This bears a striking resample-lance

SAMPLING IN R

Richie Cotton
Data Evangelist at DataCamp

With or without

Sampling without replacement

Sampling with replacement ("resampling")

Simple random sampling without replacement

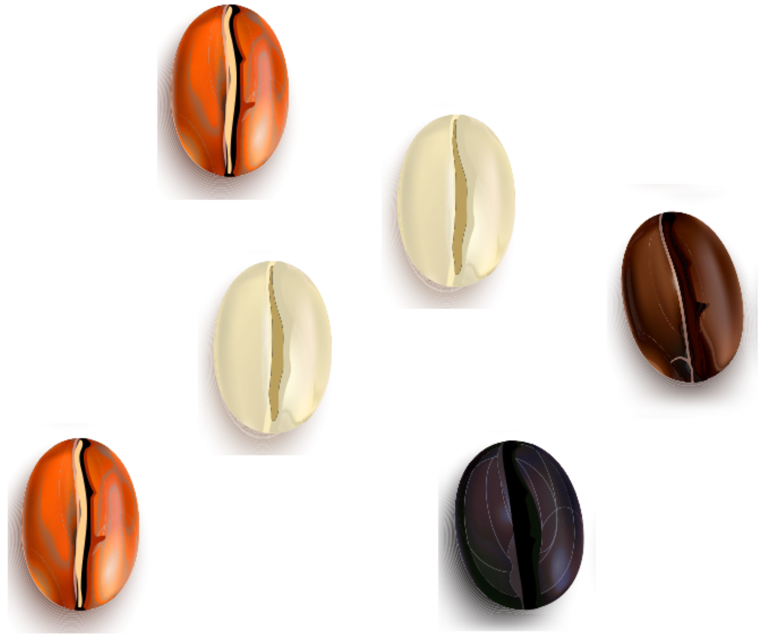
Population

Sample

Simple random sampling with replacement

Population

Sample



Why sample with replacement?

- Think of the `coffee_ratings` data as being a sample of a larger population of all coffees.
- Think about each coffee in our sample as being representative of many different coffees that we don't have in our sample, but do exist in the population.
- Sampling with replacement is a proxy for including different members of these groups in our sample.

Coffee data preparation

```
coffee_focus <- coffee_ratings %>%
  select(variety, country_of_origin, flavor) %>%
  rowid_to_column()
```

```
glimpse(coffee_focus)
```

```
Rows: 1,338
Columns: 4
$ rowid             <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, ...
$ variety           <chr> NA, "Other", "Bourbon", NA, "Other", NA, "Other", N...
$ country_of_origin <chr> "Ethiopia", "Ethiopia", "Guatemala", "Ethiopia", "E...
$ flavor            <dbl> 8.83, 8.67, 8.50, 8.58, 8.50, 8.42, 8.50, 8.33, 8.6...
```

Resampling with slice_sample()

```
coffee_resamp <- coffee_focus %>%
  slice_sample(prop = 1, replace = TRUE)
```

```
# A tibble: 1,338 x 4
   rowid variety country_of_origin flavor
   <int> <chr>   <chr>              <dbl>
 1  1253 Bourbon Guatemala           6.92
 2   186 Caturra Colombia            7.58
 3  1185 Bourbon Guatemala           7.42
 4  1273 NA      Philippines         6.5
 5  1042 Caturra Honduras            7.33
 6   195 Caturra Guatemala           7.75
 7  1219 Typica  Mexico              7
 8   952 Caturra Honduras            7.5
 9    41 Caturra Thailand            8.33
10   460 Caturra Honduras            7.67
# ... with 1,328 more rows
```

Repeated coffees

```r
coffee_resamp %>%
  count(rowid, sort = TRUE)
```

```
# A tibble: 844 x 2
   rowid     n
   <int> <int>
 1   704     5
 2   913     5
 3  1070     5
 4    16     4
 5   180     4
 6   230     4
 7   234     4
 8   342     4
 9   354     4
10   423     4
# ... with 834 more rows
```

Missing coffees

```
coffee_resamp %>%
  summarize(
    coffees_included = n_distinct(rowid),
    coffees_not_included = n() - coffees_included
  )
```

```
# A tibble: 1 x 2
  coffees_included coffees_not_included
             <int>                <int>
1              844                  494
```

