yrbss2 %>%
  rep_sample_n(size = 30,
               reps = 10000,
               replace = FALSE)
samp_n30_rep10000
```

```
# A tibble: 300,000 × 4
# Groups:   replicate [10,000]
   replicate    id height.ft weight.lb
       <int> <int>     <dbl>     <dbl>
 1         1  3871      5.25      115.
 2         1 12090      5.15      125.
 3         1   241      5.58      119.
 4         1  4570      5.58      140.
 5         1  4131      5.35      143.
 6         1 11513      5.35      135.
 7         1  9663      5.25      125.
 8         1  3789      5.25      160.
 9         1   442      5.15      130.
10         1 11528      5.51      200.
# ℹ 299,990 more rows
```

Calculate the mean for each of the 10,000 random samples:

```
means_hght_samp_n30_rep10000 <-
  samp_n30_rep10000 %>%
  group_by(replicate) %>%
  summarise(mean_height =
              mean(height.ft))

means_hght_samp_n30_rep10000
```

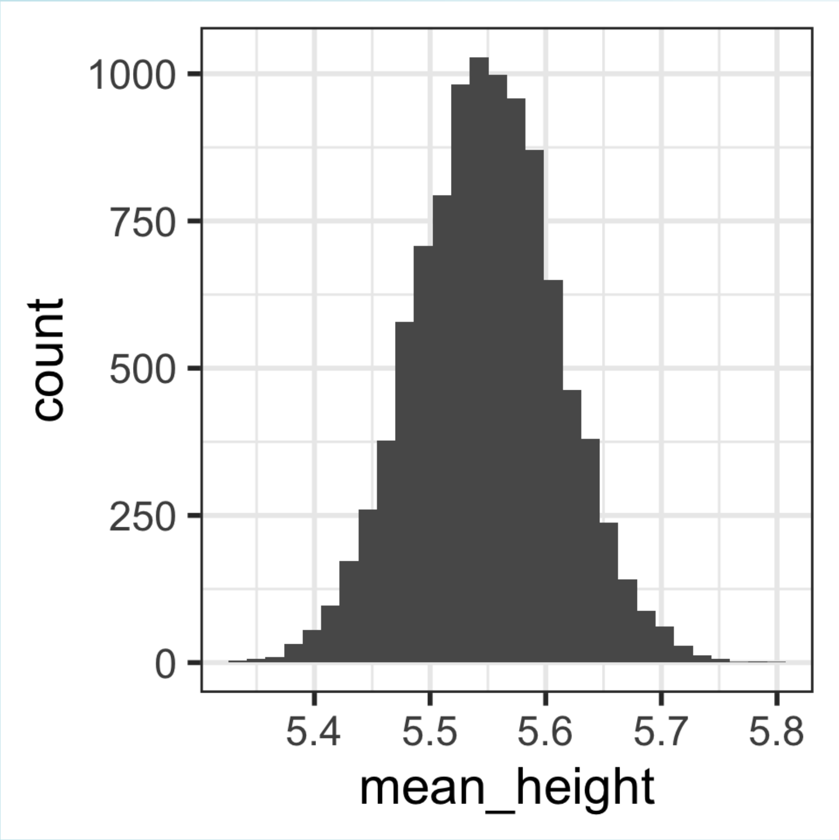
```
# A tibble: 10,000 × 2
   replicate mean_height
       <int>       <dbl>
 1         1        5.48
 2         2        5.63
 3         3        5.46
 4         4        5.46
 5         5        5.51
 6         6        5.54
 7         7        5.56
 8         8        5.51
 9         9        5.51
10        10        5.50
# ℹ 9,990 more rows
```

How close are the mean heights for each of the 10,000 random samples?

Distribution of 10,000 sample mean heights (n = 30)

Describe the distribution shape.

