IS5 in R: The Standard Deviation as a Ruler and the Normal Model (Chapter 5)

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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. 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 (https://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 5: The Standard Deviation as a Ruler and the Normal Model

```
library(mosaic)
library(readr)
library(janitor)
WomenHeptathlon2016 <-
  read_csv("http://nhorton.people.amherst.edu/is5/data/Womens_Heptathlon_2016.csv") %>%
  janitor::clean_names()
```

By default, `read_csv()` prints the variable names. These messages were 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).

```
# page 123
df_stats(~long_jump, data = WomenHeptathlon2016)
```

```
##    response  min   Q1 median   Q3  max     mean        sd  n missing
## 1 long_jump 5.51 6.08   6.19 6.31 6.58 6.169655 0.2474655 29       2
```

```
df_stats(~x200m, data = WomenHeptathlon2016)
```

```
##   response   min    Q1 median    Q3   max     mean        sd  n missing
## 1    x200m 23.26 24.12   24.6 24.99 26.32 24.58207 0.6544975 29       2
```

```
with(WomenHeptathlon2016, stem(x200m))
```

```
##
##   The decimal point is at the |
##
```

```
##   23 | 3
##   23 | 589
##   24 | 011123334
##   24 | 5667789
##   25 | 00112444
##   25 |
##   26 | 3
```

```
with(WomenHeptathlon2016, stem(long_jump))
```

```
##
##   The decimal point is 1 digit(s) to the left of the |
##
##   54 | 1
##   56 | 2
##   58 | 181
##   60 | 0588002569
##   62 | 023501145
##   64 | 38158
```

Section 5.1: Using the Standard Deviation to Standardize Values

```
filter(WomenHeptathlon2016, last_name == "Thiam") %>%
  data.frame()
```

```
##   first_name last_name x200m long_jump  x800m high_jump x100m_hurdles javelin
## 1 Nafissatou     Thiam  25.1      6.58 136.54      1.98         13.56   53.13
##   shot_put
## 1    14.91
```

```
# calculate z-score with mean and sd from df_stats
(6.58 - 6.17) / .247 # long jump
```

```
## [1] 1.659919
```

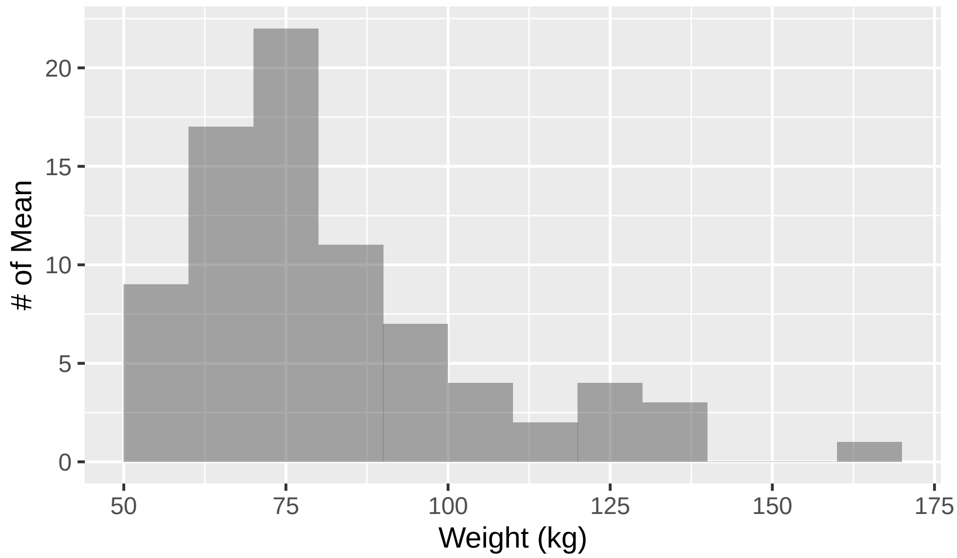
```
filter(WomenHeptathlon2016, last_name == "Johnson-Thompson") %>%
  data.frame()
```

```
##   first_name        last_name x200m long_jump  x800m high_jump x100m_hurdles
## 1   Katarina Johnson-Thompson 23.26      6.51 130.47      1.98         13.48
##   javelin shot_put
## 1   36.36    11.68
```

`data.frame()` converts an object into a data frame.