Bootstrapping

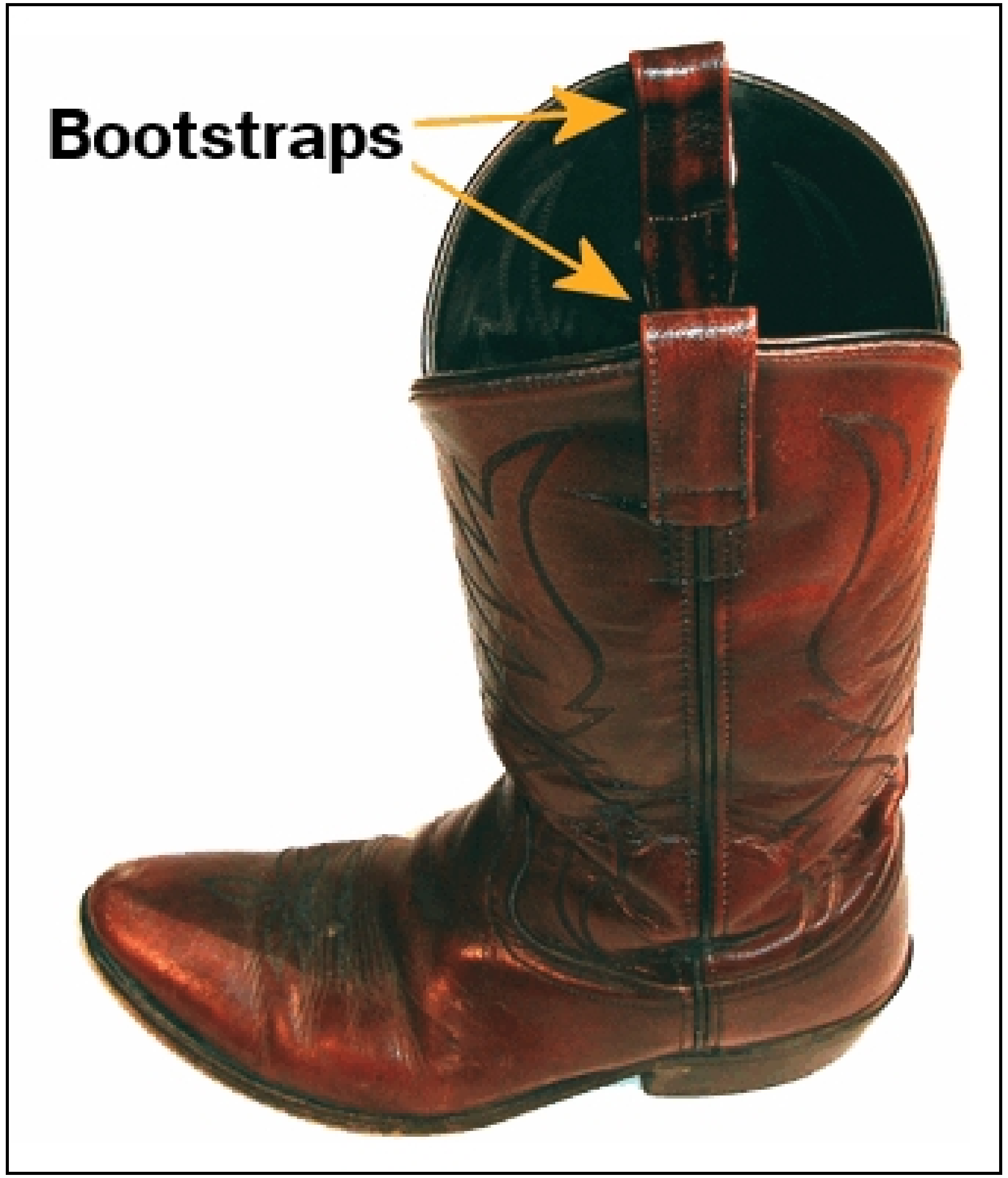
> The opposite of sampling from a population.

Sampling: going from a population to a smaller sample.

Bootstrapping: building up a theoretical population from your sample.

Bootstrapping use case

- Develop understanding of sampling variability using a single sample.



Bootstrapping process

1. Make a resample of the same size as the original sample.
2. Calculate the statistic of interest for this bootstrap sample.
3. Repeat steps 1 and 2 many times.

The resulting statistics are called *bootstrap statistics* and when viewed to see their variability a *bootstrap distribution*.

Bootstrapping coffee mean flavor

```
# Step 3. Repeat many times
mean_flavors_1000 <- replicate(
  n = 1000,
  expr = {
```

```
    coffee_focus %>%
      # Step 1. Resample
      slice_sample(prop = 1, replace = TRUE) %>%
```

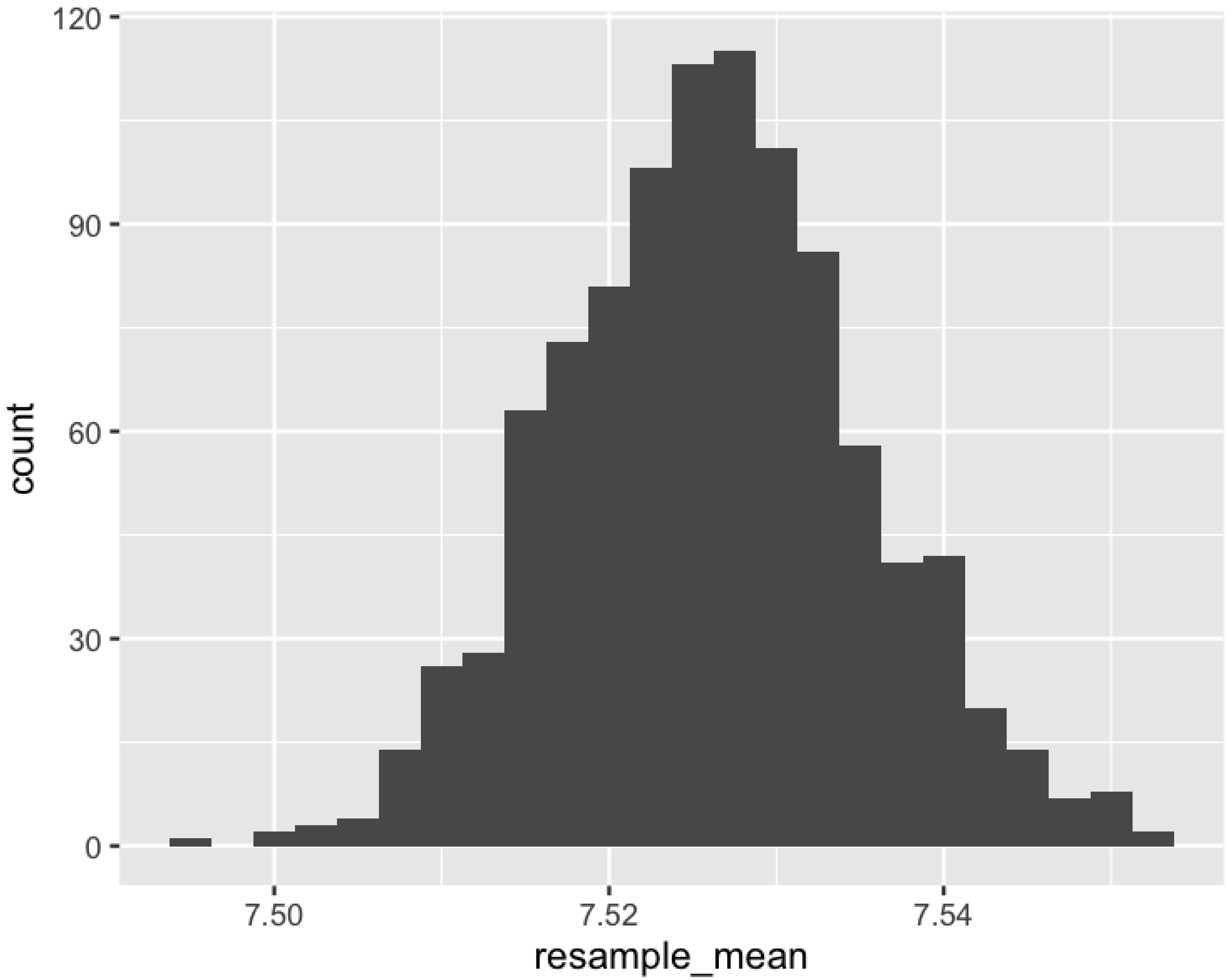
```
      # Step 2. Calculate statistic
      summarize(mean_flavor = mean(flavor, na.rm = TRUE)) %>%
      pull(mean_flavor)
```

```
  })
```

