

# Week 6 synchronous class and video code

Prof. Caetano

2021-02-22

```
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.0.3
```

```
## Warning: package 'tibble' was built under R version 4.0.3
```

```
## Warning: package 'readr' was built under R version 4.0.3
```

## Synchronous class

### [Case study 1]

(a) Select 1000 samples of size 20 from the population of claims stored in the `auto_claims_population.csv` data set (each sample is taken without replacement, so there are no repeated observations within each sample). Compute the mean age of claimants for each sample and produce appropriate summaries of the simulated sample means.

```
AutoClaimsPop <- read_csv("auto_claims_population.csv")
```

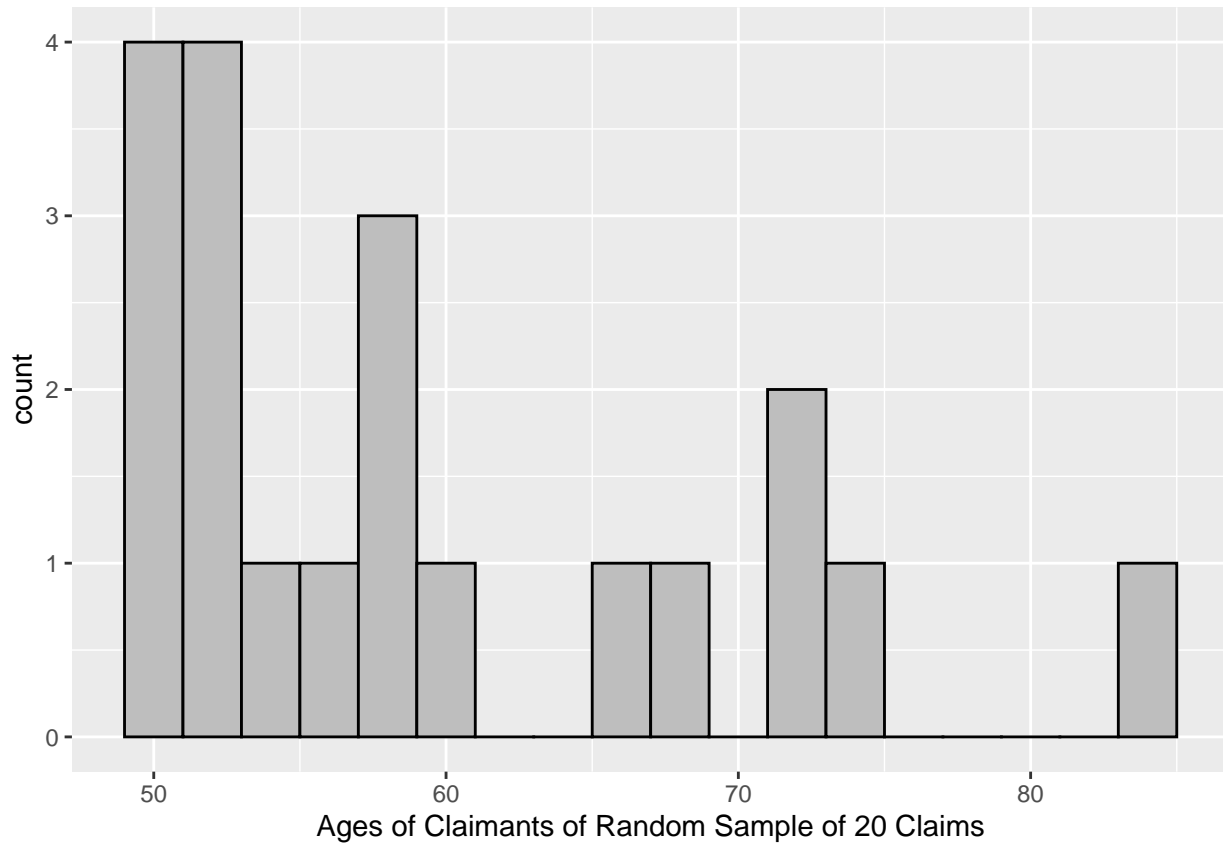
```
##  
## -- Column specification -----  
## cols(  
##   STATE = col_character(),  
##   CLASS = col_character(),  
##   GENDER = col_character(),  
##   AGE = col_double(),  
##   PAID = col_double()  
## )
```

(b) Now suppose we only had data for ONE random sample of 20 car insurance claims, and that these 20 observations are stored in `ages20`.

```
set.seed(321)  
ages20 <- tibble(age=sample(AutoClaimsPop$AGE,size = 20, replace=FALSE))  
glimpse(ages20)
```

```
## Rows: 20
## Columns: 1
## $ age <dbl> 75, 72, 68, 52, 50, 59, 52, 57, 53, 73, 84, 51, 51, 51, 61, 52,...
```

```
ages20 %>% ggplot(aes(x = age)) +
  geom_histogram(binwidth = 2, colour = "black", fill = "grey") +
  labs(x="Ages of Claimants of Random Sample of 20 Claims")
```



```
summarise(ages20,
  min=min(age),
  mean = mean(age),
  median = median(age),
  max=max(age),
  sd = sd(age),
  n=n())
```

```
## # A tibble: 1 x 6
##   min mean median max sd n
##   <dbl> <dbl> <dbl> <dbl> <dbl> <int>
## 1    50  60.0   57.5   84  9.88   20
```

Use R to take 1000 bootstrap samples from the ages of the claimants of the claims sampled and stored in `ages20`. Compute the mean age of claimants for each bootstrap sample of claims and produce appropriate summaries of the bootstrap sample means.

(c) What distribution do the distributions we simulated in (a) and (b) both estimate? Comment on the similarities and differences in the estimates we obtained.

## [Case study 2]

In this question we will look at data from the Child Health and Development Studies. Our data are adapted from the `Gestation` data set in the `mosaicData` package. Birth weight, date, and gestational period were collected as part of the Child Health and Development Studies in 1961 and 1962 for a sample of 400 mothers who had babies in these two years. Information about the baby's parents—age, education, height, weight, and whether the mother smoked—was also recorded.

We will find confidence intervals for parameters related to the distribution of the mother's age, which for this sample is stored in the variable `age`.

