

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

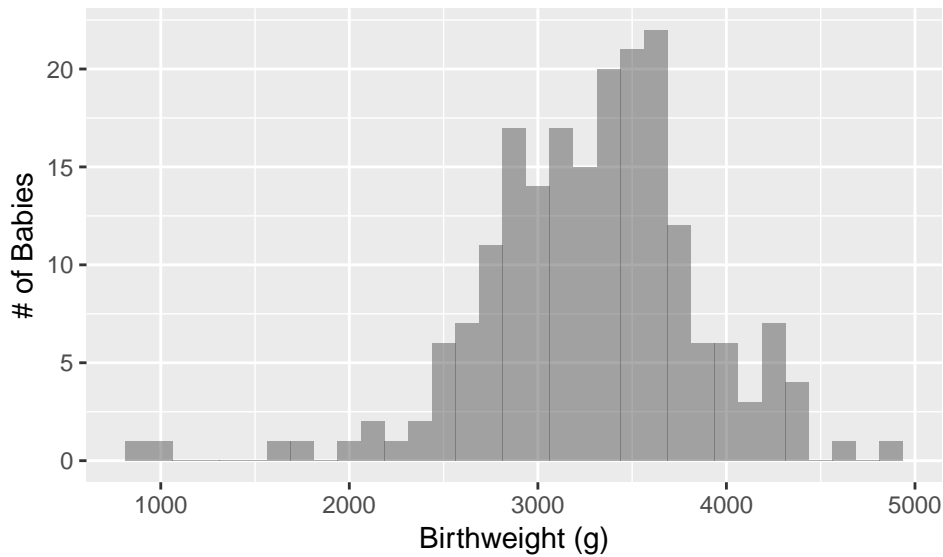
```
library(mosaic)
library(readr)
library(janitor)
Babies <- read_csv("http://nhorton.people.amherst.edu/is5/data/Babysamp_98.csv") %>%
  clean_names()
```

```
## 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) # To ensure we get the same values when we run it multiple times
numsim <- 10000 # Number of simulations

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

## [1] 3214.53

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

## [1] 3290.34

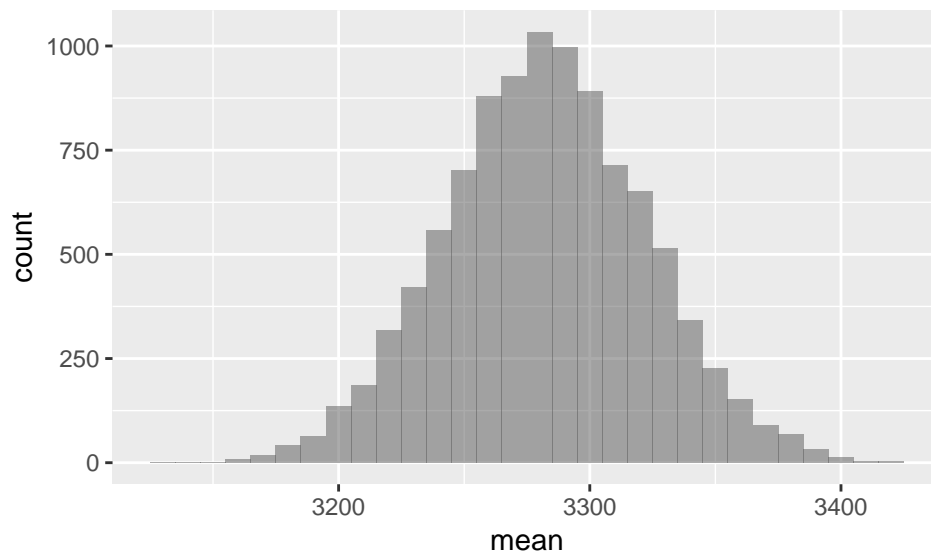
do(2) * mean(~ weight, data = sample(Babies, size = 100)) # Calculates the mean twice

##          mean
## 1 3297.84
## 2 3286.70

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

The `do()` function repeatedly calculates the mean of a random sample of 100 baby 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
```