Bootstrap distribution histogram

```
bootstrap_distn <- tibble(
  resample_mean = mean_flavors_1000
)
```

```
ggplot(bootstrap_distn, aes(resample_mean)) +
  geom_histogram(binwidth = 0.0025)
```



Let's practice!

SAMPLING IN R

A breath of fresh error

SAMPLING IN R

Richie Cotton

Data Evangelist at DataCamp

Coffee focused subset

```r
set.seed(19790801)
coffee_sample <- coffee_ratings %>%
  select(variety, country_of_origin, flavor) %>%
  rowid_to_column() %>%
  slice_sample(n = 500)
glimpse(coffee_sample)
```

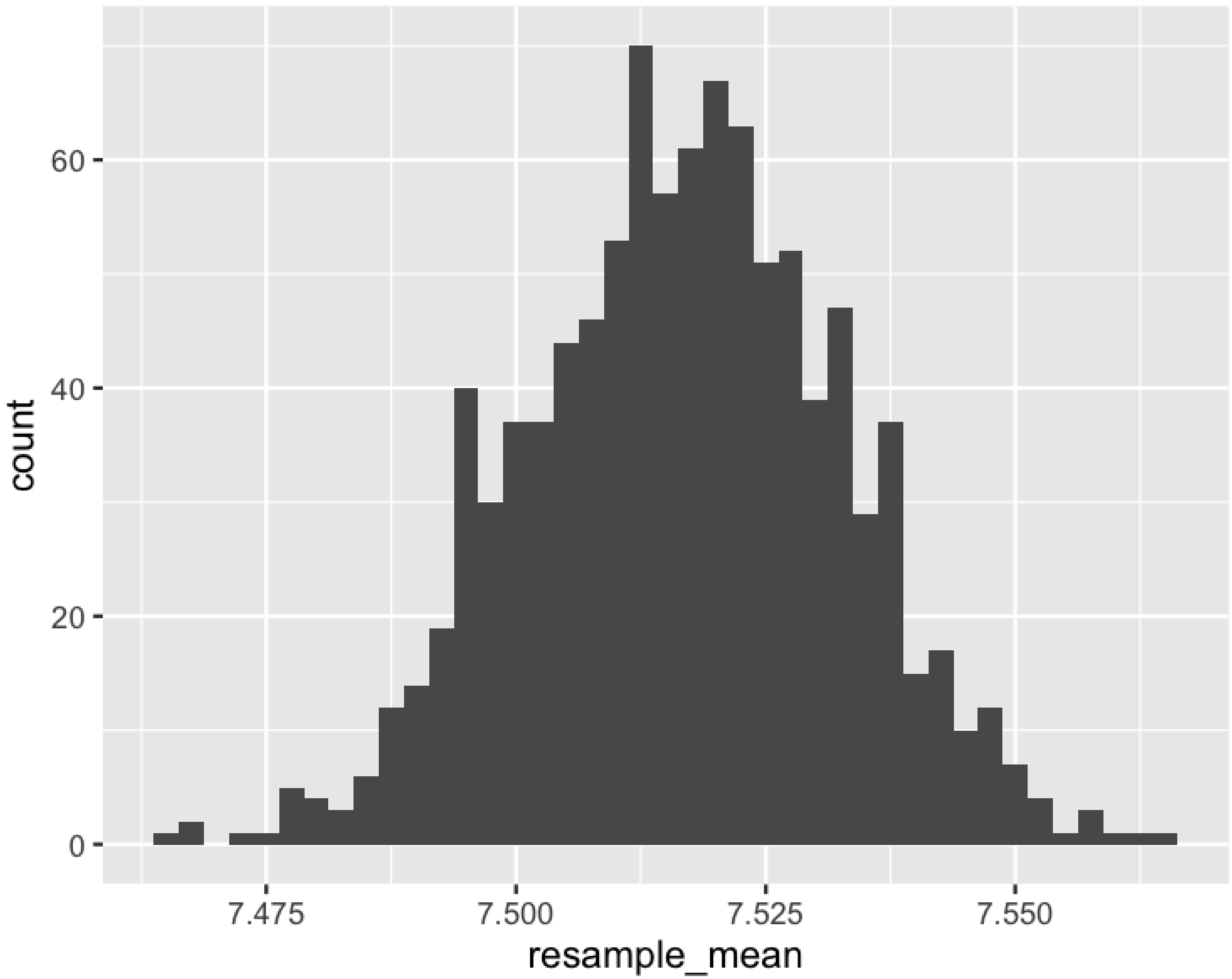
```
Rows: 500
Columns: 4
$ rowid             <int> 10, 278, 458, 622, 131, 385, 1292, 47, 904, 1020, 5...
$ variety           <chr> "Other", "Bourbon", NA, "Caturra", "Caturra", "Yell...
$ country_of_origin <chr> "Ethiopia", "Guatemala", "Colombia", "Thailand", "C...
$ flavor            <dbl> 8.58, 7.75, 7.75, 7.50, 8.00, 7.83, 7.17, 8.08, 7.3...
```