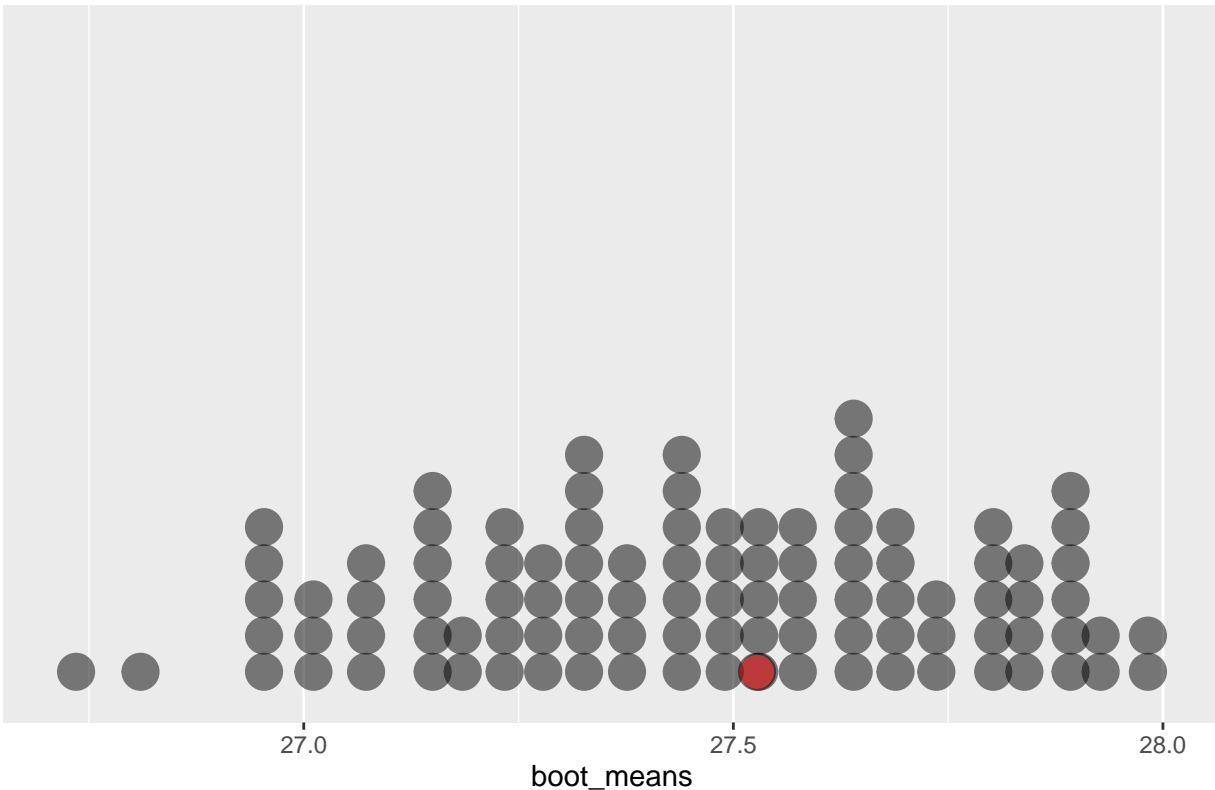
```
Gestation <- read_csv("gestation.csv")
```

```
##
## -- Column specification -----
## cols(
##   .default = col_double(),
##   drace = col_character()
## )
## i Use 'spec()' for the full column specifications.
```

(a) Suppose we are interested in how means of random samples of  $n=400$  mothers vary across possible samples of 400 mothers we could take from the population. Explain why it is not possible to use these data (i.e., 'Gestation') to estimate this like we did in Case Study 1, question a).

(b) The plot below shows the bootstrap distribution for the mean of mother's age for 100 bootstrap samples. The red dot is the estimate of the mean for the first bootstrap sample, and the grey dots are the estimates of the mean for the other 99 bootstrap samples.

Bootstrap distribution for mean of mother's age



```
## # A tibble: 1 x 6
##   min mean median max sd n
##   <dbl> <dbl> <dbl> <dbl> <dbl> <int>
## 1  26.7  27.5  27.5  28.0 0.299  100
```

- (i) Explain how the value of the red dot is calculated.
- (ii) Using this plot, estimate a 90% confidence interval for the mean of mother's age.

(c)

- (i) Use R to find a 99% bootstrap confidence interval for the mean of mother's age. Use 2000 bootstrap samples. *NOTE:* More bootstrap samples is better, but if you find your analysis times out or takes too long in RStudio Cloud, try using 1000 bootstrap samples instead.
- (ii) Explain why the interpretation “We are 99% sure that the true mean of a mother's age at the time this sample was taken is between 26.8 and 27.7 years.” is *INCORRECT*. What is a correct interpretation?

(d)

- (i) Use R to find a 95% bootstrap confidence interval for the *median* of mother's age. Use 2000 bootstrap samples. *NOTE:* More bootstrap samples is better, but if you find this times out or takes too long in RStudio Cloud, try using 1000 bootstrap samples instead.
- (ii) Write an interpretation of this interval.

## Video code

### Setting up the flights data

```
#install.packages("nycflights13")
library(tidyverse)
library(nycflights13)

## Warning: package 'nycflights13' was built under R version 4.0.3

# Save data in a data frame called SF
SF <- flights %>% filter(dest=="SFO" & !is.na(arr_delay))
dim(SF)

## [1] 13173    19
```

### Summarise the flights data

```
SF %>% summarise(
  mean_delay = mean(arr_delay),
  median_delay = median(arr_delay),
  max_delay = max(arr_delay))

## # A tibble: 1 x 3
##   mean_delay median_delay max_delay
##   <dbl>         <dbl>         <dbl>
## 1      2.67           -8          1007

# We'll save the population mean,
# so we can use it later on
population_mean <- SF %>%
  summarize(population_mean_delay =
    mean(arr_delay))

population_mean <-
  as.numeric(population_mean)
```

### Take a sample

```
# sample of 25 flights from our population
# by default, replace = FALSE (i.e. sampling without replacement)
sample25 <- SF %>% sample_n(size=25, replace = FALSE)
```

What is the difference between `sample()` and `sample_n()`?

```
sample(c("H", "T"), prob=c(0.5, 0.5),
       size=10, replace=TRUE)
sample(1:6, replace=FALSE)
```

The `sample()` function samples elements from a **vector**, with or without replacement

```
# Create our sample
SF %>% sample_n(size=25, replace=FALSE)
```

The `sample_n()` samples rows (observations) from a data frame, with or without replacement

## Calculate summary values for this sample

```
sample25 %>% summarise(mean_delay = mean(arr_delay),
                        median_delay = median(arr_delay),
                        max_delay = max(arr_delay))
```

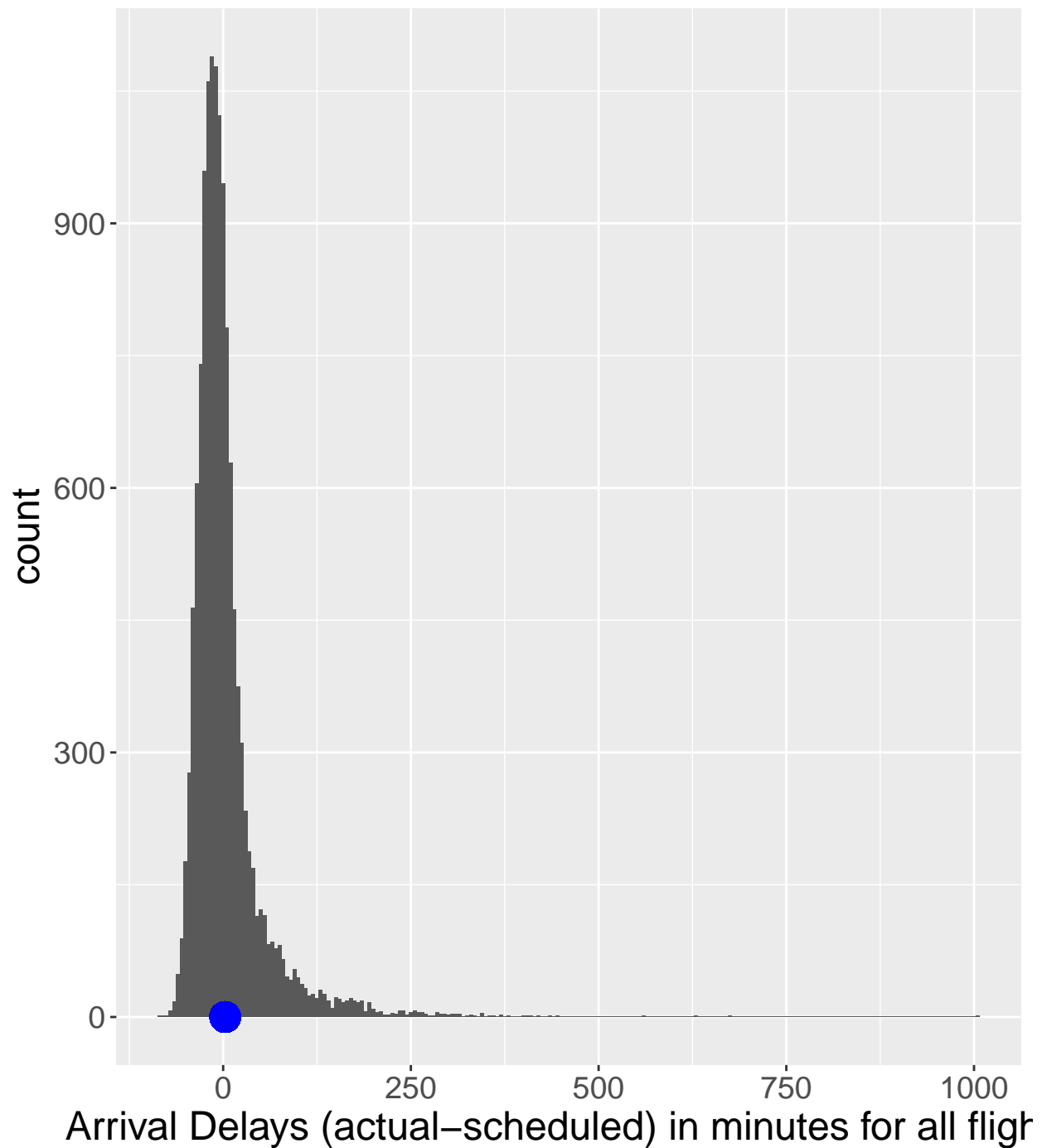
```
## # A tibble: 1 x 3
##   mean_delay median_delay max_delay
##       <dbl>         <dbl>     <dbl>
## 1         1.8          -10        208
```