```
ggplot(
  means_hght_samp_n30_rep10000,
  aes(x = mean_height)) +
  geom_histogram()
```



Calculate the mean and SD of the 10,000 mean heights from the 10,000 samples:

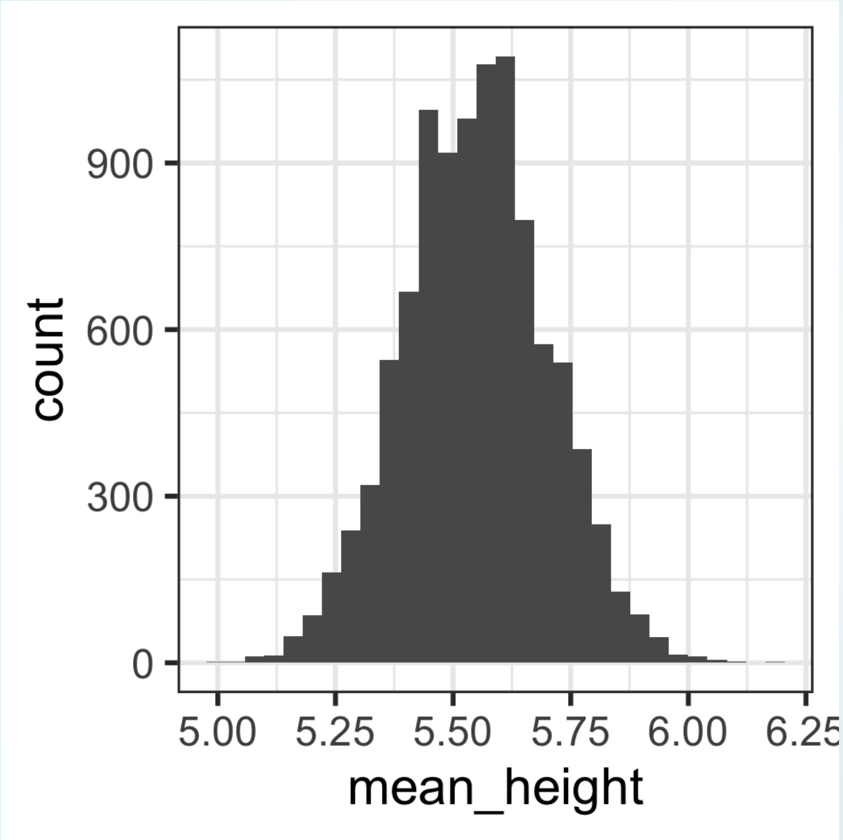
```
stats_means_hght_samp_n30_rep10000<-
  means_hght_samp_n30_rep10000 %>%
  summarise(
   mean_mean_height=mean(mean_height),
   sd_mean_height = sd(mean_height)
   )
stats_means_hght_samp_n30_rep10000
```

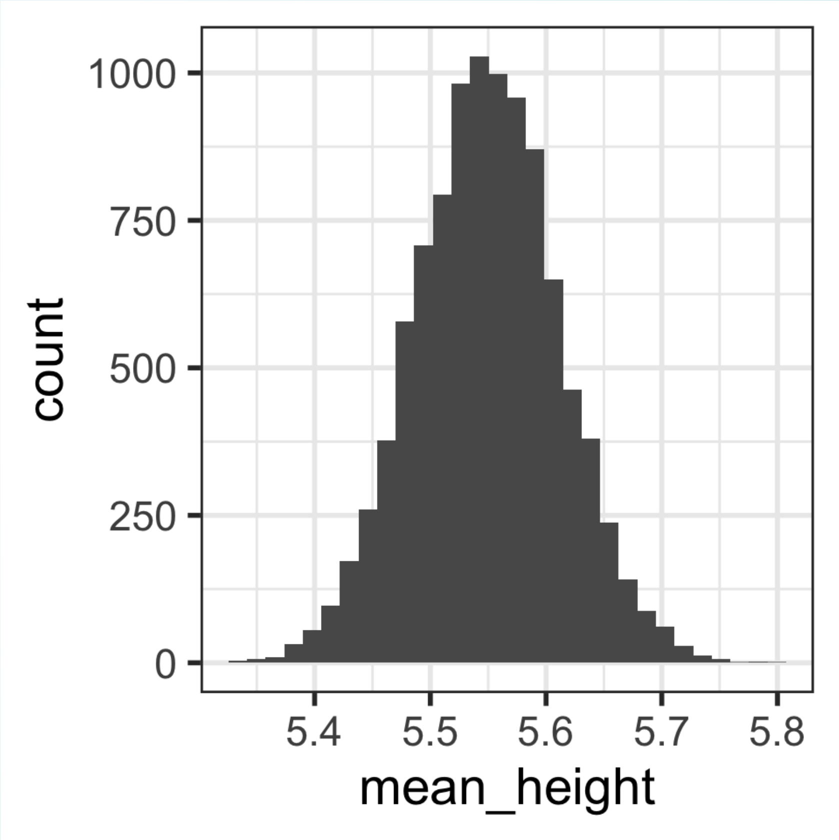
```
# A tibble: 1 × 2
  mean_mean_height sd_mean_height
             <dbl>          <dbl>
1             5.55         0.0623
```

Is the mean of the means close to the “center” of the distribution?

Compare distributions of 10,000 sample mean heights when n = 5 (left) vs. n = 30 (right)

How are the center, shape, and spread similar and/or different?