The bootstrap of mean coffee flavors

```
mean_flavors_1000 <- replicate(
  n = 1000,
  expr = coffee_sample %>%
    slice_sample(prop = 1, replace = TRUE) %>%
    summarize(mean_flavor = mean(flavor, na.rm = TRUE)) %>%
    pull(mean_flavor)
)
bootstrap_distn <- tibble(
  resample_mean = mean_flavors_1000
)
```

Mean flavor bootstrap distribution

```
ggplot(bootstrap_distn, aes(resample_mean)) +
 geom_histogram(binwidth = 0.0025)
```



Sample, bootstrap distribution, population means

Sample mean

```
coffee_sample %>%
  summarize(mean_flavor = mean(flavor)) %>%
  pull(mean_flavor)
```

```
7.5163
```

Estimated population mean

```
bootstrap_distn %>%
  summarize(mean_mean_flavor = mean(resample_mean)) %>%
  pull(mean_flavor)
```

```
7.5167
```

True population mean

```
coffee_ratings %>%
  summarize(mean_mean_flavor = mean(resample_mean)) %>%
  pull(mean_flavor)
```

```
7.5260
```

Interpreting the means

- The bootstrap distribution mean is usually almost identical to the sample mean.
- It may not be a good estimate of the population mean.
- Bootstrapping cannot correct biases due to differences between your sample and the population.

Sample sd vs bootstrap distribution sd

Sample standard deviation

```
coffee_focus %>%
  summarize(sd_flavor = sd(flavor)) %>%
  pull(sd_flavor)
```

```
0.3525
```

Estimated population standard deviation?

```
bootstrap_distn %>%
  summarize(sd_mean_flavor = sd(resample_mean)) %>%
  pull(sd_mean_flavor)
```

```
0.01572
```

Sample, bootstrap dist'n, pop'n standard deviations

Sample standard deviation

```
coffee_focus %>%
  summarize(sd_flavor = sd(flavor)) %>%
  pull(sd_flavor)
```

```
0.3525
```

True standard deviation

```
coffee_ratings %>%
  summarize(sd_flavor = sd(flavor)) %>%
  pull(sd_flavor)
```

```
0.3414
```

Estimated population standard deviation

```
standard_error <- bootstrap_distn %>%
  summarize(sd_mean_flavor = sd(resample_mean)) %>%
  pull(sd_mean_flavor)
```

```
standard_error * sqrt(500)
```

```
0.3515
```

Standard error is the standard deviation of the statistic of interest.

Standard error times square root of sample size estimates the population standard deviation.

Interpreting the standard errors

- *Estimated standard error* is the standard deviation of the bootstrap distribution for a sample statistic.
- The bootstrap distribution standard error times the square root of the sample size estimates the standard deviation in the population.

Let's practice!

SAMPLING IN R

Venus infers

SAMPLING IN R

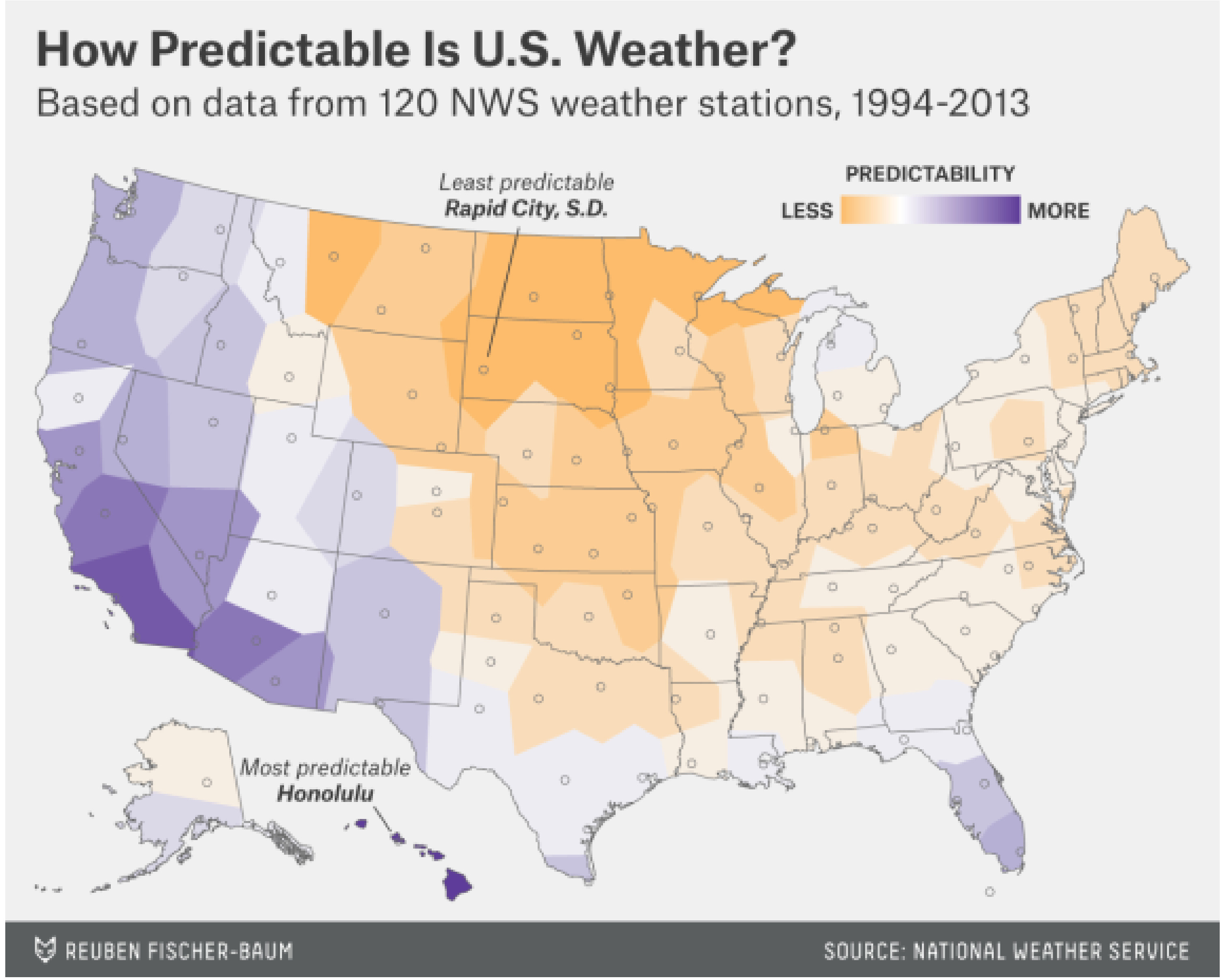
Richie Cotton
Data Evangelist at DataCamp

