IS5 in R: Confidence Intervals for Means (Chapter 14)

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Introduction and background

This document is intended to help describe how to undertake analyses introduced as examples in the Fifth Edition of *Intro Stats* (2018) by De Veaux, Velleman, and Bock. More information about the book can be found at http://wps.aw.com/aw_deveaux_stats_series. This file as well as the associated R Markdown reproducible analysis source file used to create it can be found at http://nhorton.people.amherst.edu/is5.

This work leverages initiatives undertaken by Project MOSAIC (http://www.mosaic-web.org), an NSF-funded effort to improve the teaching of statistics, calculus, science and computing in the undergraduate curriculum. In particular, we utilize the `mosaic` package, which was written to simplify the use of R for introductory statistics courses. A short summary of the R needed to teach introductory statistics can be found in the mosaic package vignettes (http://cran.r-project.org/web/packages/mosaic). A paper describing the mosaic approach was published in the *R Journal*: https://journal.r-project.org/archive/2017/RJ-2017-024.

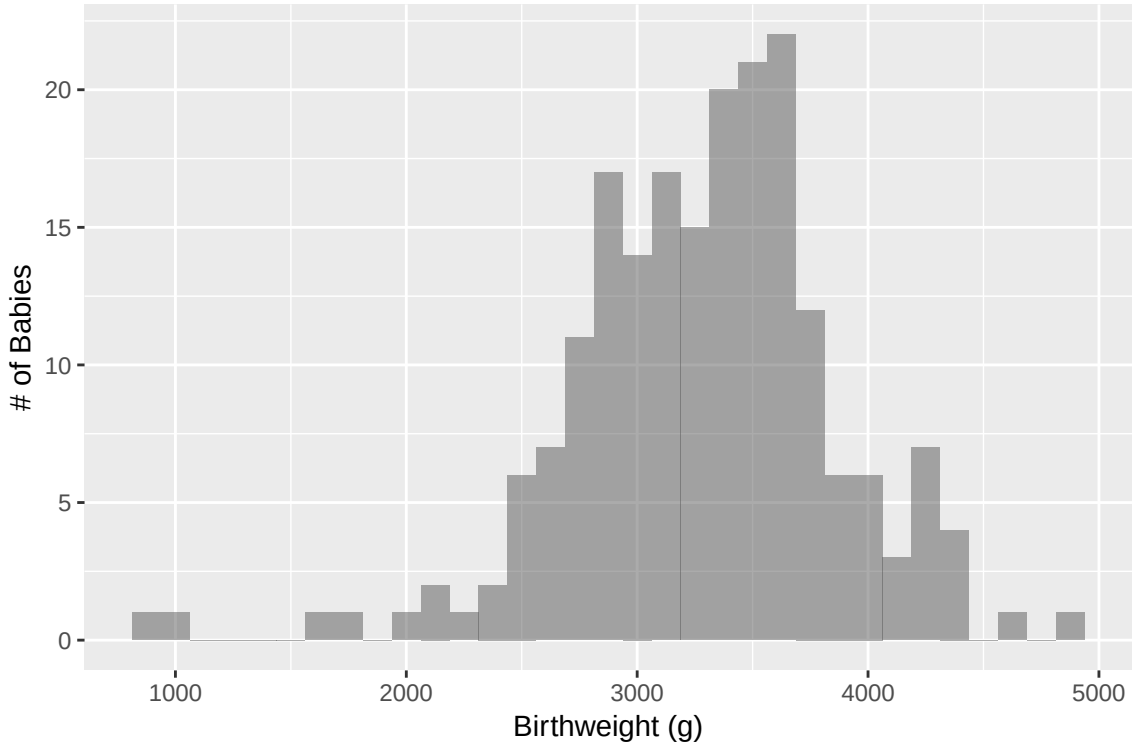
Chapter 14: Confidence Intervals for Means

```
library(mosaic)
library(readr)
library(janitor)
Babies <- read_csv("http://nhorton.people.amherst.edu/is5/data/Babysamp_98.csv") %>%
  clean_names()
```

```
## Parsed with column specification:
## cols(
##   MomAge = col_integer(),
##   DadAge = col_integer(),
##   MomEduc = col_integer(),
##   MomMarital = col_integer(),
##   numlive = col_integer(),
##   dobmm = col_integer(),
##   gestation = col_integer(),
##   sex = col_character(),
##   weight = col_integer(),
##   prenatalstart = col_integer(),
##   orig.id = col_integer(),
##   preemie = col_logical()
## )
```

By default, `read_csv()` prints the variable names. These messages can be suppressed using the `message = FALSE` code chunk option to save space and improve readability.
Here we use the `clean_names()` function from the `janitor` package to sanitize the names of the columns (which would otherwise contain special characters or whitespace).

```
# Figure 14.1, page 441
gf_histogram(~ weight, data = Babies, binwidth = 125) %>%
  gf_labs(x = "Birthweight (g)", y = "# of Babies")
```




```
# Figure 14.2
set.seed(12346) # For reproducibility
numsim <- 10000 # Number of simulations

# What does do() do?
mean(~ weight, data = sample(Babies, 100)) # Mean of a random sample of 100
```

```
## [1] 3214.53
```

```
mean(~ weight, data = sample(Babies, 100)) # Mean of another random sample
```

```
## [1] 3290.34
```