## Looking at multiple samples of size n=25

```
## Warning: Use of 'SF$arr_delay' is discouraged. Use 'arr_delay' instead.
```



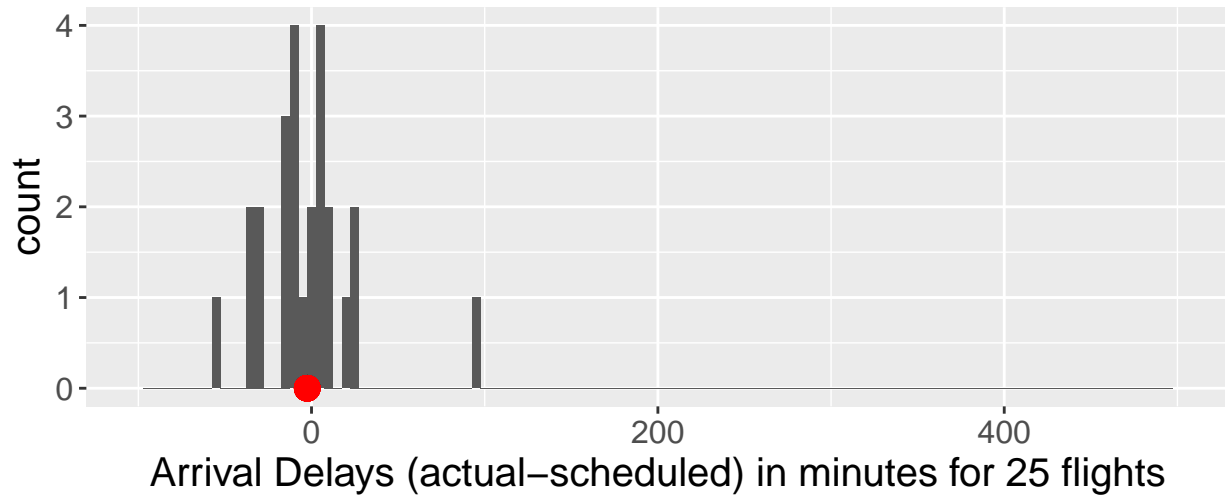
## Distribution of arrival delays for all flights, with population mean of 2.67



```
## Warning: Use of 'd25$arr_delay' is discouraged. Use 'arr_delay' instead.
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

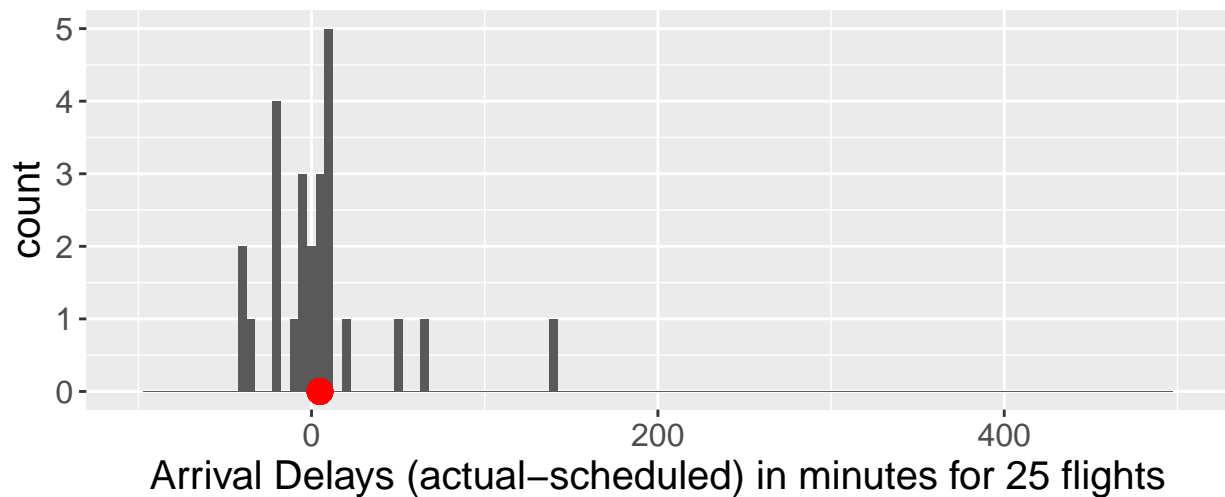
Sample of 25 flights, with sample mean of  $-2.48$



```
## Warning: Use of 'd25$arr_delay' is discouraged. Use 'arr_delay' instead.
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

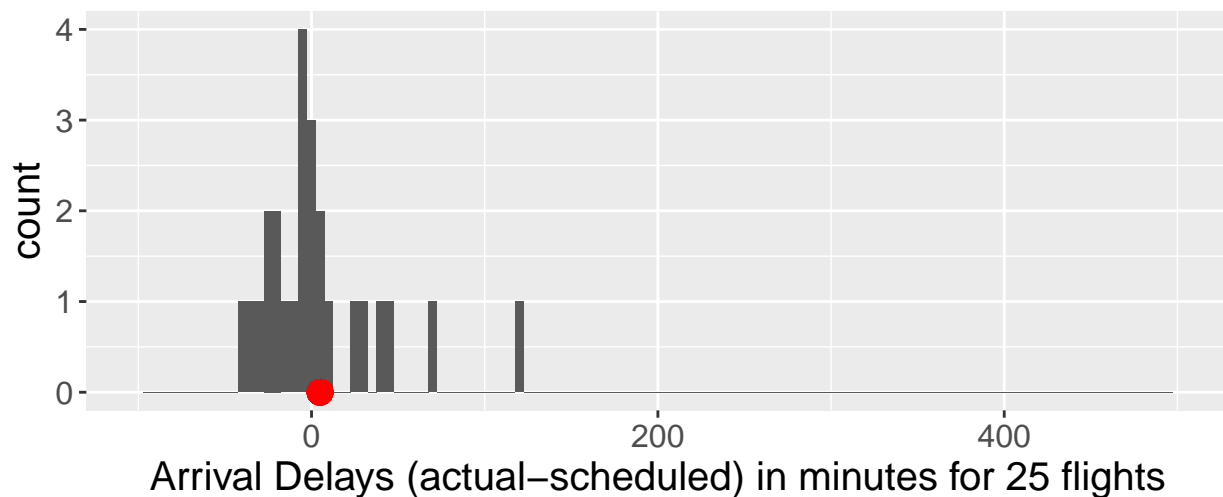
Sample of 25 flights, with sample mean of  $4.88$



```
## Warning: Use of 'd25$arr_delay' is discouraged. Use 'arr_delay' instead.
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

## Sample of 25 flights, with sample mean of 4.92



### Review: Sampling distributions

Recall, the **sampling distribution** of the mean of `arr_delay` is the distribution of all the values that `mean_delay` could be for random samples of size  $n = 25$

To estimate the sampling distribution, let's look at 1000 values of `mean_delay`, calculated from 1000 random samples of size  $n = 25$  from our population