Confidence intervals

- "Values within one standard deviation of the mean" includes a large number of values from each of these distributions.
- We'll define a related concept called a *confidence interval.*

Predicting the weather

- Rapid City, South Dakota in the United States has the least predictable weather.
- Your job is to predict the high temperature there tomorrow.



How Predictable Is U.S. Weather?

Based on data from 120 NWS weather stations, 1994-2013

REUBEN FISCHER-BAUM

SOURCE: NATIONAL WEATHER SERVICE

Your weather prediction

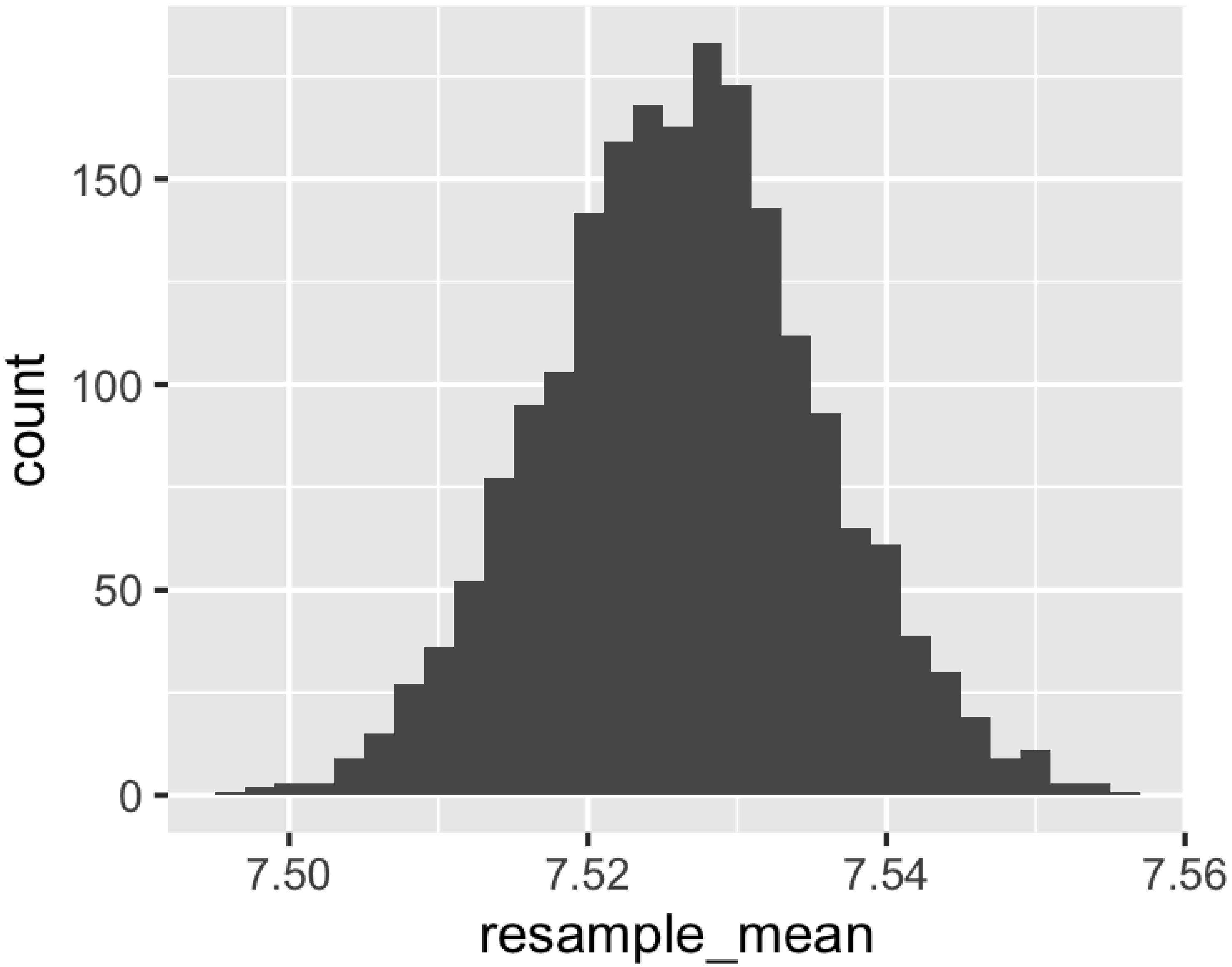
- point estimate = 47 °F (8.3 °C)
- range of plausible high temperature values = 40 to 54 °F (4.4 to 12.8 °C)