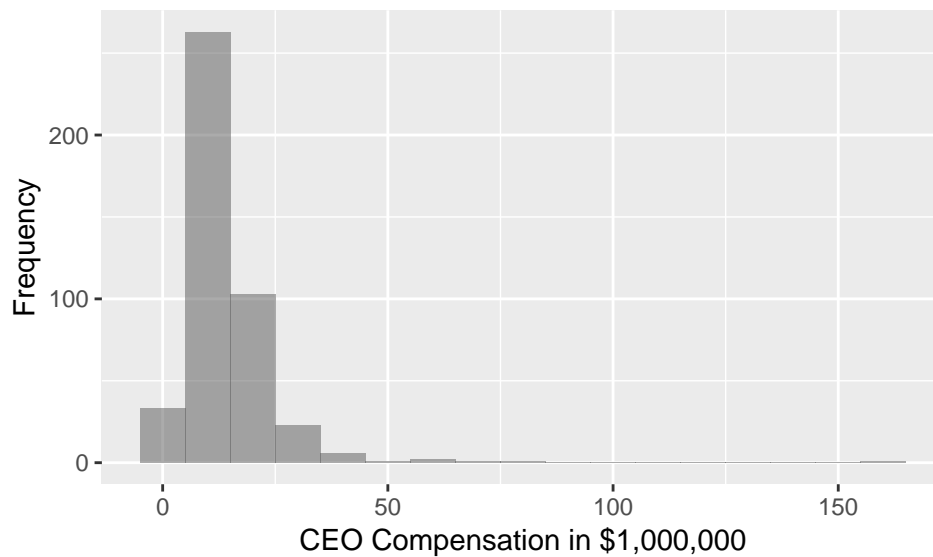
Section 14.1: The Central Limit Theorem

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

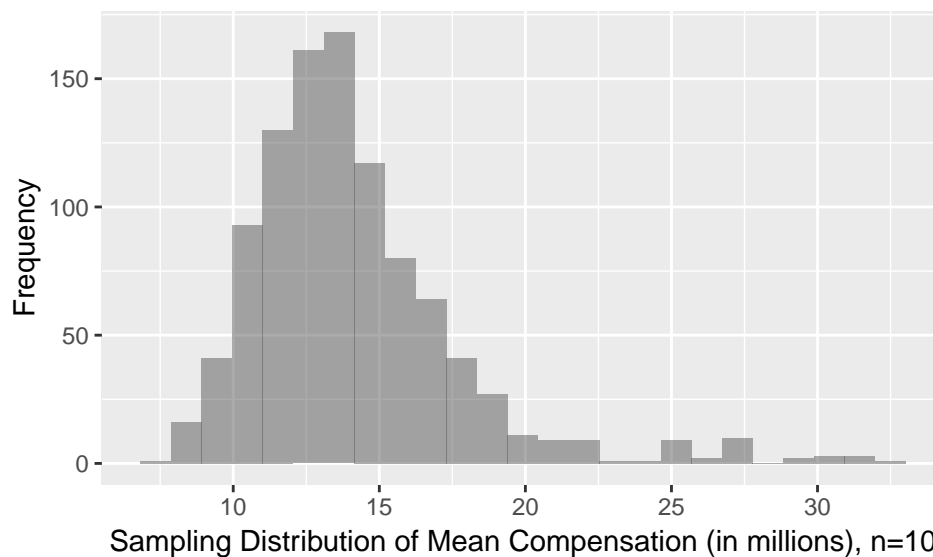
```
## Parsed with column specification:
## cols(
##   Employer = col_character(),
##   CEO = col_character(),
##   CEO_Compensation = col_integer(),
##   Median_Worker_Comp = col_integer(),
##   Ratio = col_integer(),
##   Company_Rating = col_double(),
##   `CEO_Compensation_($M)` = col_double()
##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

Figure 14.3

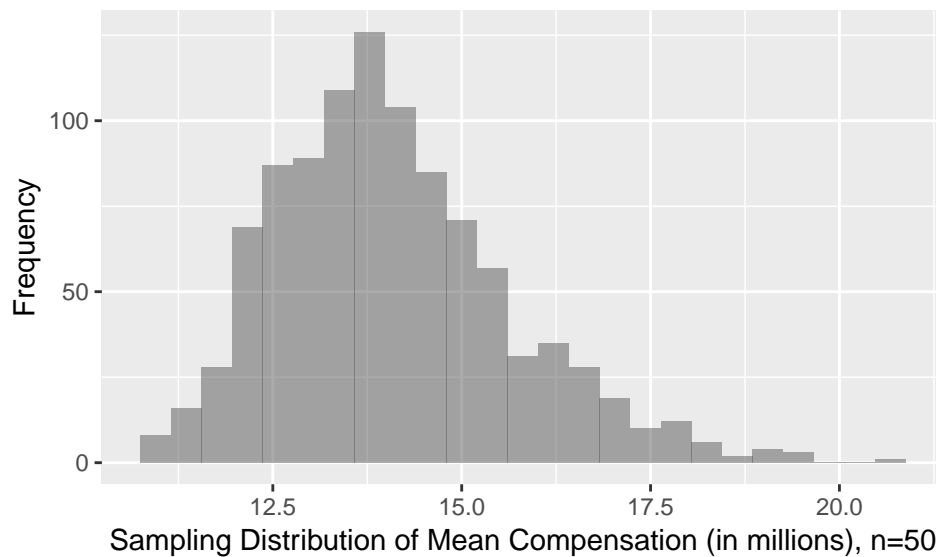
```
gf_histogram(~ ceo_compensation_m, data = CEOComp, binwidth = 10) %>%