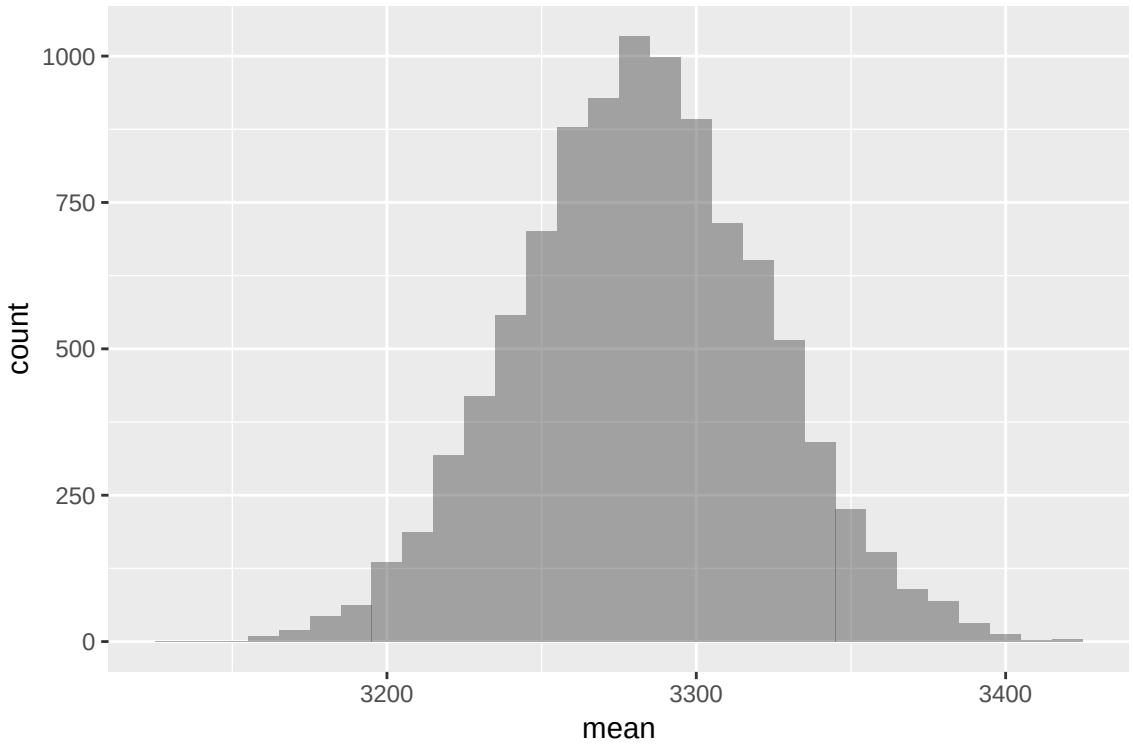
```
do(2) * mean(~ weight, data = sample(Babies, 100)) # Finds the mean twice
```

```
##      mean
## 1 3297.84
## 2 3286.70
```

```
# For the visualization, we need 10,000 means
WeightMeans <- do(numsim) * mean(~ weight, data = sample(Babies, 100))
```

Here, the `do()` function finds, 10,000 times, the mean of a random sample of 100 Babies weights.

```
gf_histogram(~ mean, data = WeightMeans, binwidth = 10)
```




```
favstats(~ mean, data = WeightMeans)
```

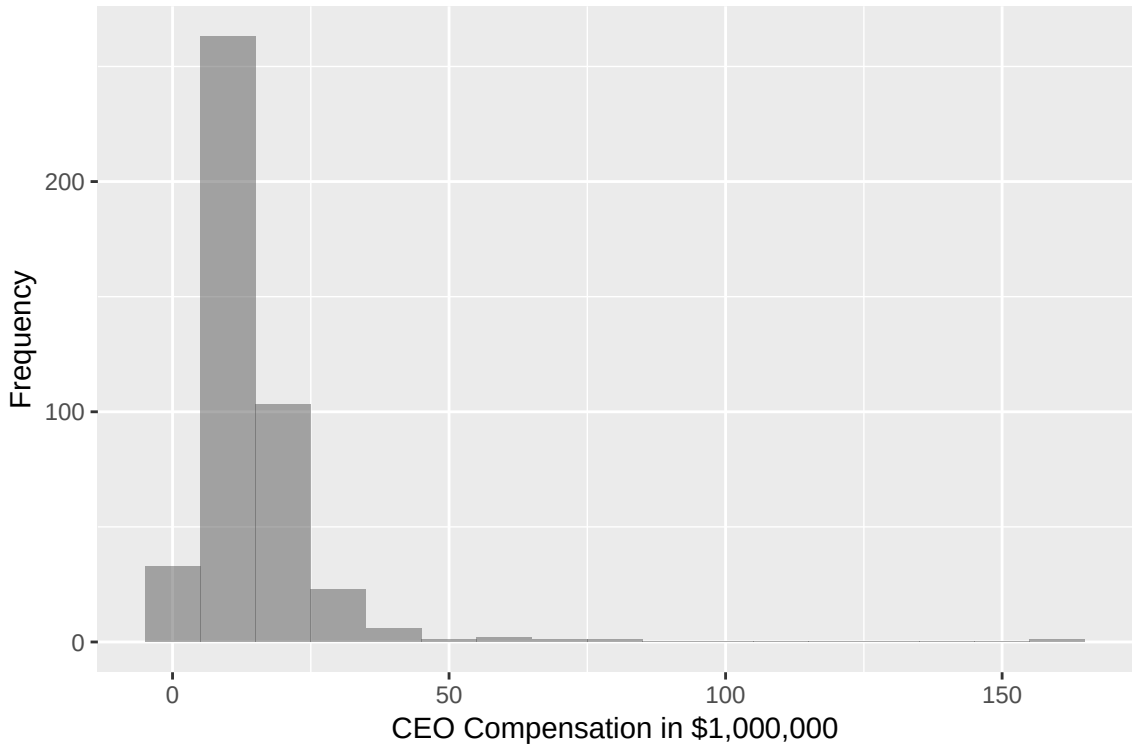
```
##      min      Q1  median       Q3     max     mean       sd     n missing
##  3132.17 3255.54 3282.14 3309.163 3422.09 3282.299 40.01813 10000       0
```