You just reported a confidence interval

- 40 to 54 °F is a *confidence interval*
- Sometimes written as 47 °F (40 °F, 54 °F) or 47 °F [40 °F, 54 °F]
- ... or, 47 ± 7 °F
- 7 °F is the *margin of error*

Bootstrap distribution of mean flavor

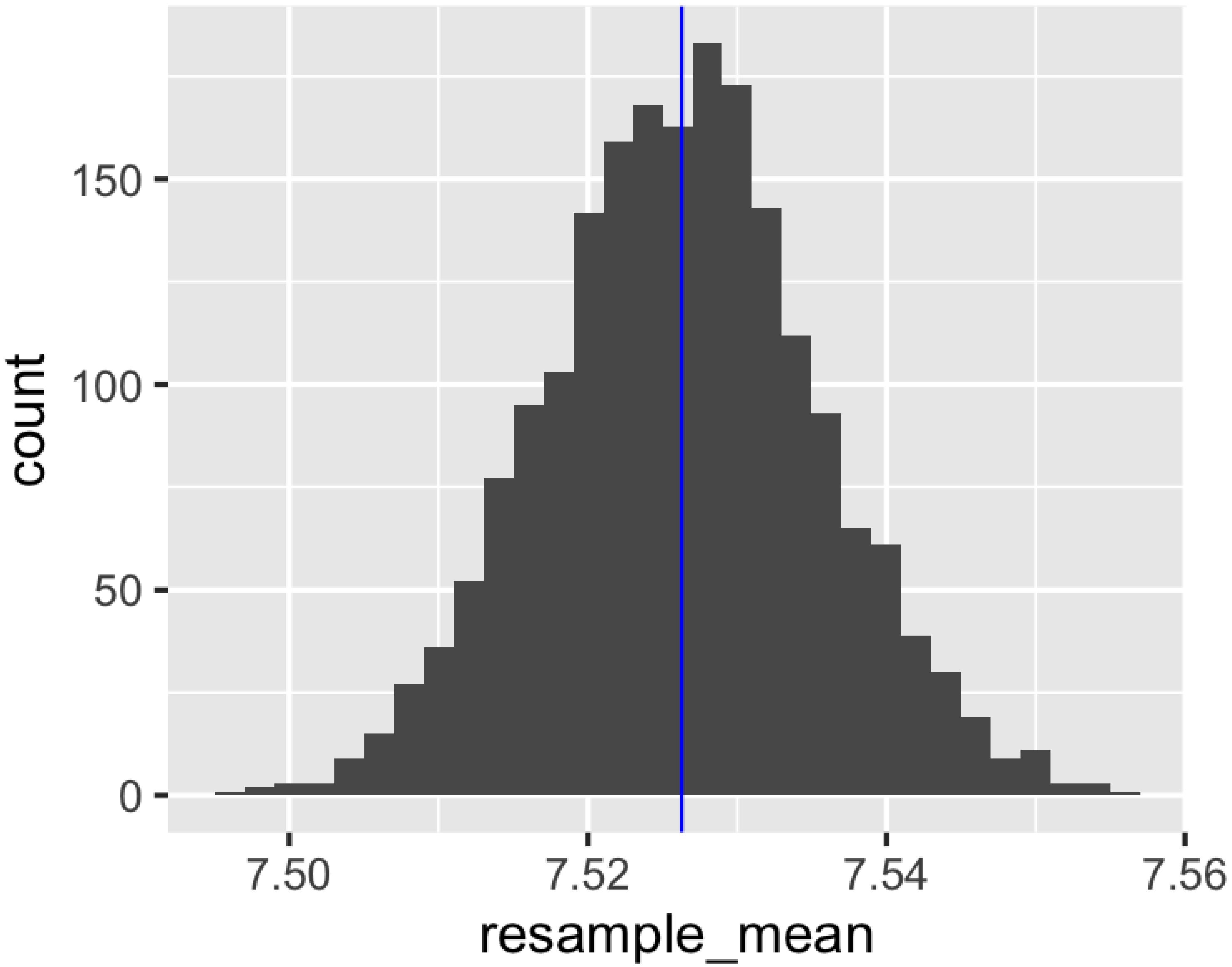
```
ggplot(coffee_boot_distn, aes(resample_mean)) +
  geom_histogram(binwidth = 0.002)
```



Mean of the resamples

```r
coffee_boot_distn %>%
  summarize(
    mean_resample_mean = mean(resample_mean)
  )
```