  gf_labs(x = "CEO Compensation in $1,000,000", y = "Frequency")
```



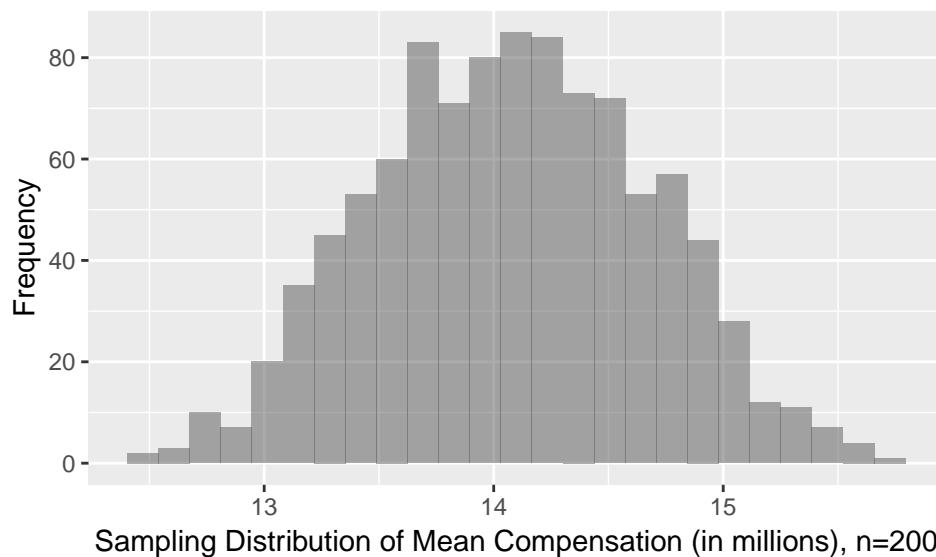
```
# Figure 14.4
set.seed(14354)
numsim <- 1000 # Here the number of simulations is 1,000
CEOMeans <- do(numsim) * mean(~ ceo_compensation_m, data = sample(CEOComp, size = 10))
gf_histogram(~ mean, data = CEOMeans) %>%
  gf_labs(x = "Sampling Distribution of Mean Compensation (in millions), n=10", y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



```
# Figure 14.5
CEOMeans2 <- do(numsim) * mean(~ ceo_compensation_m, data = sample(CEOComp, size = 50))
gf_histogram(~ mean, data = CEOMeans2) %>%
  gf_labs(x = "Sampling Distribution of Mean Compensation (in millions), n=50", y = "Frequency")
```