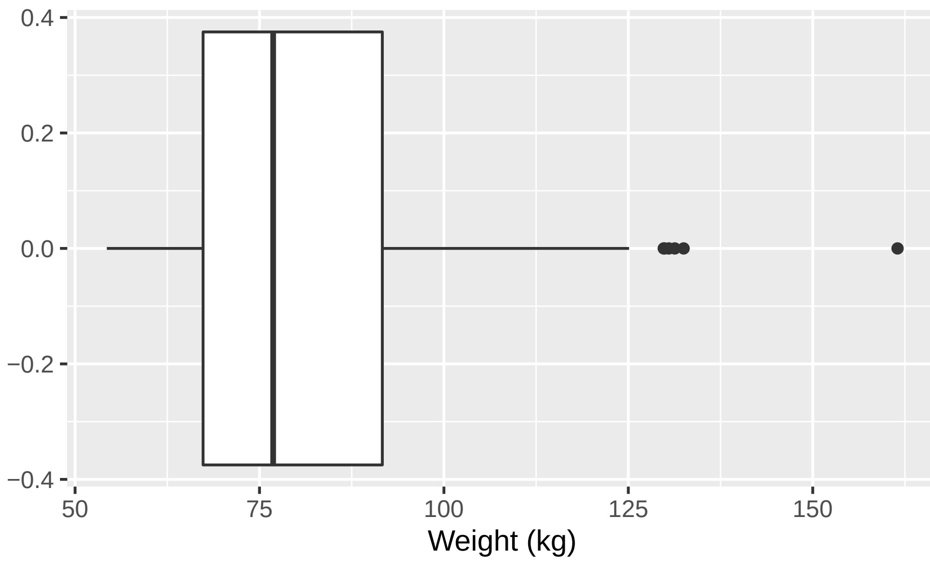
Section 5.2: Shifting and Scaling

```
MenWeight <- read_csv("http://nhorton.people.amherst.edu/is5/data/Mens_Weights.csv") %>%
  janitor::clean_names()
# Figure 5.2, page 125
gf_histogram(~weight_in_kg, data = MenWeight, binwidth = 10, center = 5) %>%
  gf_labs(x = "Weight (kg)", y = "# of Mean")
```



Shifting to Adjust the Center

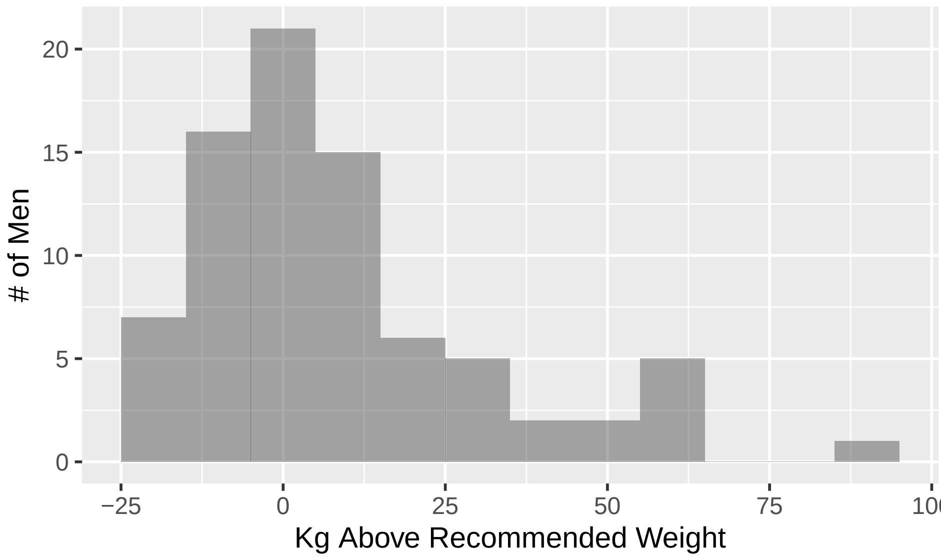
```
gf_boxplot(~weight_in_kg, data = MenWeight, xlab = "Weight (kg)")
```




```
df_stats(~weight_in_kg, data = MenWeight)
```

```
##       response  min    Q1 median    Q3   max     mean       sd  n missing
## 1 weight_in_kg 54.3 67.35  76.85 91.65 161.5 82.35625 22.26881 80       0
```

```
# Figure 5.3
gf_histogram(~ (weight_in_kg - 74), data = MenWeight, binwidth = 10) %>%
  gf_labs(x = "Kg Above Recommended Weight", y = "# of Men")
```




```r
df_stats(~weight_in_kg, data = MenWeight)
```