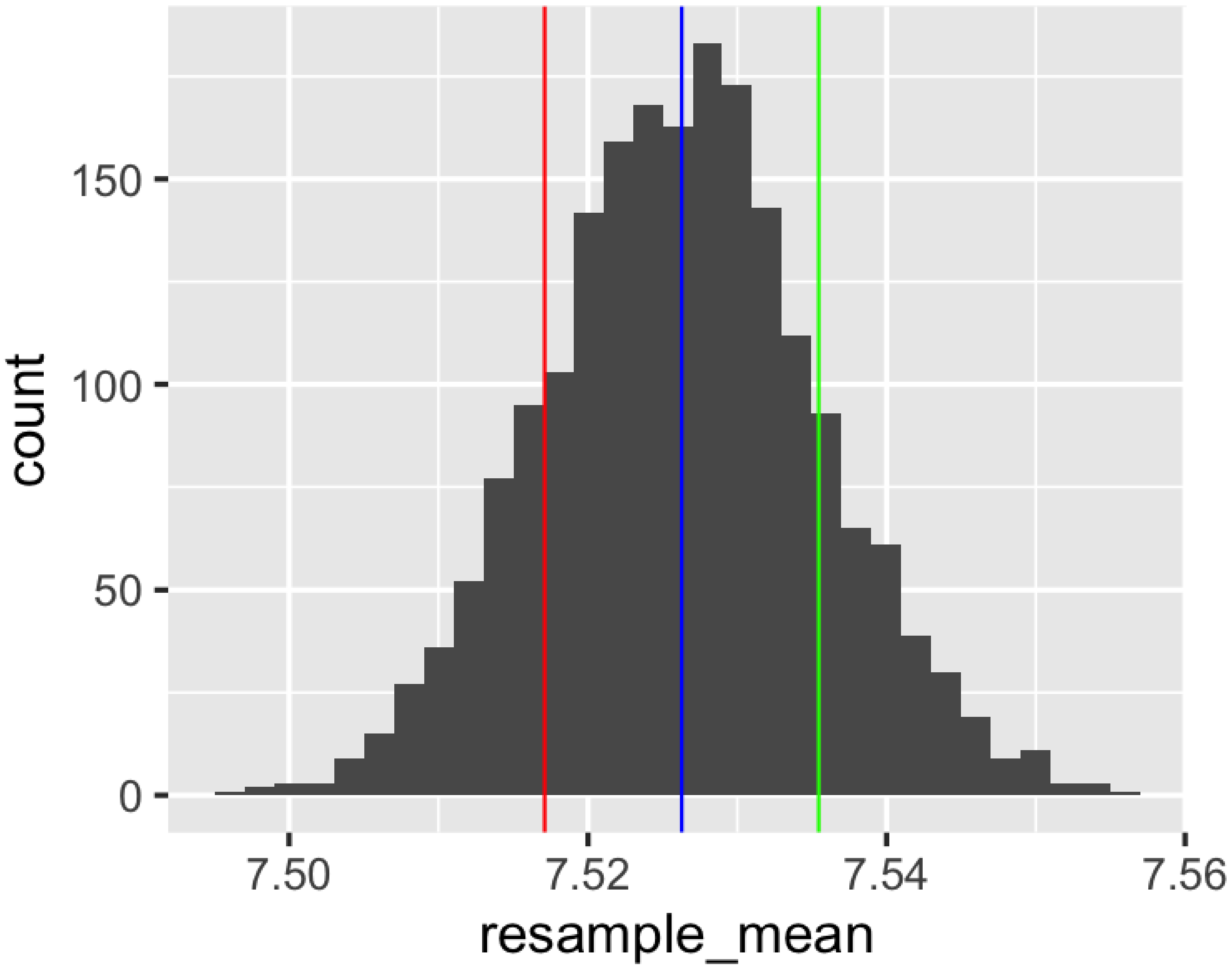
```
# A tibble: 1 x 1
  mean_resample_mean
               <dbl>
1             7.5263
```



Mean plus or minus one standard deviation

```
coffee_boot_distn %>%
  summarize(
    mean_resample_mean = mean(resample_mean),
    mean_minus_1sd = mean_resample_mean - sd(resample_mean),
    mean_plus_1sd = mean_resample_mean + sd(resample_mean)
  )
```

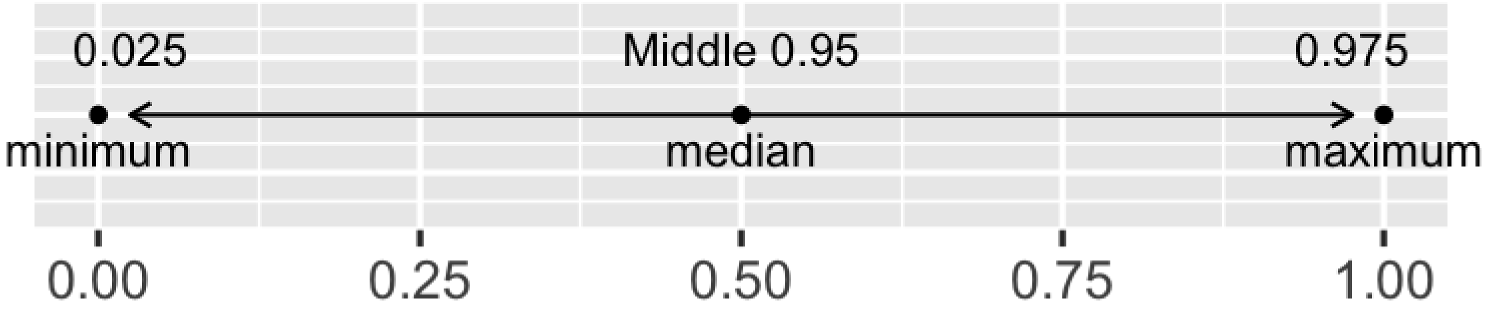
```
# A tibble: 1 x 3
  mean_resample_mean mean_plus_1sd mean_minus_1sd
               <dbl>         <dbl>          <dbl>
1             7.5263        7.5355         7.5171
```



Quantile method for confidence intervals

```
coffee_boot_distn %>%
  summarize(
    lower = quantile(resample_mean, 0.025),
    upper = quantile(resample_mean, 0.975)
  )
```

```
# A tibble: 1 x 2
   lower  upper
   <dbl>  <dbl>
1 7.5087 7.5447
```