Section 14.1: The Central Limit Theorem

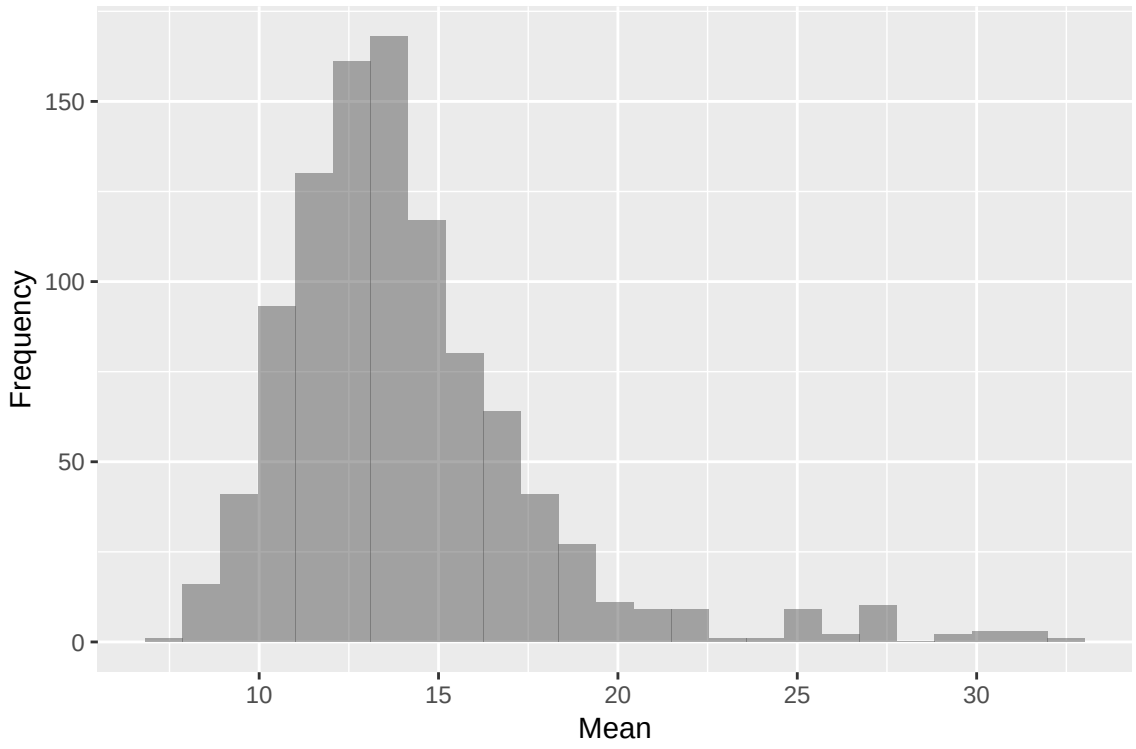
```
CEOComp <- read_csv("http://nhorton.people.amherst.edu/is5/data/CEO_Compensation_2014.csv") %>%
  clean_names()
```

```
## Parsed with column specification:
## cols(
##   Employer = col_character(),
##   CEO = col_character(),
##   CEO_Compensation = col_integer(),
##   Median_Worker_Comp = col_integer(),
##   Ratio = col_integer(),
##   Company_Rating = col_double(),
##   `CEO_Compensation_($M)` = col_double()
## )
```