```
sample_means <- rep(NA, 1000) # where we'll store the means

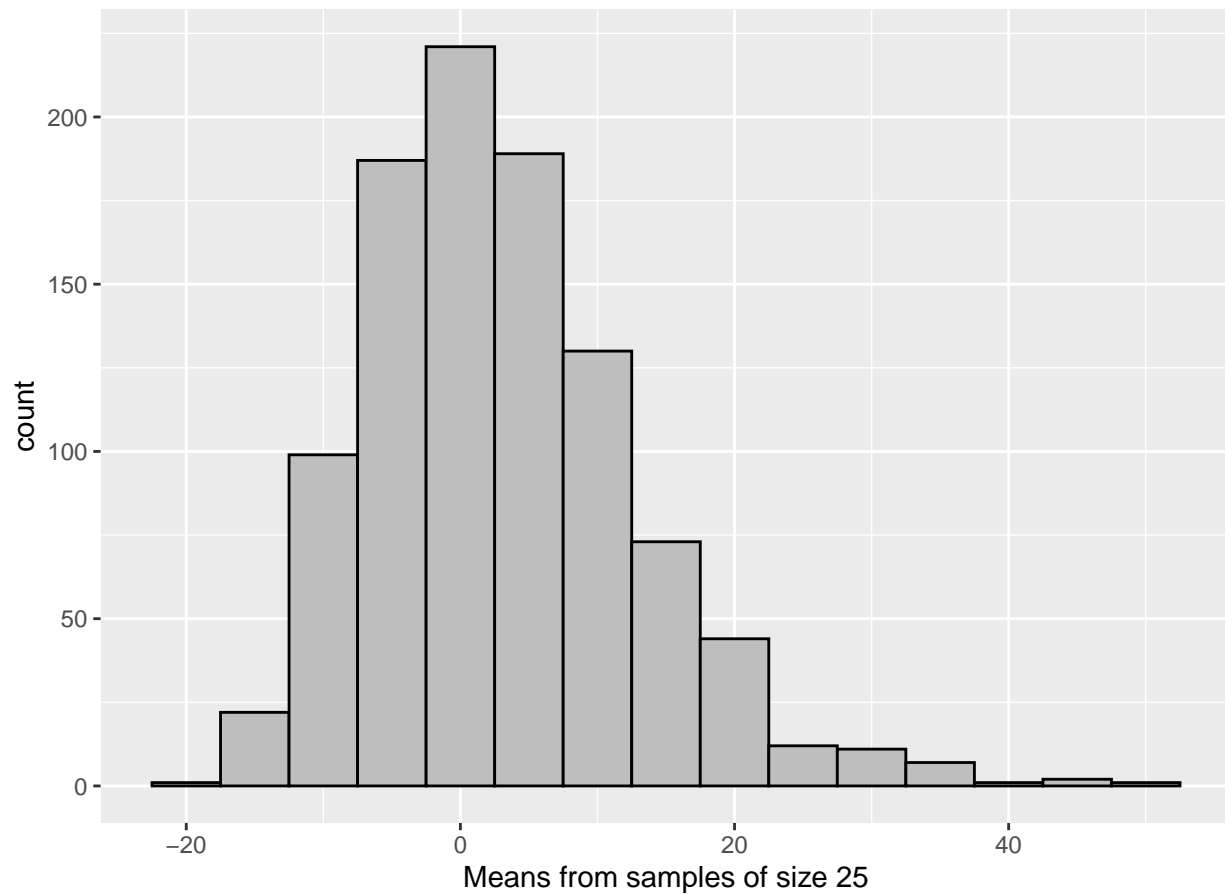
for(i in 1:1000){
  sample25 <- SF %>% sample_n(size=25)
  sample_means[i] <- as.numeric(sample25 %>%
    summarize(mean(arr_delay)))
}

sample_means <- tibble(mean_delay = sample_means)
```

### Sampling distribution of the mean

```
ggplot(sample_means, aes(x=mean_delay)) +
  geom_histogram(binwidth=5, color="black", fill="gray") +
  labs(x="Means from samples of size 25",
       title="Sampling distribution for the mean of arr_delay")
```

Sampling distribution for the mean of arr\_delay



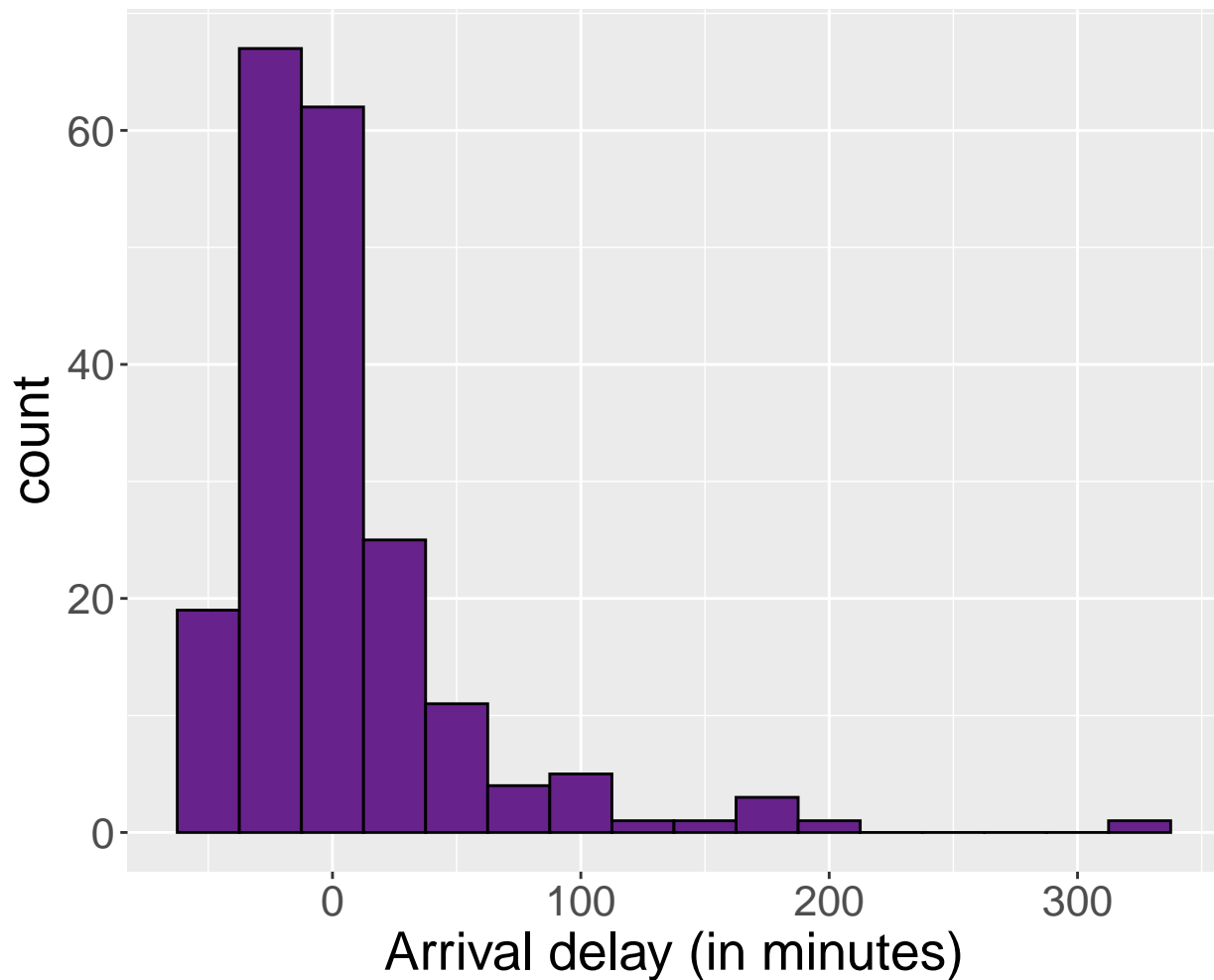
3 histograms for question prompt

## Bootstrapping with R

Suppose we do not observe the full population, and have only observed **one sample of size 200**