Rescaling to Adjust the Scale

```
##       response  min    Q1 median    Q3   max     mean       sd  n missing
## 1 weight_in_kg 54.3 67.35  76.85 91.65 161.5 82.35625 22.26881 80       0
```

```r
df_stats(~weight_in_pounds, data = MenWeight)
```

```
##           response    min     Q1 median     Q3   max     mean       sd  n
## 1 weight_in_pounds 119.46 148.17 169.07 201.63 355.3 181.1838 48.99137 80
##   missing
## 1       0
```

```r
library(tidyr) # for gather() function

# What does gather() do?
MenWeight %>%
  head() # There are two variables: weight_in_kg and weight_in_pounds. Each observation has a value for
```

```
## # A tibble: 6 x 2
##   weight_in_kg weight_in_pounds
##          <dbl>            <dbl>
## 1        107.              236.
## 2         95.7             211.
## 3         68.9             152.
## 4         60.3             133.
## 5         60.4             133.
## 6         69.7             153.
```

```r
nrow(MenWeight)
```

```
## [1] 80
```

```r
MenGather <- MenWeight %>%
  gather(key = weighttype, value = weight, weight_in_kg, weight_in_pounds)
MenGather %>%
  head() # The two variables are weighttype and weight. weighttype is a categorical variable that is ei
```

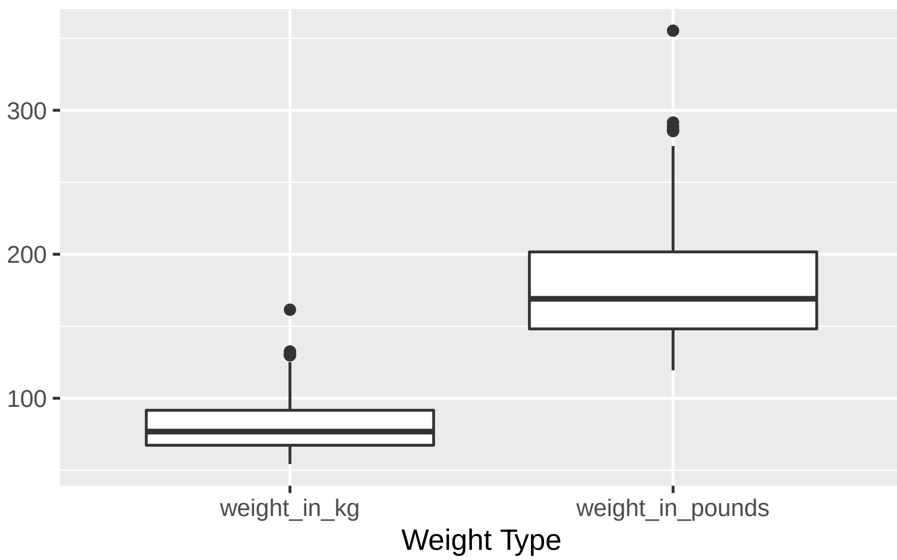
```
## # A tibble: 6 x 2
##   weighttype   weight
##   <chr>         <dbl>
## 1 weight_in_kg  107.
## 2 weight_in_kg   95.7
## 3 weight_in_kg   68.9
## 4 weight_in_kg   60.3
## 5 weight_in_kg   60.4
## 6 weight_in_kg   69.7
```

```
nrow(MenGather) # Each observation from before is now two rows
```

```
## [1] 160
```

Here we use the `gather()` function to transform the dataset into the needed format, which can be seen with the `head()` function.

```
MenGather %>%
  gf_boxplot(weight ~ weighttype) %>%
  gf_labs(x = "Weight Type", y = "")
```