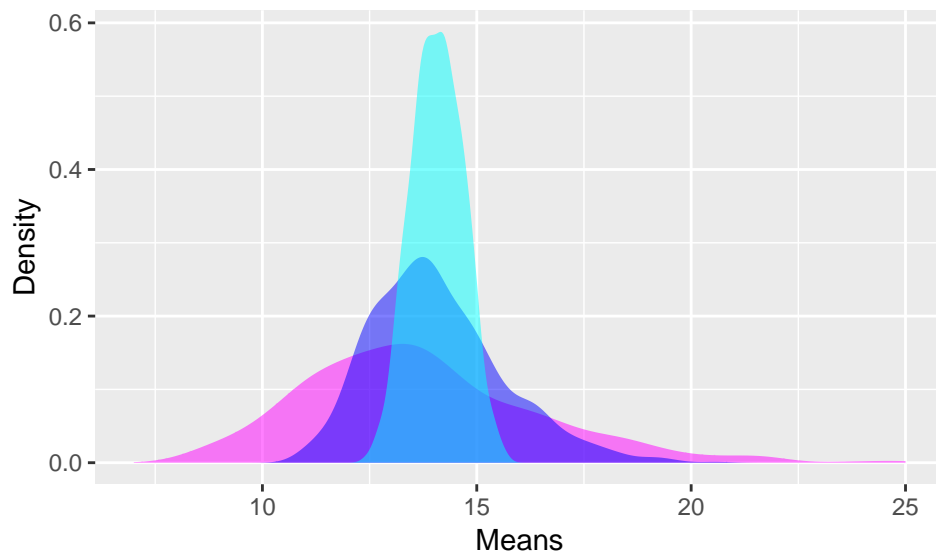
```
# Figure 14.7 (skipped 14.6 because it's similar)
CEOMeans3 <- do(numsim) * mean(~ ceo_compensation_m, data = sample(CEOComp, size = 200))
gf_histogram(~ mean, data = CEOMeans3) %>%
  gf_labs(x = "Sampling Distribution of Mean Compensation (in millions), n=200", y = "Frequency")
```



For each example sample size, the `do()` function calculates the mean of random samples of that specified size.

```
# Samples as overlaid density plots
gf_density(~ mean, data = CEOMeans, fill = 6) %>%
  gf_density(~ mean, data = CEOMeans2, fill = 4) %>%
  gf_density(~ mean, data = CEOMeans3, fill = 5) %>%
  gf_labs(y = "Density", x = "Means") +
  xlim(7, 25)
```

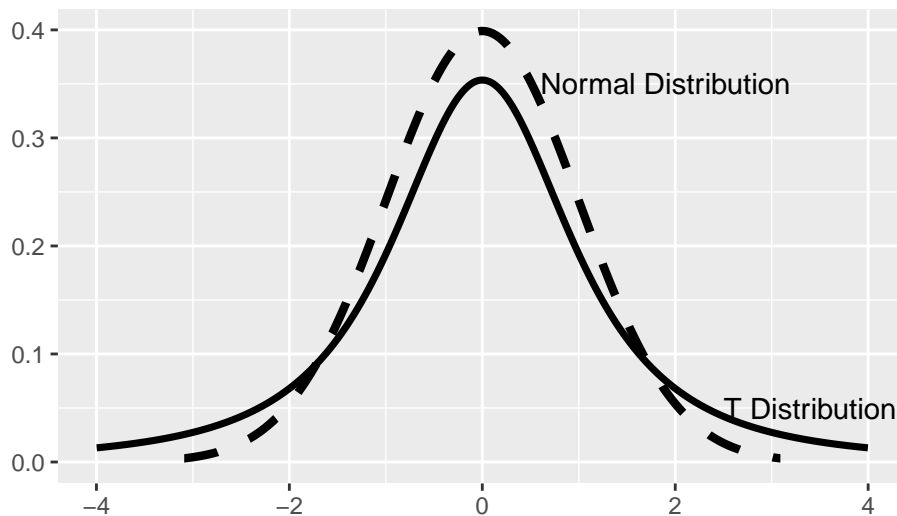
```
## Warning: Removed 27 rows containing non-finite values (stat_density).
```