```
observed_data <- SF %>%  
  sample_n(size=200)
```

## Histogram of arrival delay for a sample (n=200) from the population



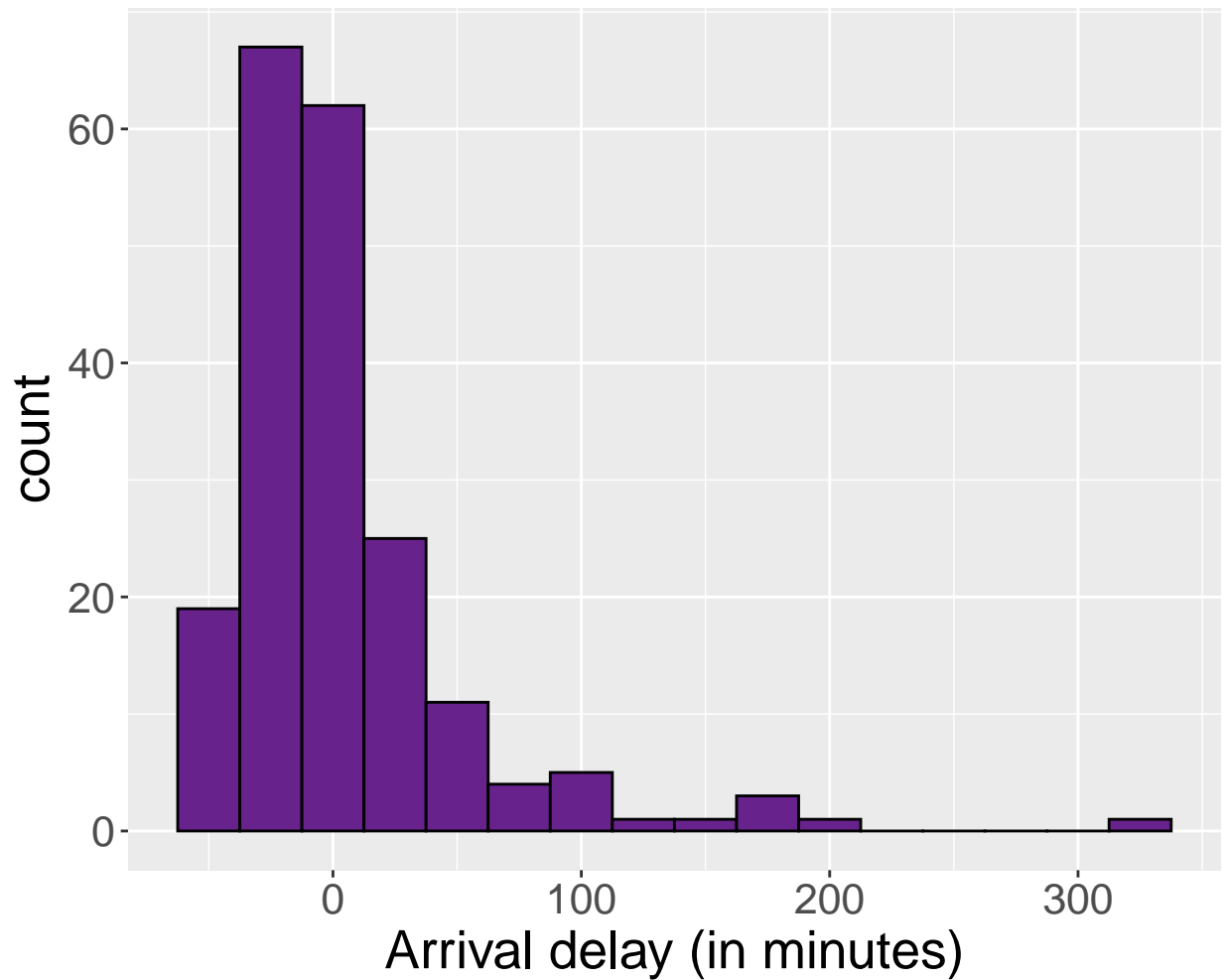
Let's calculate the mean arrival delay for this sample

```
obs_mean <- observed_data %>%  
  summarize(mean(arr_delay))  
as.numeric(obs_mean)
```

```
## [1] 4.485
```

A bootstrap sample from our observed data

## Histogram of arrival delay for a sample (n=200 from the population

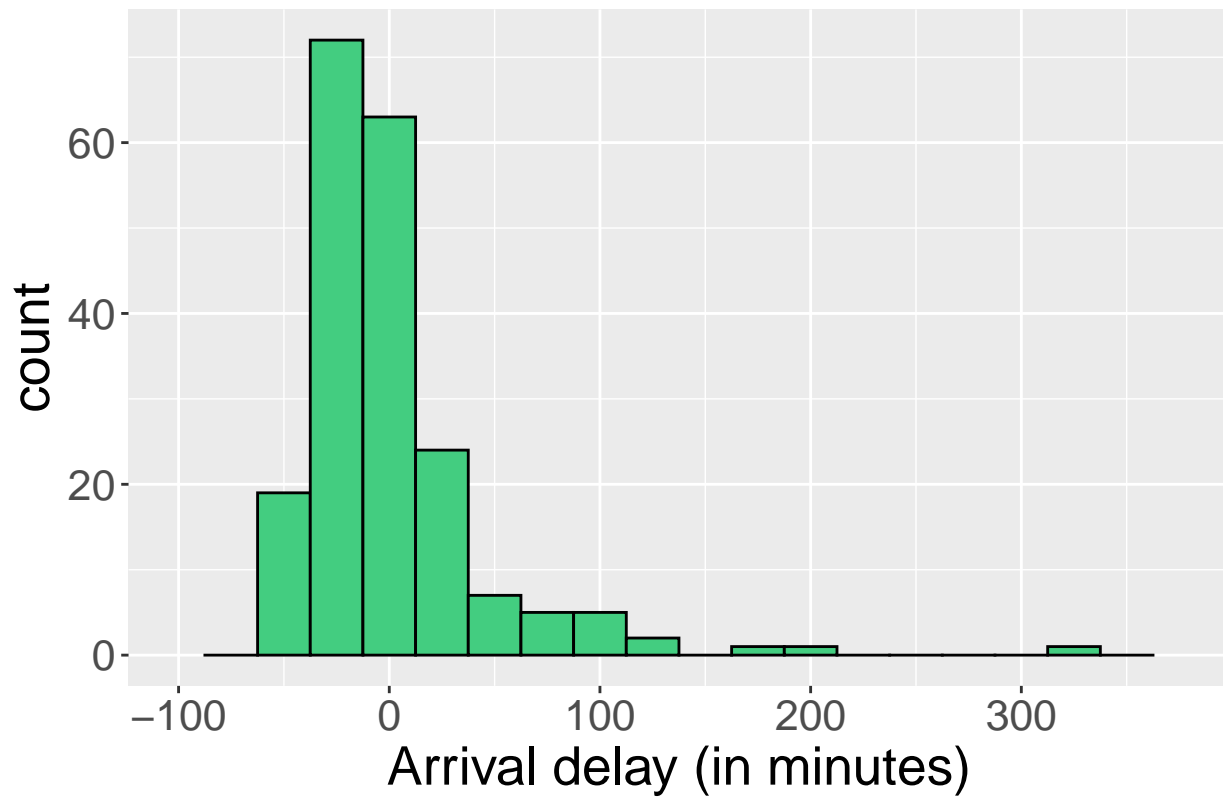