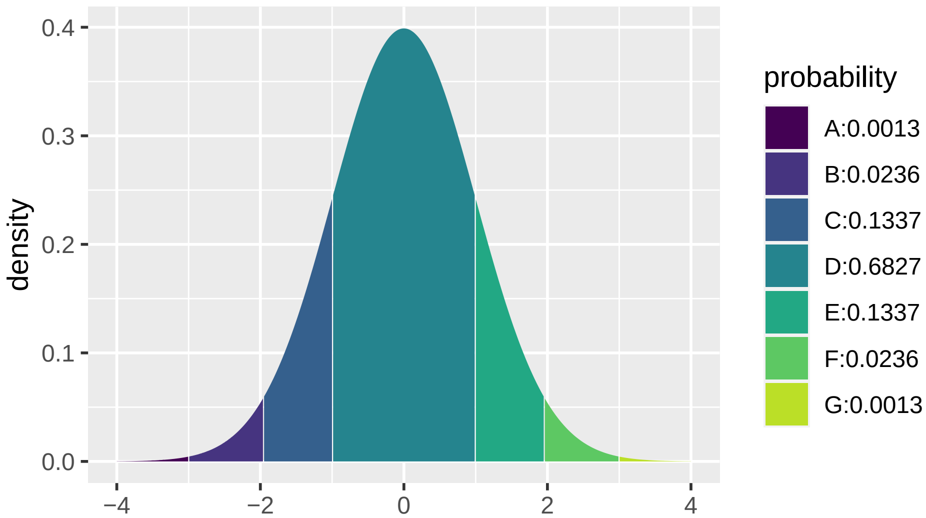
We see the use of `goal(Y ~ X)` as an example of the general modeling language for two variables in the `mosaic` package.

Shifting, Scaling, and the z-Scores

Section 5.3: Normal Models

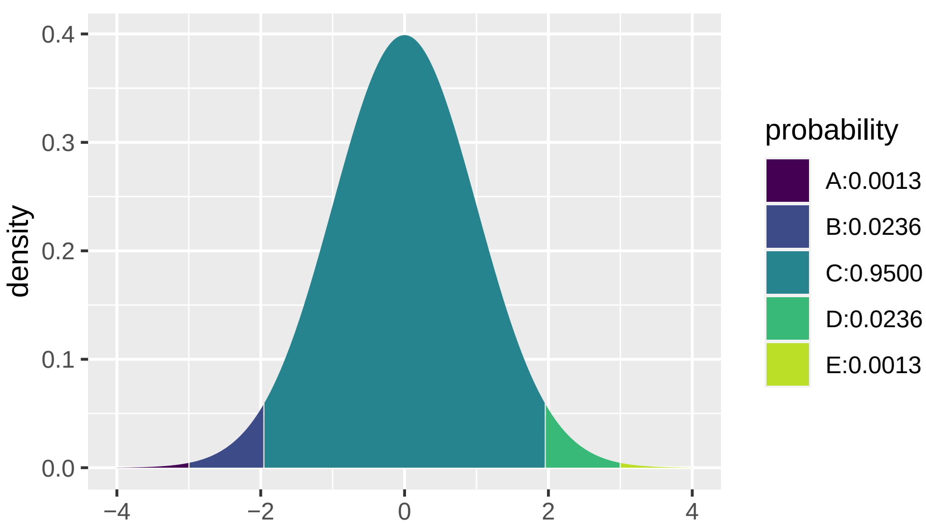
The 68-95-99.7 Rule See display on page 129.

```
# Figure 5.6
# 1, 2 (1.96), and 3 SD's
xpnorm(c(-3, -1.96, -1, 1, 1.96, 3), mean = 0, sd = 1, verbose = FALSE)
```