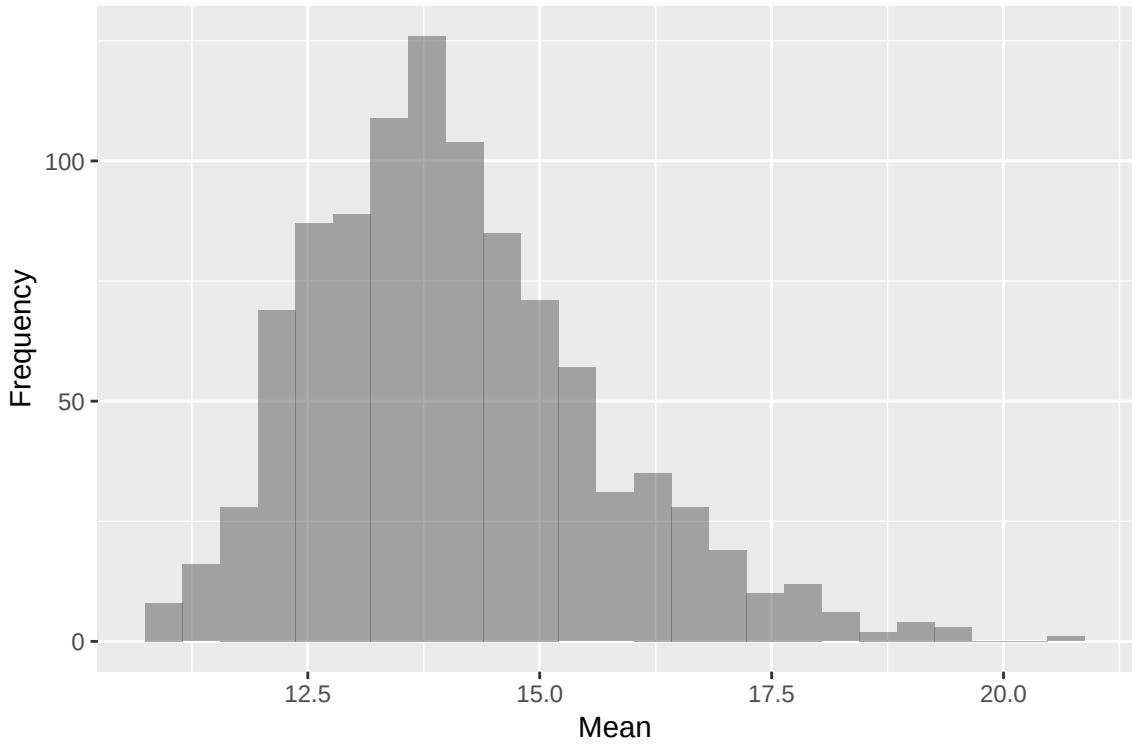
```
# Figure 14.3
gf_histogram(~ ceo_compensation_m, data = CEOComp, binwidth = 10) %>%
  gf_labs(x = "CEO Compensation in $1,000,000", y = "Frequency")
```



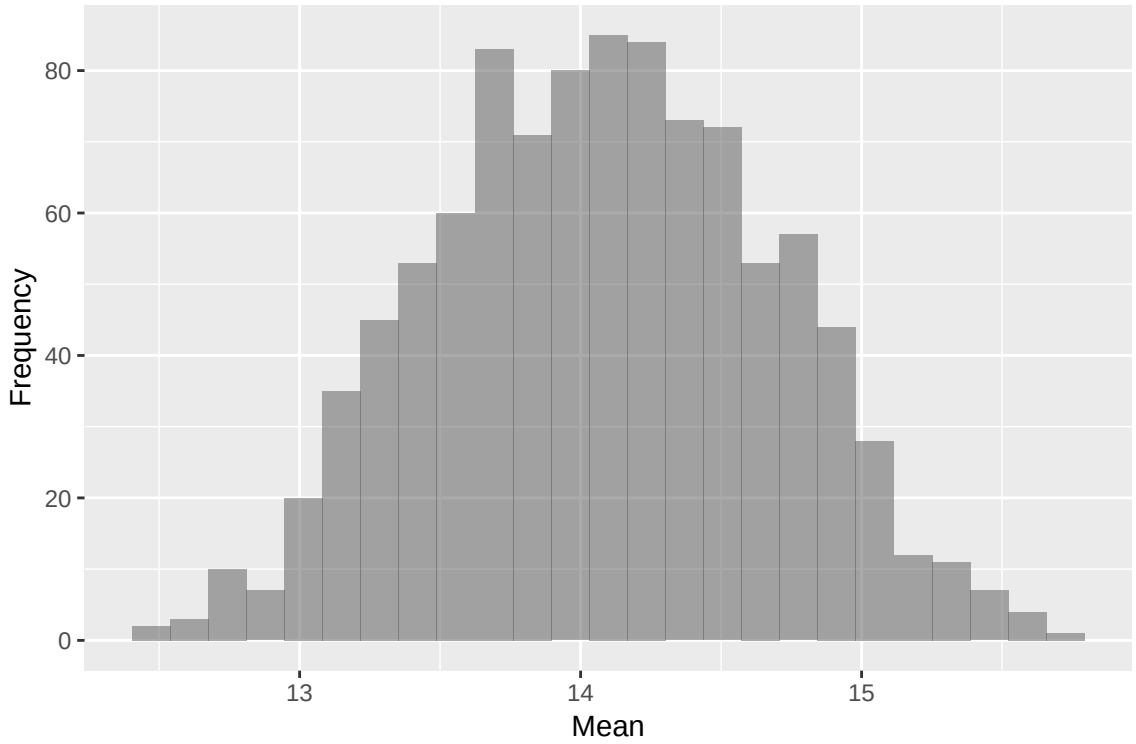

```
# Figure 14.4
set.seed(14354)
numsim <- 1000 # Here the number of simulations is 1,000
CEOMeans <- do(numsim) * mean(~ ceo_compensation_m, data = sample(CEOComp, 10))
gf_histogram(~ mean, data = CEOMeans) %>%
  gf_labs(x = "Mean", y = "Frequency")
```




```
# Figure 14.5
CEOMeans2 <- do(numsim) * mean(~ ceo_compensation_m, data = sample(CEOComp, 50))
gf_histogram(~ mean, data = CEOMeans2) %>%
  gf_labs(x = "Mean", y = "Frequency")
```



```r
# Figure 14.7 (skipped 14.6 because it's similar)
CEOMeans3 <- do(numsim) * mean(~ ceo_compensation_m, data = sample(CEOComp, 200))
gf_histogram(~ mean, data = CEOMeans3) %>%
  gf_labs(x = "Mean", y = "Frequency")
```