```
.pull-left[
```

```
boot_samp <- observed_data %>%  
  sample_n(size=200, replace=TRUE)
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

## Histogram of arrival delay for a bootstrap sample (n=200)

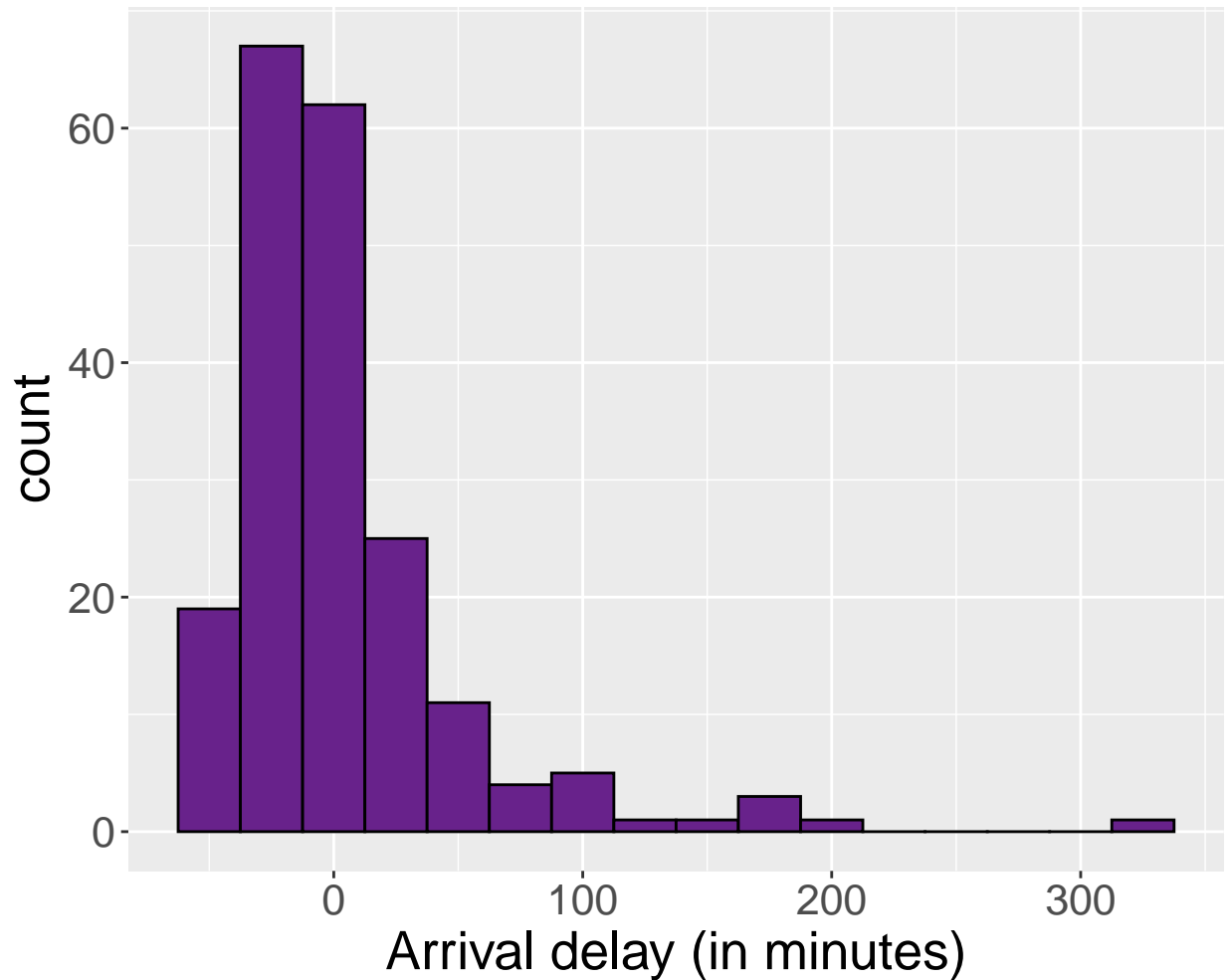


```
boot_mean <- boot_samp %>%  
  summarize(mean_delay =  
    mean(arr_delay))  
as.numeric(boot_mean)
```

```
## [1] 1.18
```