Section 14.2: A Confidence Interval for the Mean

```
# Figure 14.9, page 446
gf_dist(dist = "norm", linetype = 2, lwd = 1.5) %>%
  gf_refine(annotate(geom = "text", x = 1.9, y = .35, label = "Normal Distribution")) %>%
  gf_labs(x = "", y = "") %>%
  gf_dist(dist = "t", df = 2, lwd = 1.25) %>%
  gf_refine(annotate(geom = "text", x = 3.4, y = .05, label = "T Distribution")) +
  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

t.test(~ mirex, data = Salmon)

##
## One Sample t-test
##
## data:  mirex
## t = 22.589, df = 149, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  0.08334978 0.09933022
## sample estimates:
## mean of x
##  0.09134

salmonlm <- lm(mirex ~ 1, data = Salmon) # equiv to t.test(~ mirex)
# replication of interval from page 448
confint(salmonlm, data = Salmon)

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

tstats <- xqt(df = 149, p = c(.025, .975), plot = FALSE) # t statistics
sey <- sd(~ mirex, data = Salmon)/(150^(1/2)) # standard error
mean(~ mirex, data = Salmon) + sey * tstats # calculations match those from confint

## [1] 0.08334978 0.09933022
```

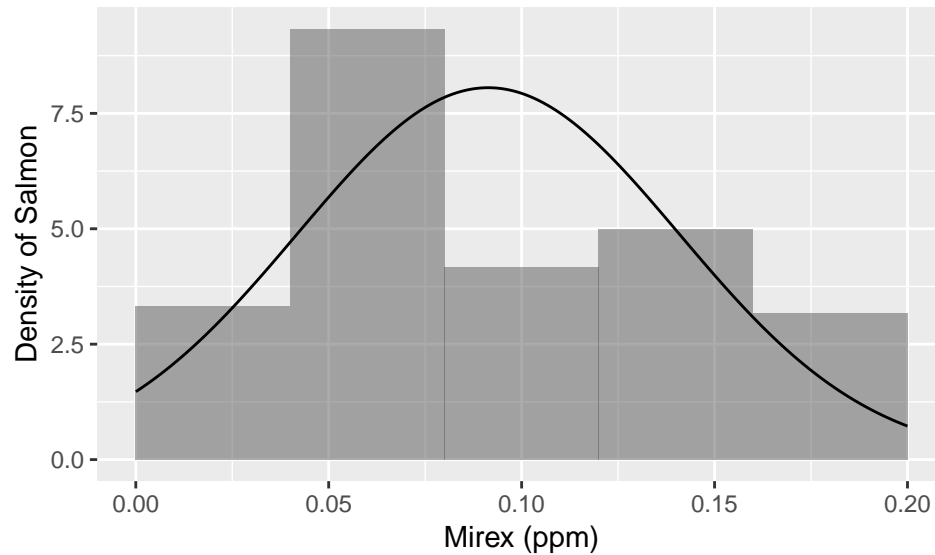
The `confint()` function takes an object, in this case a linear regression model, as an argument.

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

```
# With a normal distribution (page 450)
gf_dhistogram(~ mirex, data = Salmon, binwidth = 0.04, center = 0.02) %>%
  gf_dist(dist = "norm", mean = mean(~ mirex, data = Salmon), sd = sd(~ mirex, data = Salmon)) %>%
```