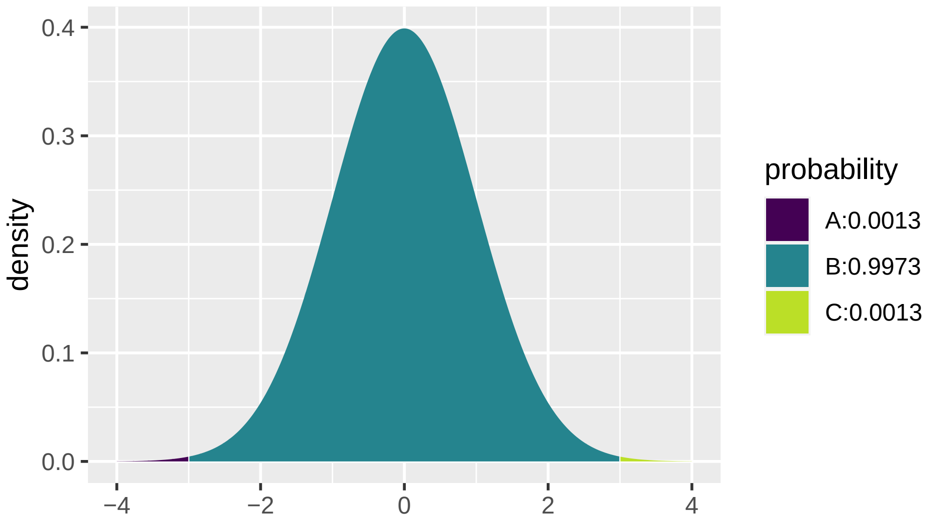

```
## [1] 0.001349898 0.024997895 0.158655254 0.841344746 0.975002105 0.998650102
```

```r
# 2 (1.96) and 3 SD's
xpnorm(c(-3, -1.96, 1.96, 3), mean = 0, sd = 1, verbose = FALSE)
```




```
## [1] 0.001349898 0.024997895 0.975002105 0.998650102
```

```r
# 3 SD's
xpnorm(c(-3, 3), mean = 0, sd = 1, verbose = FALSE)
```



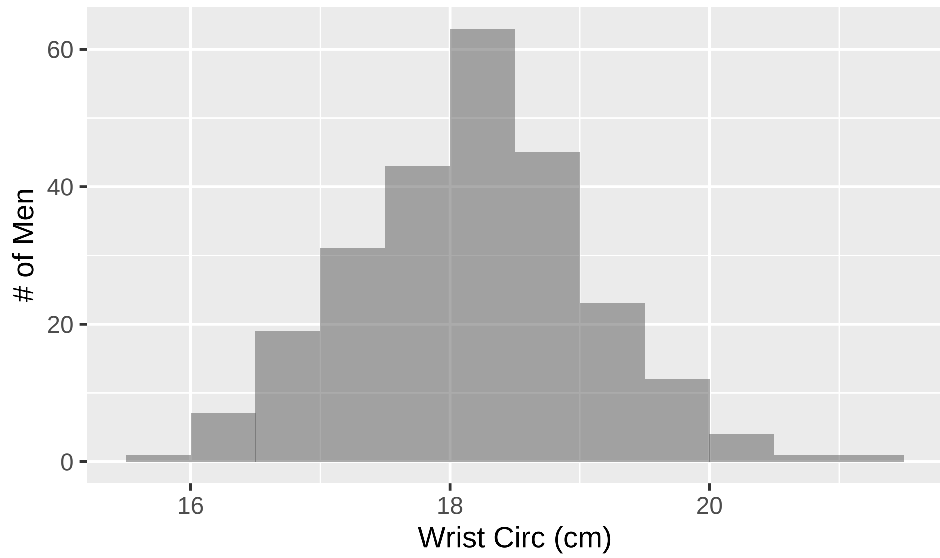

```
## [1] 0.001349898 0.998650102
```

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

Example 5.4: Using the 68-95-99.7 Rule

```
##
## -- Column specification --------------------------------------------------------------------------------
## cols(
##   Density = col_double(),
##   Pct.BF = col_double(),
##   Age = col_double(),
##   Weight = col_double(),
##   Height = col_double(),
##   Neck = col_double(),
##   Chest = col_double(),
##   Abdomen = col_double(),
##   Waist = col_double(),
##   Hip = col_double(),
##   Thigh = col_double(),
##   Knee = col_double(),
##   Ankle = col_double(),
##   Bicep = col_double(),
##   Forearm = col_double(),
##   Wrist = col_double()
## )
```