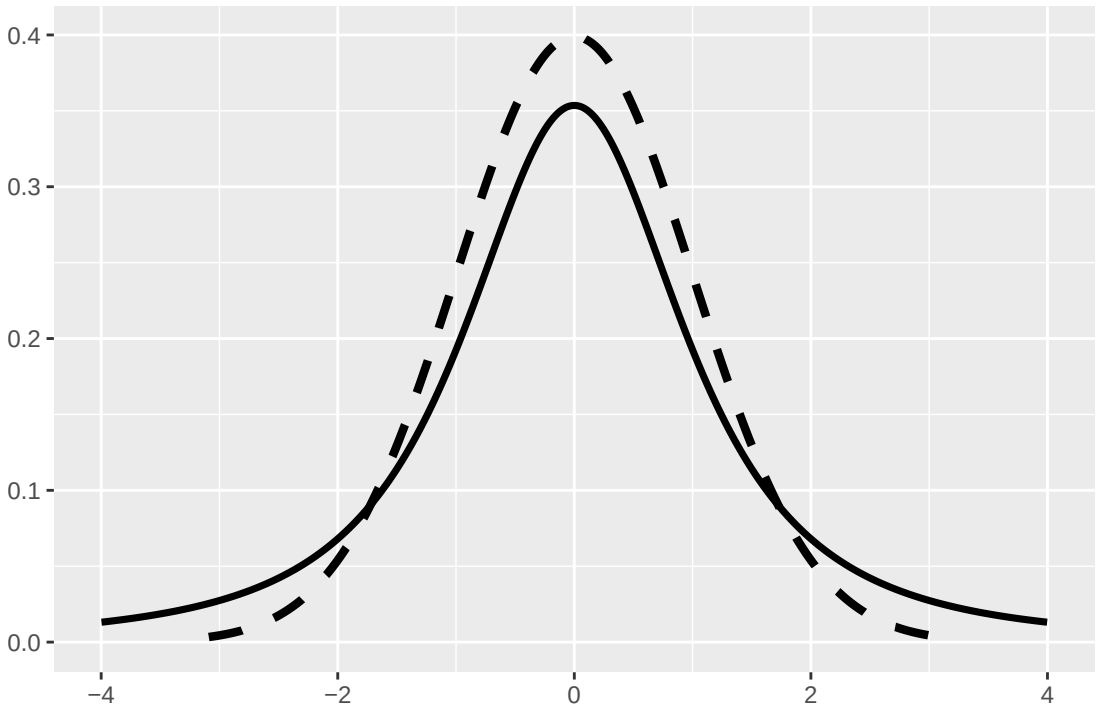


Here, in each example, the `do()` function finds the mean of random samples of 10, 50, and 200 CEO compensations.

Section 14.2: A Confidence Interval for the Mean

```r
# Figure 14.9, page 446
gf_dist(dist = "norm", linetype = 2, lwd = 1.5) %>%
  gf_labs(x = "", y = "") %>%
  gf_dist(dist = "t", df = 2, lwd = 1.25) +
  xlim(-4, 4)
```

```
## Warning: Removed 4104 rows containing missing values (geom_path).
```



Example 14.1: A One-Sample *t*-Interval for the Mean

```
Salmon <- read_csv("http://nhorton.people.amherst.edu/is5/data/Farmed_salmon.csv") %>%
  clean_names()
```

```
## Parsed with column specification:
## cols(
##   Kind = col_character(),
##   Location = col_character(),
##   Mirex = col_double(),
##   Hexachlorobenzene = col_double(),
##   HCH_gamma = col_double(),
##   `Heptachlor Epoxide` = col_double(),
##   Dieldrin = col_double(),
##   Endrin = col_double(),
##   `Total Chlordane` = col_double(),
##   `Total DDT` = col_double(),
##   Dioxin = col_double(),
##   `Total Pesticides` = col_double(),
##   `Total PCBs` = col_integer()
## )
```

```
Salmon <- Salmon %>%
  filter(mirex != "NA")
favstats(~ mirex, data = Salmon)
```

```
##  min    Q1 median      Q3   max    mean         sd   n missing
##    0 0.056  0.079 0.13475 0.194 0.09134 0.04952388 150       0
```