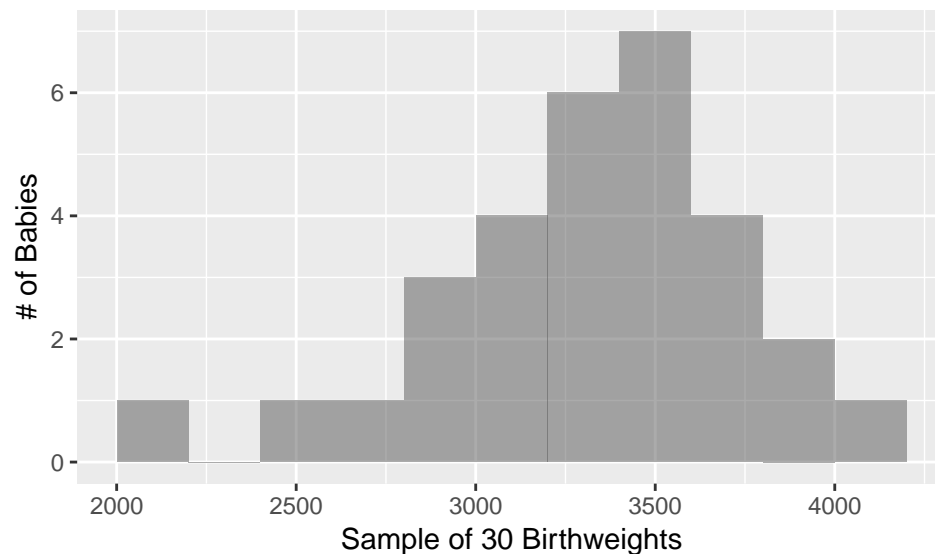
```
gf_labs(x = "Mirex (ppm)", y = "Density of Salmon") +
xlim(0, .2)
```

```
## Warning: Removed 1733 rows containing missing values (geom_path).
```



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

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



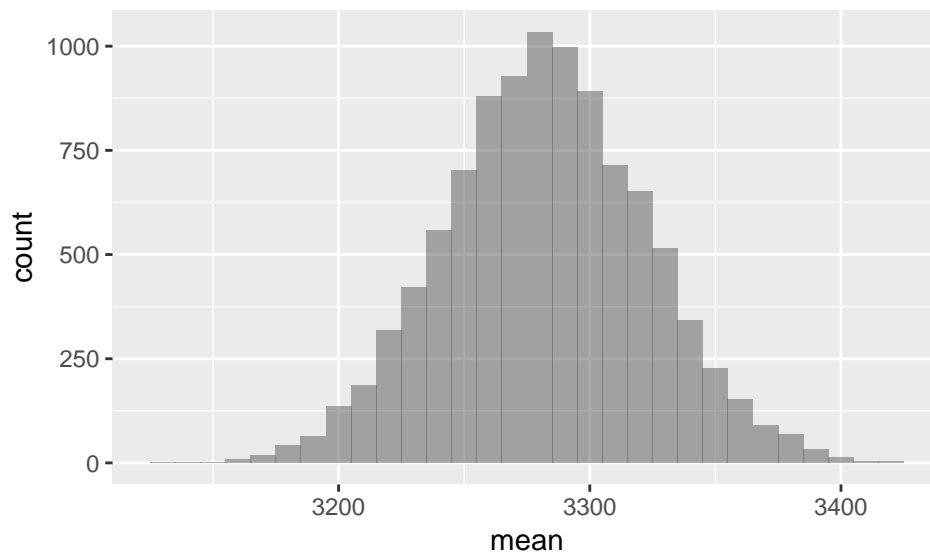
```
babieslm <- lm(weight ~ 1, data = BabiesSample)
confint(babieslm, level = 0.90)
```

```
##              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)
```