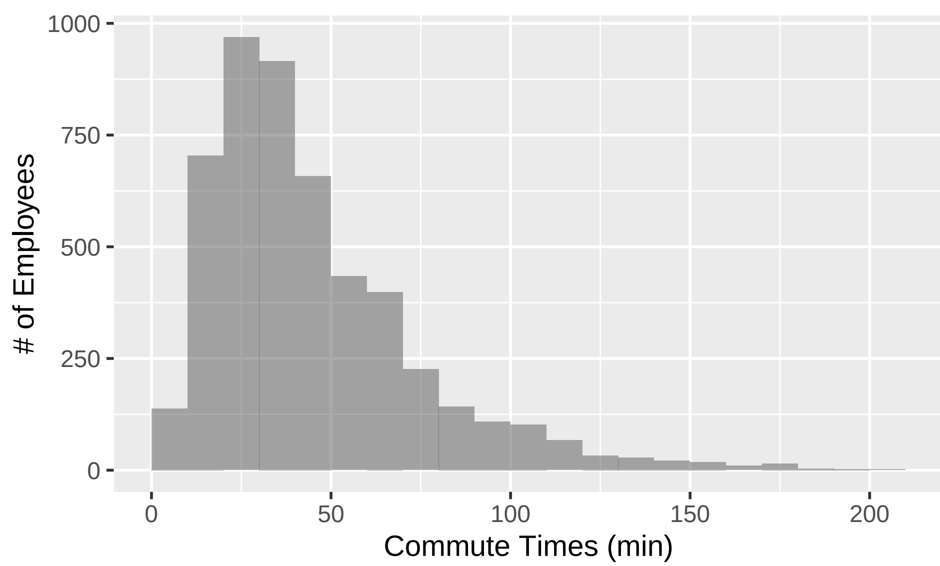
```
gf_histogram(~Wrist,
  data = BodyFat, binwidth = .5,
  center = -.25
) %>%
  gf_labs(x = "Wrist Circ (cm)", y = "# of Men")
```



Random Matters Starts on page 133.

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

gf_histogram(~commute_time, data = Commute, binwidth = 10, center = 5) %>%
  gf_labs(x = "Commute Times (min)", y = "# of Employees")
```




```
set.seed(2143) # To ensure we get the same values when we run it multiple times
numsim <- 10000 # Number of simulations


mean(~commute_time, data = sample(Commute, size = 100)) # Mean of one random sample
```

```
## [1] 45.79
```

```
mean(~commute_time, data = sample(Commute, size = 100)) # Mean of another random sample
```

```
## [1] 44.7
```

The `do()` command allows us to run a command multiple times, saving the result as a data frame.

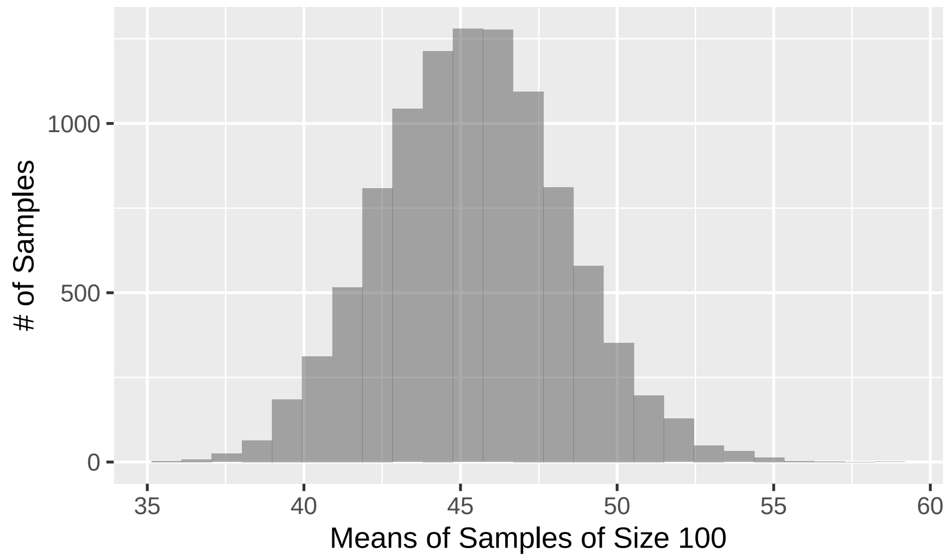
```r
do(2) * mean(~commute_time, data = sample(Commute, size = 100))
```

```
##    mean
## 1 47.43
## 2 45.97
```

```r
# For the visualization, we use do() 10,000 times
Commute_sample <- do(numsim) * mean(~commute_time, data = sample(Commute, size = 100))
```

The `do()` function generates 10,000 samples of size 100 and for each calculates the sample mean.