```
# A tibble: 1 × 2
  mean_mean_height sd_mean_height
             <dbl>          <dbl>
1             5.55          0.153
```

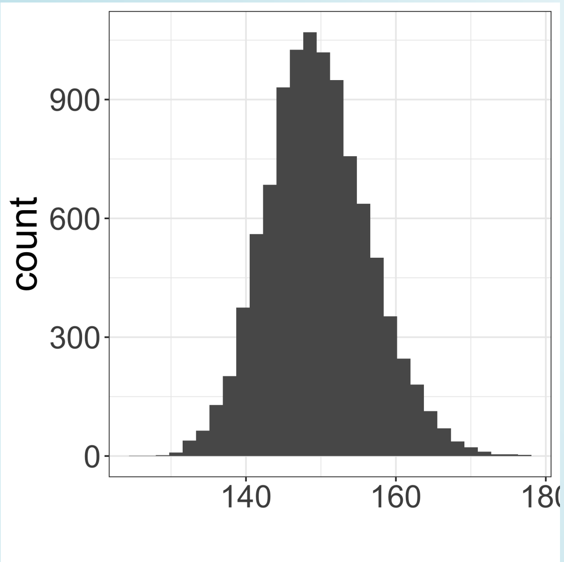
```
# A tibble: 1 × 2
  mean_mean_height sd_mean_height
             <dbl>          <dbl>
1             5.55         0.0623
```

Sampling high schoolers' weights

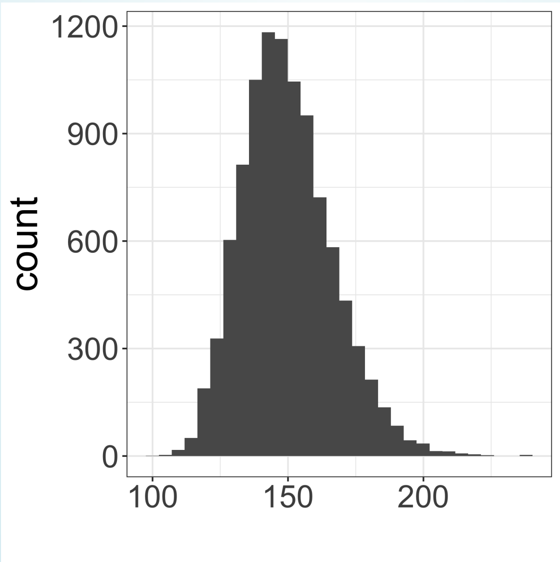
Which figure is which?

- Population distribution of weights
- Sampling distribution of mean heights when $n = 5$
- Sampling distribution of mean heights when $n = 30$.