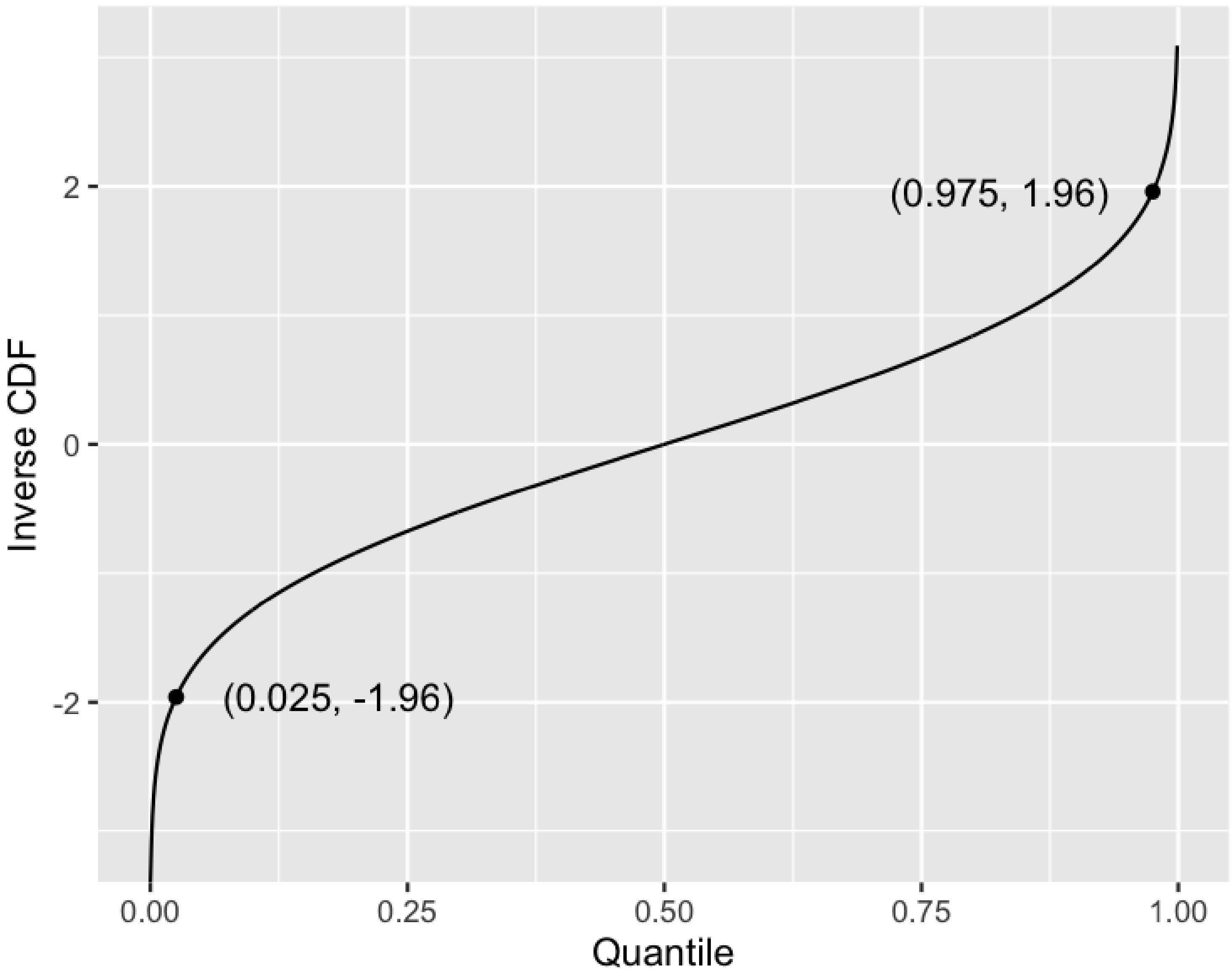


Inverse cumulative distribution function

- PDF: The bell curve
- CDF: integrate to get area under bell curve
- Inv. CDF: flip x and y axes

```r
normal_inv_cdf <- tibble(
  p = seq(-0.001, 0.999, 0.001),
  inv_cdf = qnorm(p)
)
```

```r
ggplot(normal_inv_cdf, aes(p, inv_cdf)) +
  geom_line()
```



[1] See "Introduction to Statistics in R", Ch3, "The Normal Distribution"

Standard error method for confidence interval

```
coffee_boot_distn %>%
  summarize(
    point_estimate = mean(resample_mean),
    std_error = sd(resample_mean),
    lower = qnorm(0.025, point_estimate, std_error),
    upper = qnorm(0.975, point_estimate, std_error)
  )
```

```
# A tibble: 1 x 4
  point_estimate std_error  lower  upper
           <dbl>     <dbl>  <dbl>  <dbl>
1         7.5263 0.0091815 7.5083 7.5443
```

Let's practice!

SAMPLING IN R

Congratulations

SAMPLING IN R

Richie Cotton

Data Evangelist at DataCamp

Recap

Chapter 1

- Sampling basics
- Selection bias
- Pseudo-random sampling

Chapter 2

- Simple random sampling
- Systematic sampling
- Stratified sampling
- Cluster sampling

Chapter 3

- Sample size and population parameters
- Creating sampling distributions
- Approximate vs. actual sampling dist'ns
- Central limit theorem

Chapter 4

- Bootstrapping from a single sample
- Standard error
- Confidence intervals

The most important things

- The standard deviation of the sampling distribution (a.k.a. the standard error) of a statistic is well-approximated by the standard deviation of the bootstrap distribution of a statistic.
- When calculating confidence intervals, it's OK to assume that bootstrap distributions are approximately normally distributed.

What's next?

- Analyzing Survey Data in R and Survey and Measurement Development in R
- Experimental Design in R and A/B Testing in R
- Foundations of Inference in R
- Foundation of Probability in R and Fundamentals of Bayesian Data Analysis in R

Let's practice!

SAMPLING IN R