```r
gf_histogram(~mean, data = Commute_sample) %>%
  gf_labs(x = "Means of Samples of Size 100", y = "# of Samples")
```

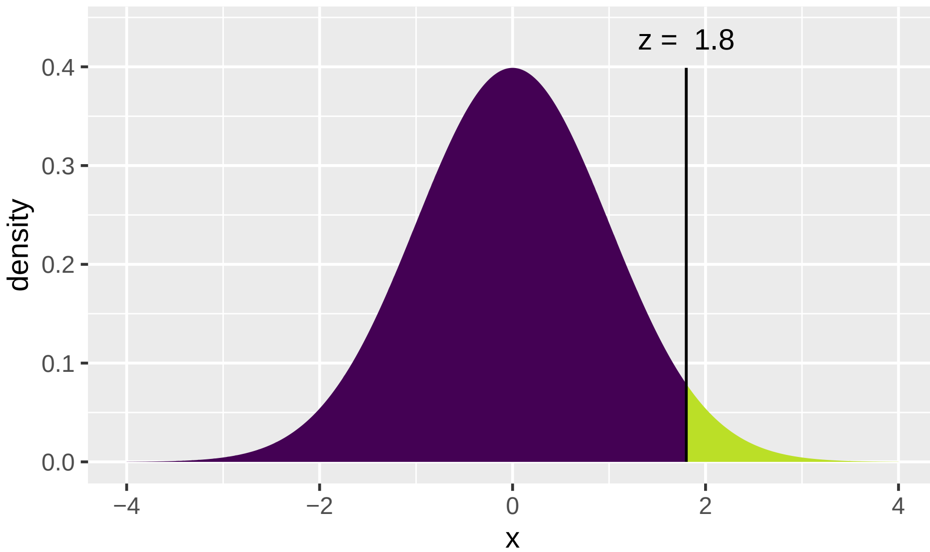


Section 5.4: Working with Normal Percentiles

The `pnorm()` function calculates normal probabilities. The `xpnorm()` function from the mosaic package adds a graphical depiction and additional output that may be helpful to new users.

```r
xpnorm(1.8, mean = 0, sd = 1)
```

```
##
## If X ~ N(0, 1), then
##  P(X <= 1.8) = P(Z <= 1.8) = 0.9641
##  P(X >  1.8) = P(Z >  1.8) = 0.03593
##
```

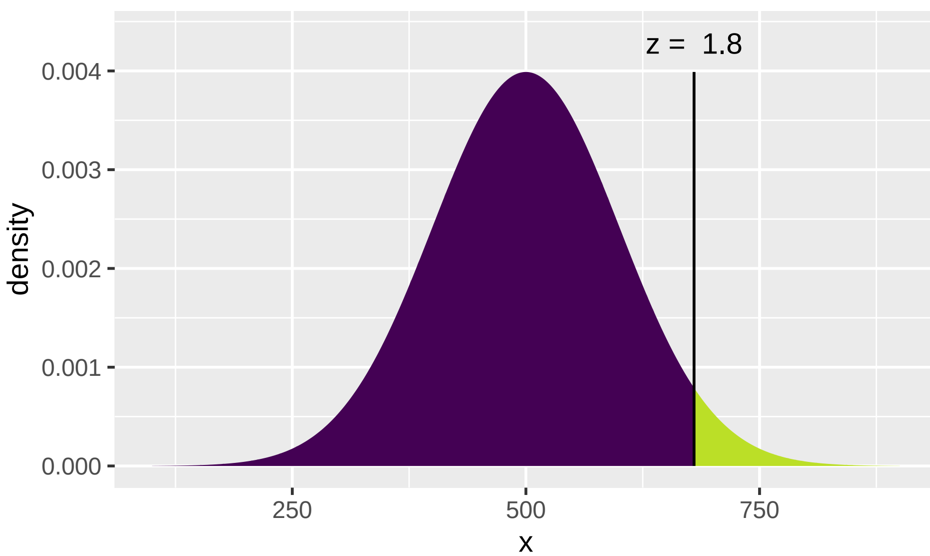



```
## [1] 0.9640697
```

The `qnorm()` function finds the inverse of normal probabilities.