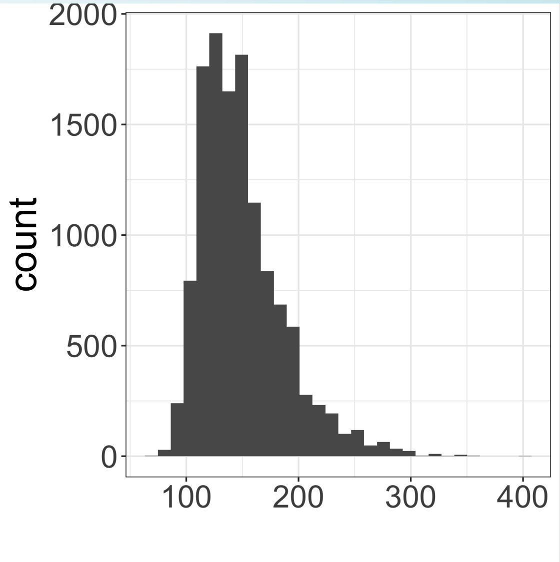
A



B

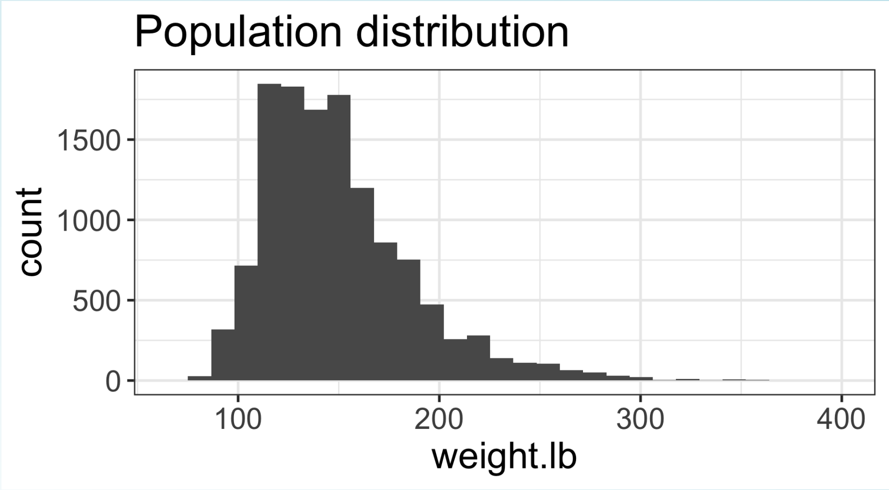


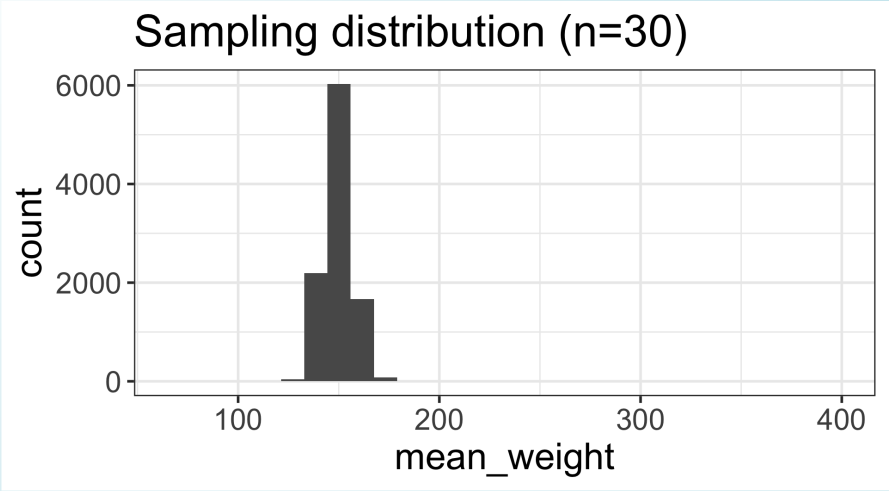
C



The sampling distribution of the mean

- The **sampling distribution** of the mean is the distribution of sample means calculated from repeated random samples of *the same size* from the same population
- Our simulations show approximations of the sampling distribution of the mean for various sample sizes
- The theoretical sampling distribution is based on all possible samples of a given sample size n.