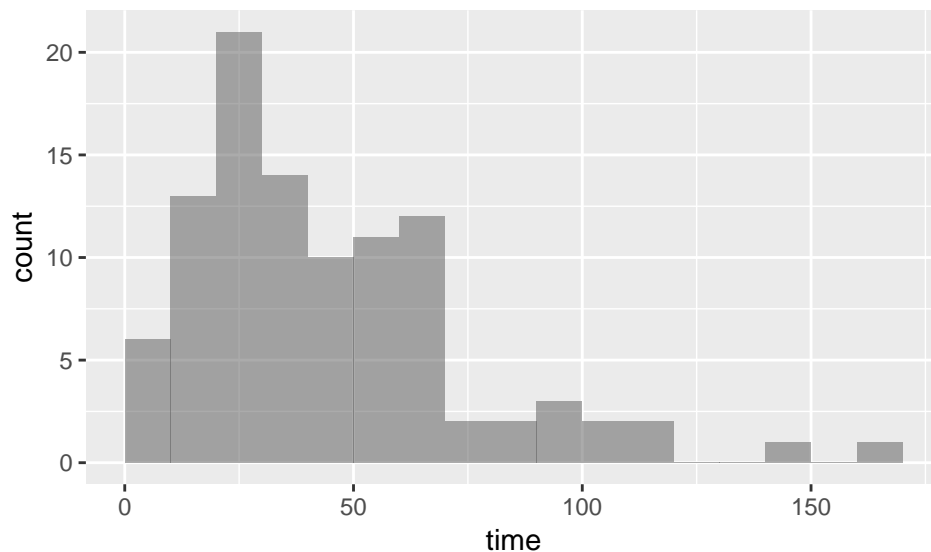


Step-By-Step Example: A Bootstrap Confidence Interval for the Mean

```
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) # To ensure we get the same values when we run it multiple times
numsim <- 10000
commutebootstrap <- do(numsim) * mean(~ time, data = resample(CommuteSample))
```

The `resample()` function samples of that data set size with replacement.

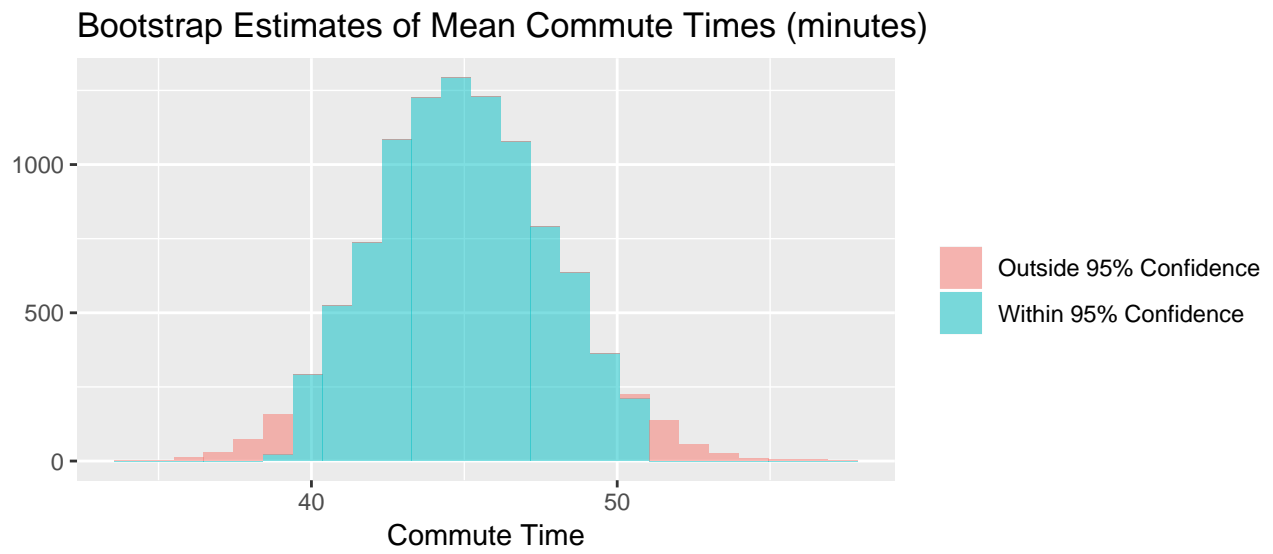
```
qdata(~ mean, p = c(.025, .975), data = commutebootstrap) # grab the percentiles with qdata
```

```
##      quantile      p
## 2.5%      39.28 0.025
## 97.5%      50.98 0.975
```

```
confint(commutebootstrap, method = "quantile") # an equivalent quantile approach
```

```
##   name lower upper level      method estimate
## 1 mean 39.28 50.98  0.95 percentile      44.98
```

```
commutebootstrap <- commutebootstrap %>%
  mutate(interval = ifelse(mean > 39.28 & mean < 50.98, "Within 95% Confidence",
                           "Outside 95% Confidence")) # for fill
gf_histogram(~ mean, fill = ~ interval, data = commutebootstrap,
             title = "Bootstrap Estimates of Mean Commute Times (minutes)") %>%
  gf_labs(x = "Commute Time", y = "", fill = "")
```



Section 14.5: Thoughts About Confidence Intervals