Another bootstrap sample from our observed data

## Histogram of arrival delay for a sample (n=200) from the population



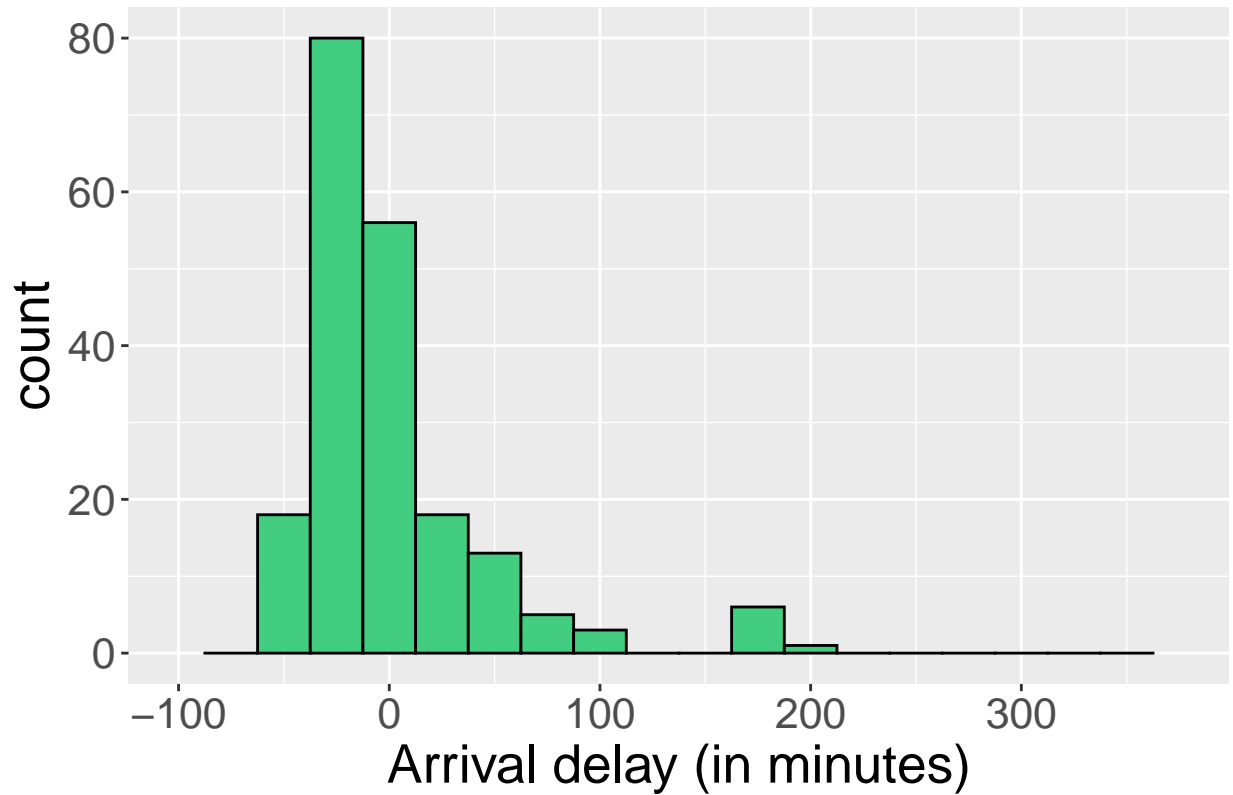
```
.pull-left[
```

```
boot_samp <- observed_data %>%  
  sample_n(size=200, replace=TRUE)
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```



## Histogram of arrival delay for a bootstrap sample (n=200)

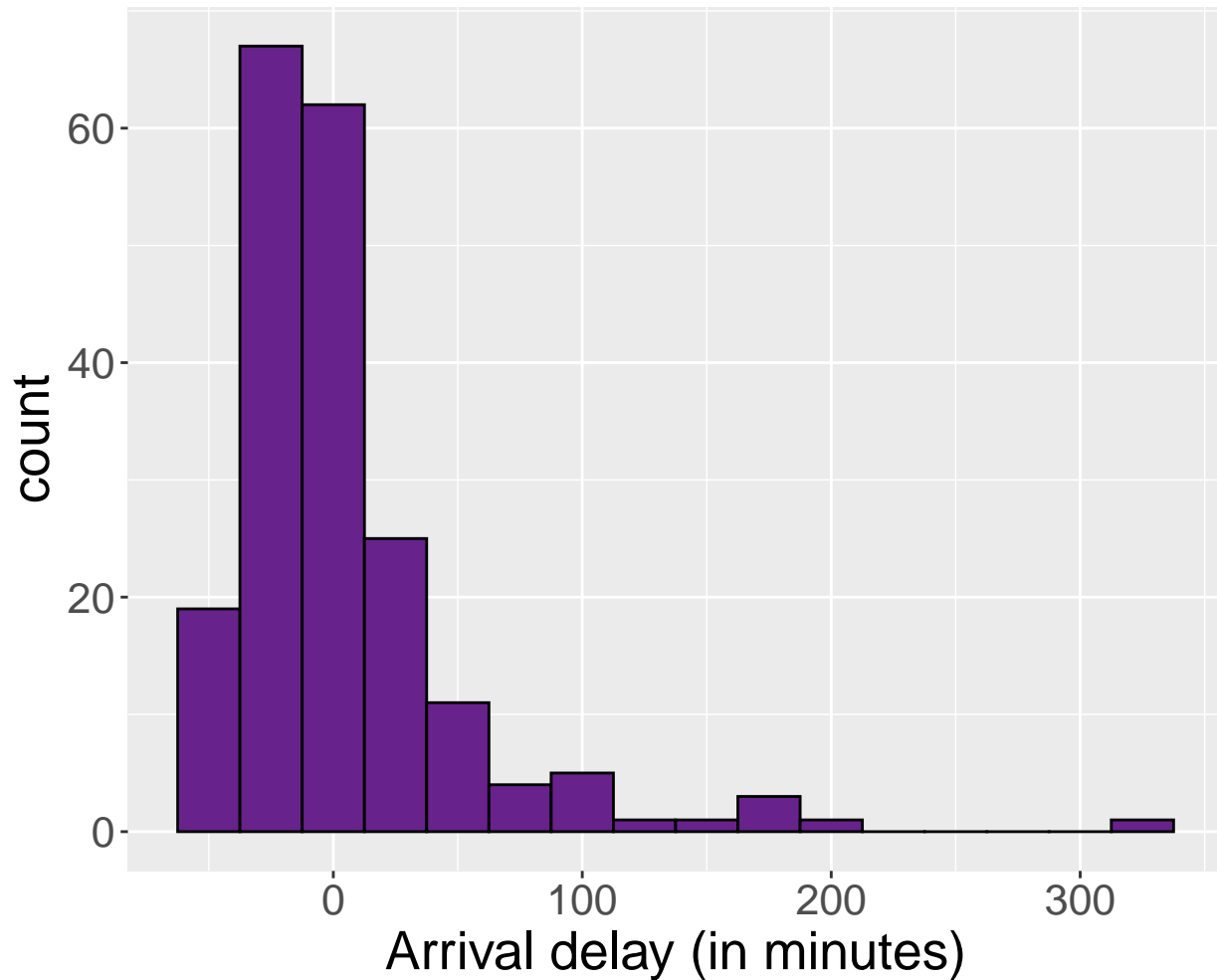


```
boot_mean <- boot_samp %>%  
  summarize(mean_delay =  
    mean(arr_delay))  
as.numeric(boot_mean)
```

```
## [1] 2.24
```

And another bootstrap sample...

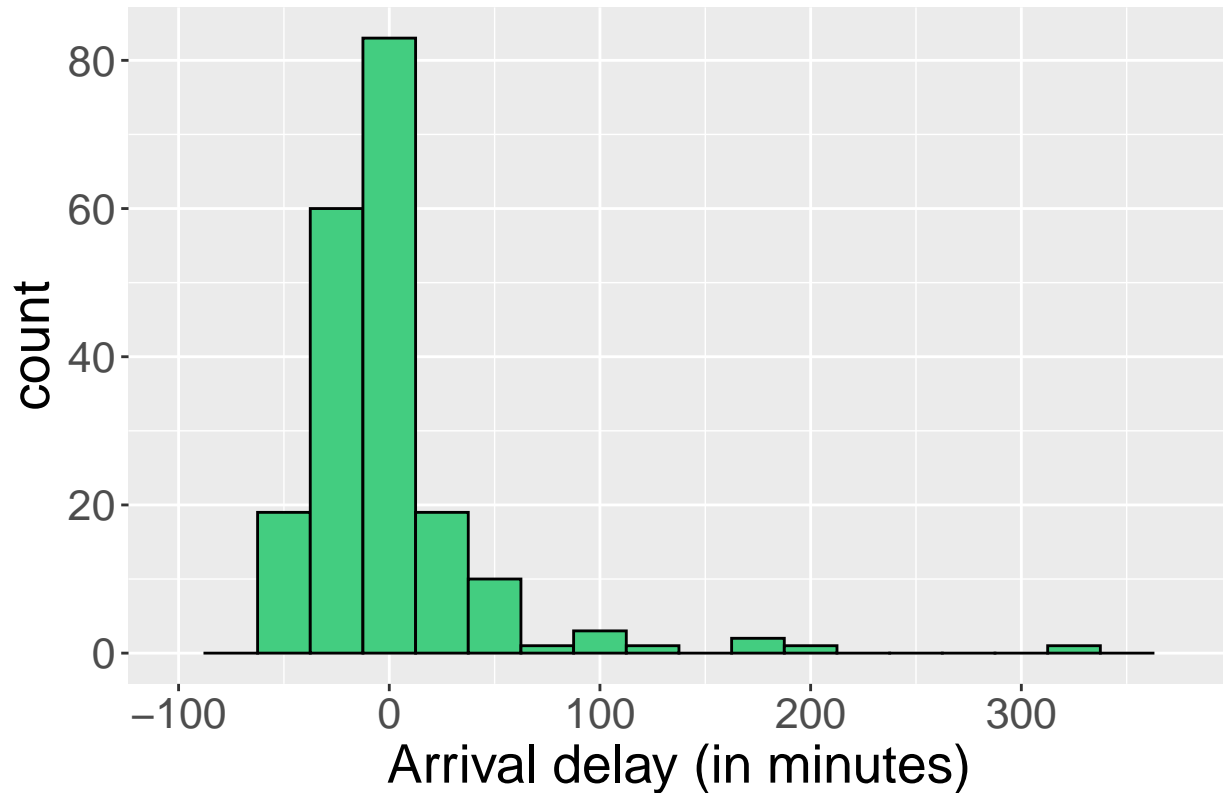
## Histogram of arrival delay for a sample (n=200) from the population