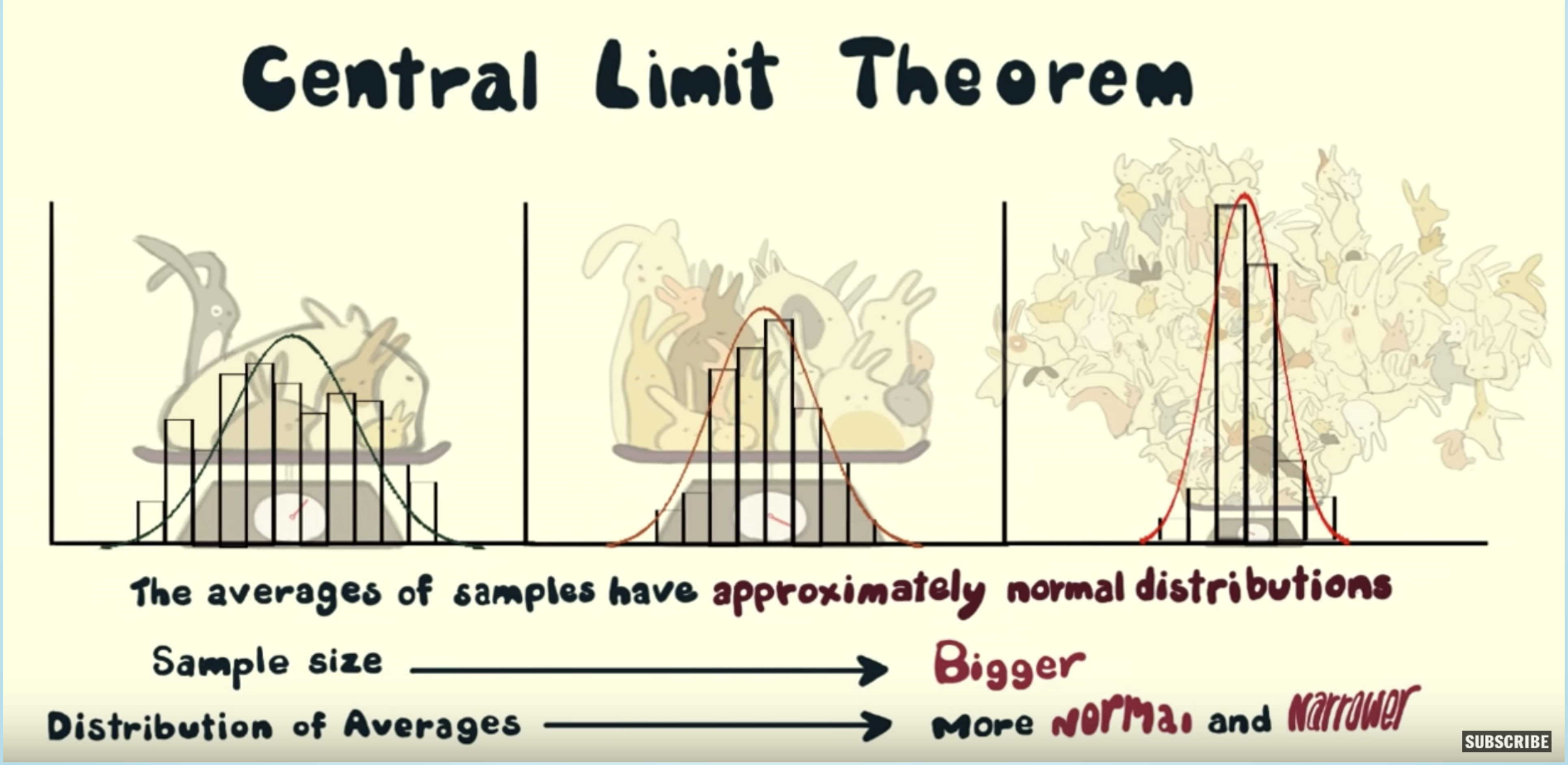
The Central Limit Theorem (CLT)

- For **“large” sample sizes** ($n \geq 30$),
  - the **sampling distribution** of the sample mean
  - can be approximated by a **normal distribution**,with
    - *mean* equal to the *population mean* value μ, and
    - *standard deviation* $\frac{\sigma}{\sqrt{n}}$

- For **small sample sizes**, if the population is known to be normally distributed, then
  - the **sampling distribution** of the sample mean