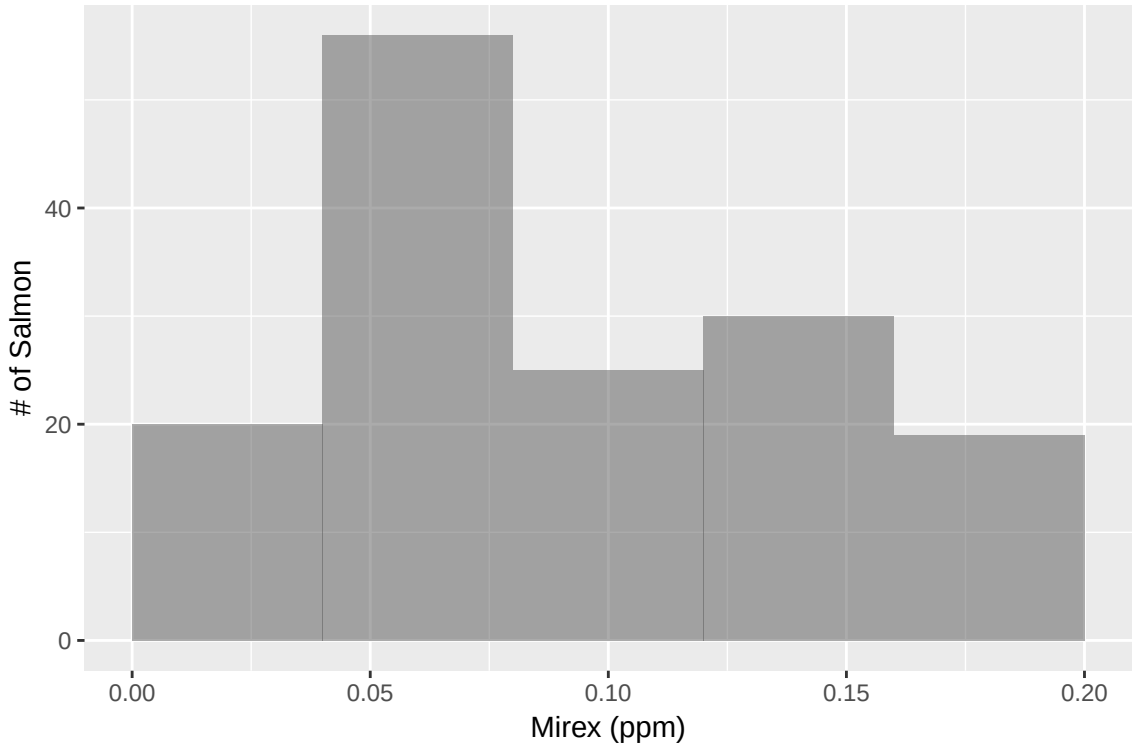
```
salmonlm <- lm(mirex ~ 1, data = Salmon)
confint(salmonlm, data = Salmon)
```

```
##                  2.5 %     97.5 %
## (Intercept) 0.08334978 0.09933022
```

The `confint()` function takes an object, such as a linear model, as an argument.

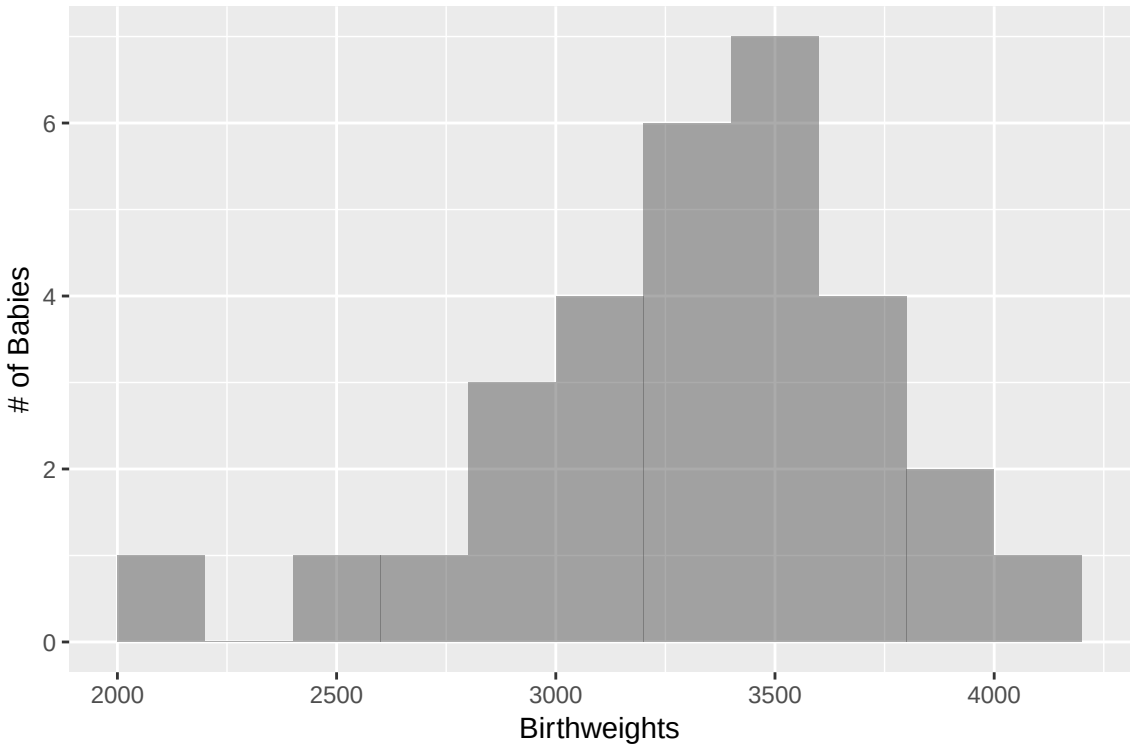
Example 14.2: Checking Assumptions and Conditions for Student's t

```
gf_histogram(~ mirex, data = Salmon, binwidth = 0.04, center = 0.02) %>%
  gf_labs(x = "Mirex (ppm)", y = "# of Salmon")
```