```
boot_samp <- observed_data %>%  
  sample_n(size=200, replace=TRUE)
```

```
## Warning: Removed 2 rows containing missing values (geom_bar).
```

## Histogram of arrival delay for a bootstrap sample (n=200)



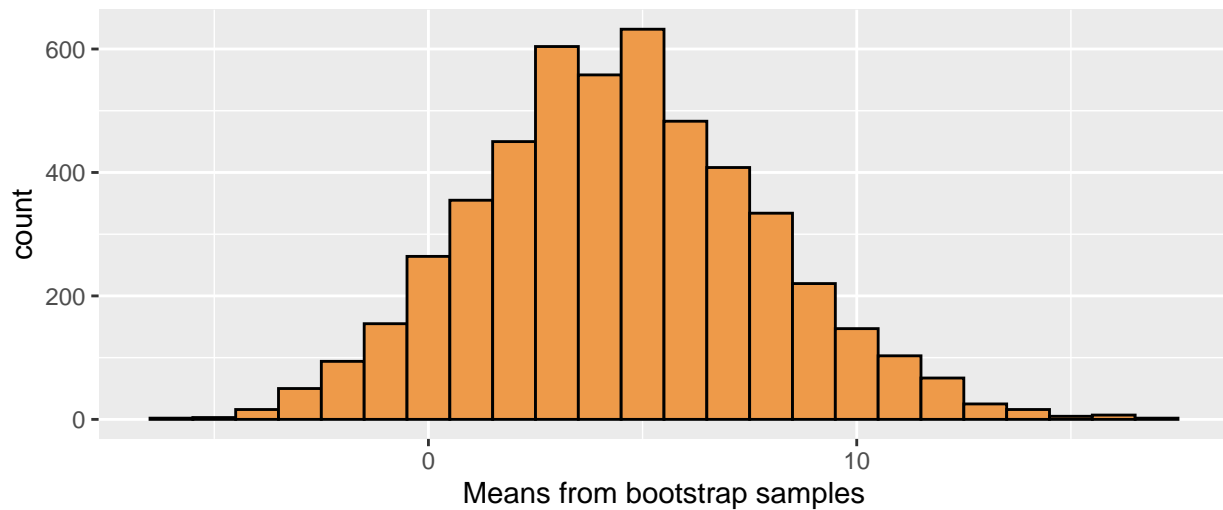
```
boot_mean <- boot_samp %>%  
  summarize(mean_delay =  
    mean(arr_delay))  
as.numeric(boot_mean)
```

```
## [1] -0.15
```

```
boot_means <- rep(NA, 5000) # where we'll store the means  
for(i in 1:5000){  
  boot_samp <- observed_data %>% sample_n(size=200, replace=TRUE)  
  boot_means[i] <-  
    as.numeric(boot_samp %>%  
      summarize(mean_delay = mean(arr_delay)))  
}  
boot_means <- tibble(mean_delay = boot_means)
```

```
ggplot(boot_means, aes(x=mean_delay)) +  
  geom_histogram(binwidth=1, fill="tan2", color="black") +  
  labs(x="Means from bootstrap samples",  
       title="Bootstrap sampling distribution for the mean arrival delay")
```

### Bootstrap sampling distribution for the mean arrival delay



### Percentiles (quantiles): an extension of quartiles

For a number  $p$  between 0 and 100, the  $p$ th percentile is the smallest value that is larger or equal to  $p\%$  of all the values

- Median ( $Q_2$ ): 50th percentile
- First quartile ( $Q_1$ ): 25th percentile
- Third quartile ( $Q_3$ ): 75th percentile

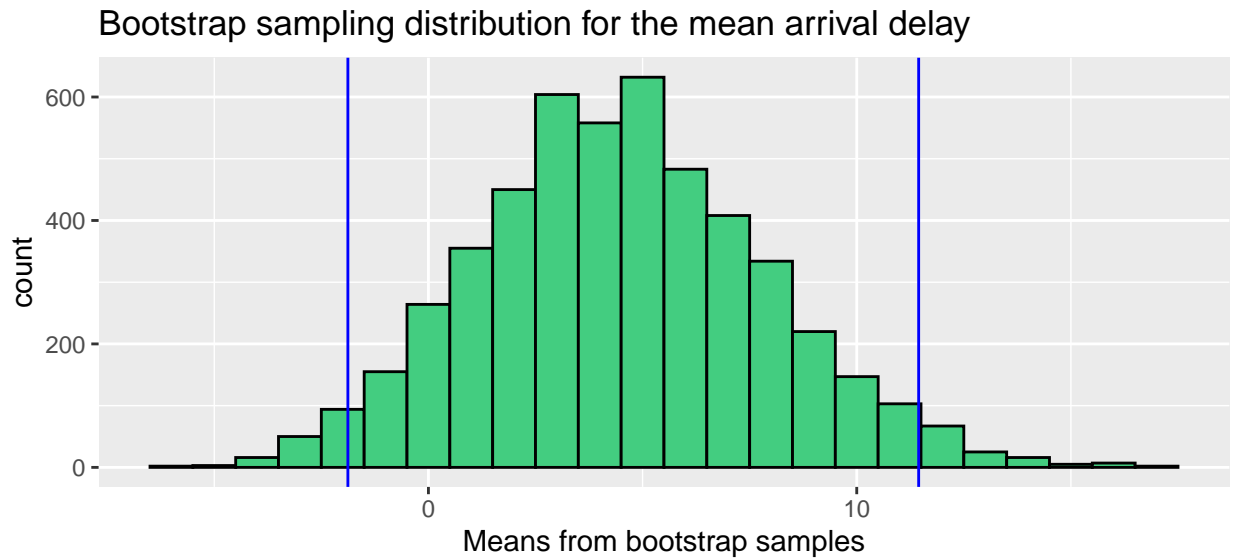
Use the `quantile()` function in R to calculate these:

```
# Calculate Q1, median, and Q3
quantile(boot_means$mean_delay, c(0.25, 0.5, 0.75))
```

```
##    25%    50%    75%
## 2.205 4.395 6.695
```

```
# Can also calculate any other percentiles
quantile(boot_means$mean_delay, c(0.025, 0.4, 0.57))
```

```
##      2.5%      40%      57%
## -1.880125  3.520000  4.970000
```



2.5th and 97.5th percentiles:

```
quantile(boot_means$mean_delay,  
         c(0.025, 0.975))
```

```
##      2.5%      97.5%  
## -1.880125 11.445625
```

Recall true population mean:

```
as.numeric(population_mean)
```

```
## [1] 2.672892
```

**How often does this procedure give an interval that captures the population mean?**

This code is for the curious but NOT something we'll ask you to be able to make yourself. It also takes aaaaaages to run, so that is why we have saved the output as a csv for you.

100 bootstrap confidence intervals for the mean,  
based on random samples from the population (n=200)