  - is a **normal distribution**, with
    - *mean* equal to the *population mean* value μ, and
    - *standard deviation* $\frac{\sigma}{\sqrt{n}}$

The cutest statistics video on YouTube

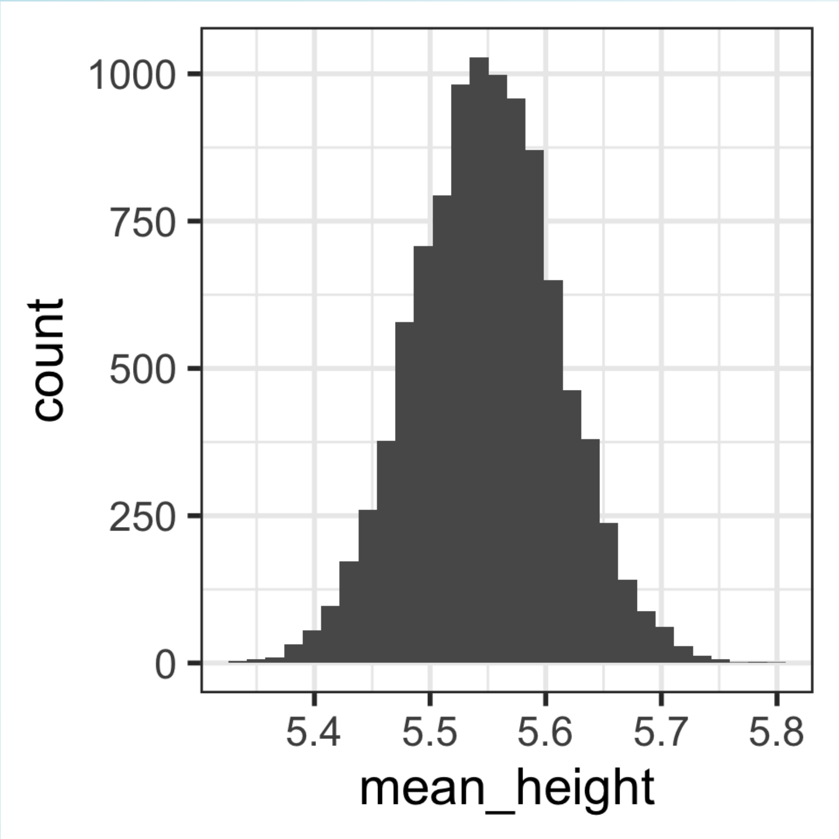
- *Bunnies, Dragons and the 'Normal' World: Central Limit Theorem*
  - Creature Cast from the New York Times
  - https://www.youtube.com/watch?v=jvoxEYmQHNM&feature=youtu.be

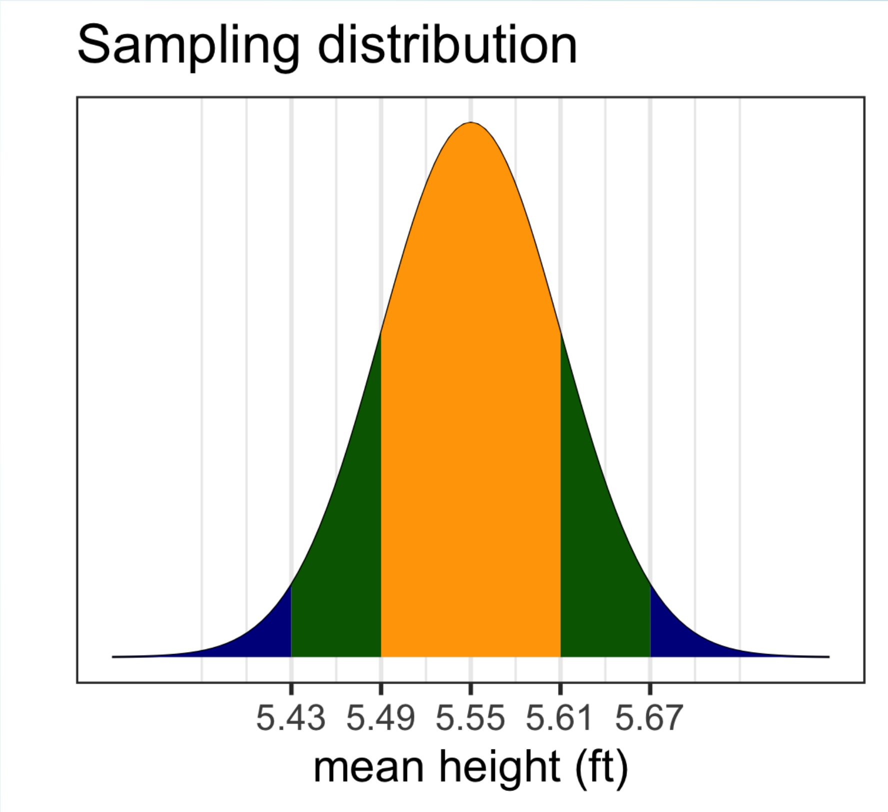


Sampling distribution of mean heights when n = 30 (1/2)