Step-By-Step Example: A One-Sample t-Interval for the Mean

```
set.seed(34)
BabiesSample <- sample(Babies, 30)
gf_histogram(~ weight, data = BabiesSample, binwidth = 200, center = 100) %>%
  gf_labs(x = "Birthweights", y = "# of Babies")
```




```
favstats(~ weight, data = BabiesSample)
```

```
##   min      Q1 median   Q3  max   mean       sd  n missing
##  2182 3056.25 3382.5 3572 4054 3316.6 423.2446 30       0
```

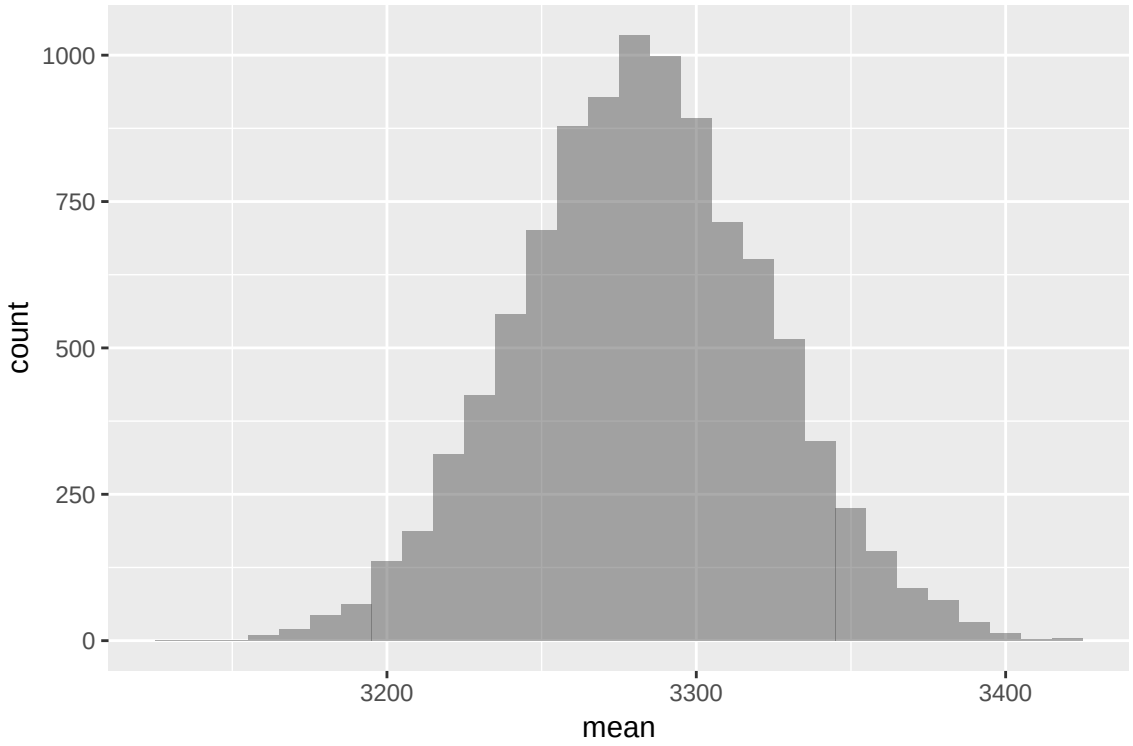
```
babieslm <- lm(weight ~ 1, data = BabiesSample)
confint(babieslm, level = 0.90)
```

```
##                   5 %     95 %
## (Intercept) 3185.302 3447.898
```

Section 14.3: Interpreting Confidence Intervals

Section 14.4: Picking Our Interval up by Our Bootstraps

```
gf_histogram(~ mean, data = WeightMeans, binwidth = 10)
```

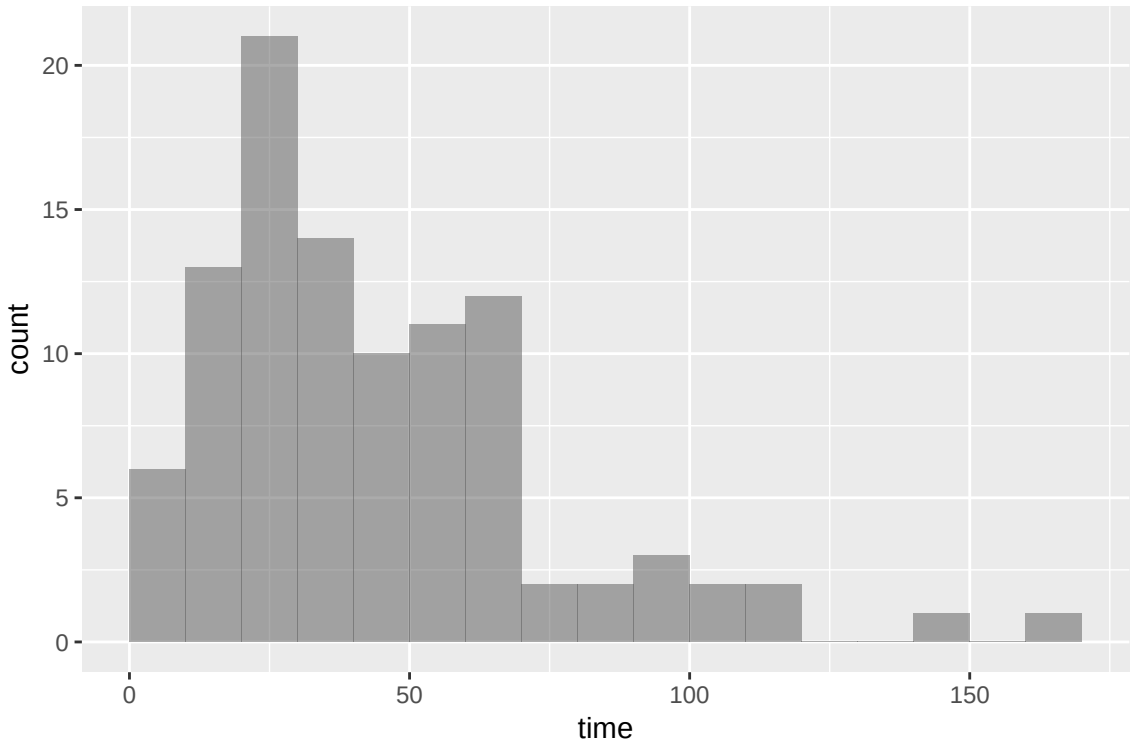


Step-By-Step Example: A Bootstrap Confidence Interval for the Mean

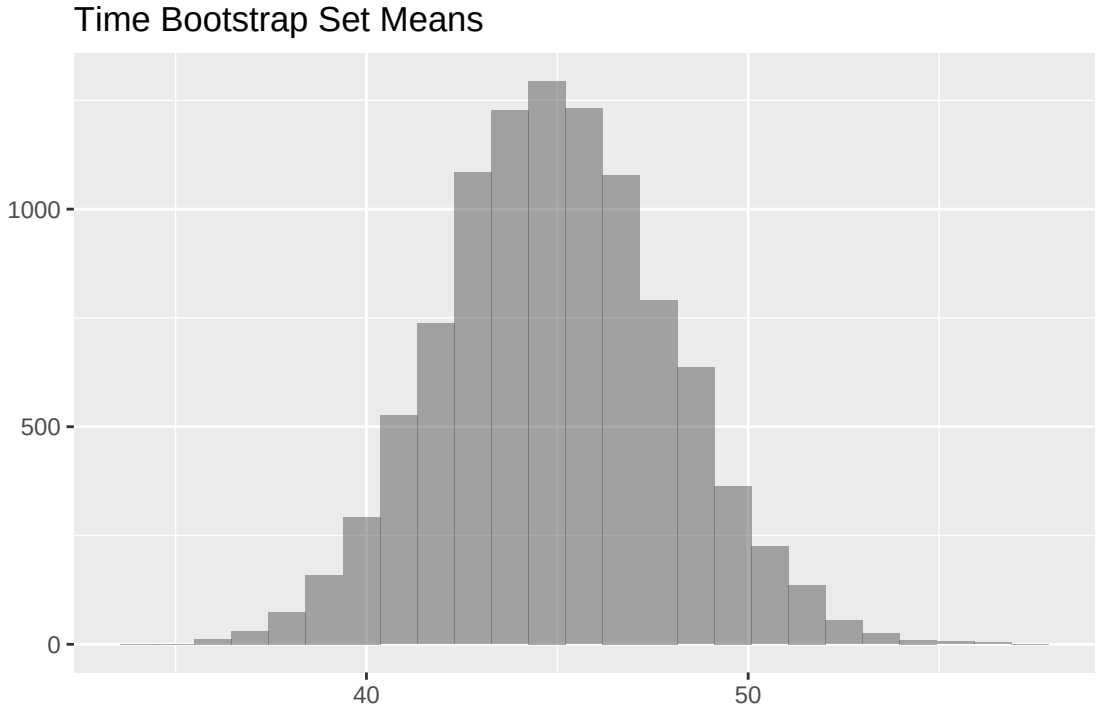
```
CommuteSample <- read_csv("http://nhorton.people.amherst.edu/is5/data/Commuter_sample.csv")
```

```
## Parsed with column specification:
## cols(
##   time = col_integer()
## )
```

```
gf_histogram(~ time, data = CommuteSample, binwidth = 10, center = 5)
```




```
# Bootstrap
set.seed(134)
numsim <- 10000
commutebootstrap <- do(numsim) * mean(~ time, data = resample(CommuteSample))
gf_histogram(~ mean, data = commutebootstrap, title = "Time Bootstrap Set Means") %>%
  gf_labs(x = "", y = "")
```



```r
cbootlm <- lm(mean ~ 1, data = commutebootstrap) # grab the percentiles with qdata
confint(cbootlm)
```

```
##                 2.5 %   97.5 %
## (Intercept) 44.90009 45.01683
```

Section 14.5: Thoughts About Confidence Intervals