```r
ggplot(
  means_hght_samp_n30_rep10000,
  aes(x = mean_height)) +
  geom_histogram()
```

CLT tells us that we can model the sampling distribution of mean heights using a normal distribution.





Sampling distribution of mean heights when n = 30 (2/2)

Mean and SD of population:

```
(mean_height.ft <- mean(yrbss2$height.ft))
```

```
[1] 5.548691
```

```
(sd_height.ft <- sd(yrbss2$height.ft))
```

```
[1] 0.3434949
```

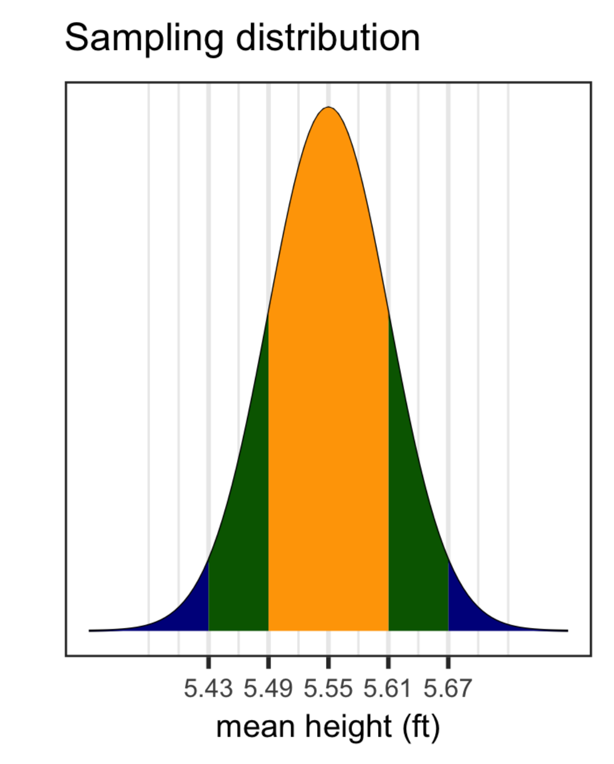
```
sd_height.ft/sqrt(30)
```

```
[1] 0.06271331
```

Mean and SD of simulated sampling distribution:

```
stats_means_hght_samp_n30_rep10000<-
  means_hght_samp_n30_rep10000 %>%
  summarise(
   mean_mean_height=mean(mean_height),
   sd_mean_height = sd(mean_height)
   )
stats_means_hght_samp_n30_rep10000
```

```
# A tibble: 1 × 2
  mean_mean_height sd_mean_height
             <dbl>          <dbl>
1             5.55         0.0623
```



Why is the mean μ & the standard error $\frac{\sigma}{\sqrt{n}}$?

Applying the CLT

What is the probability that for a random sample of 30 high schoolers, that their mean height is greater than 5.6 ft?

Class Discussion

Problems from Homework 4:

- R1: Youth weights (YRBSS)
- Book exercise: 4.2
- Non-book exercise: Ethan Allen