```r
xqnorm(0.964, mean = 500, sd = 100) # inverse of pnorm()
```

```
##
## If X ~ N(500, 100), then
##  P(X <= 679.9118) = 0.964
##  P(X >  679.9118) = 0.036
##
```




```
## [1] 679.9118
```

```r
qnorm(0.964, mean = 0, sd = 1) # what is the z-score?
```

```
## [1] 1.799118
```

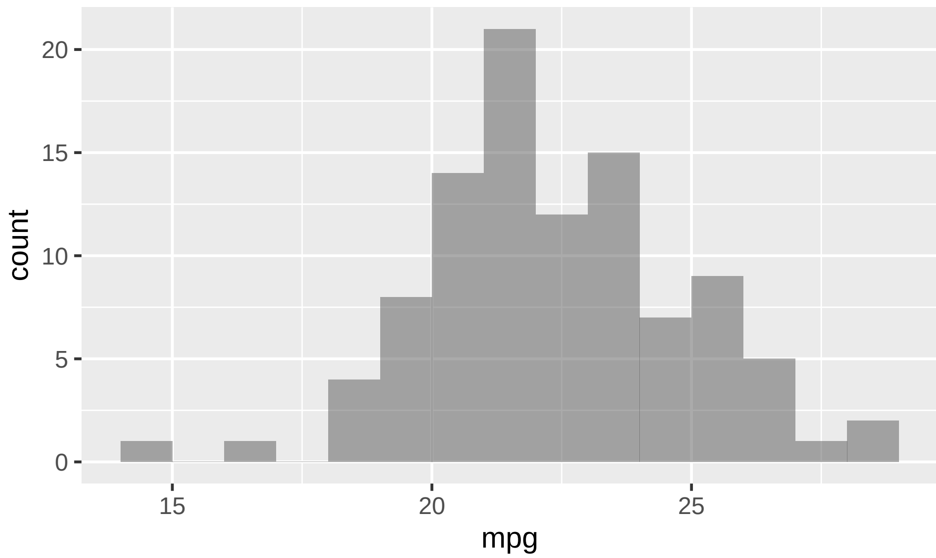
See examples on pages 136-140.

Section 5.5: Normal Probability Plots

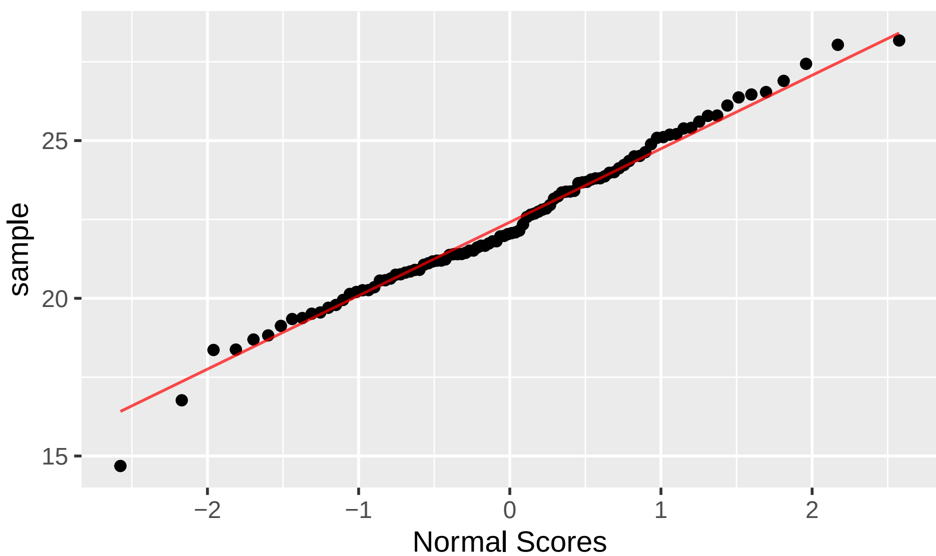
```
Nissan <- read_csv("http://nhorton.people.amherst.edu/is5/data/Nissan.csv")
```

```
##
## -- Column specification ------------------------------------------------------------------------
## cols(
##   mpg = col_double()
## )
```

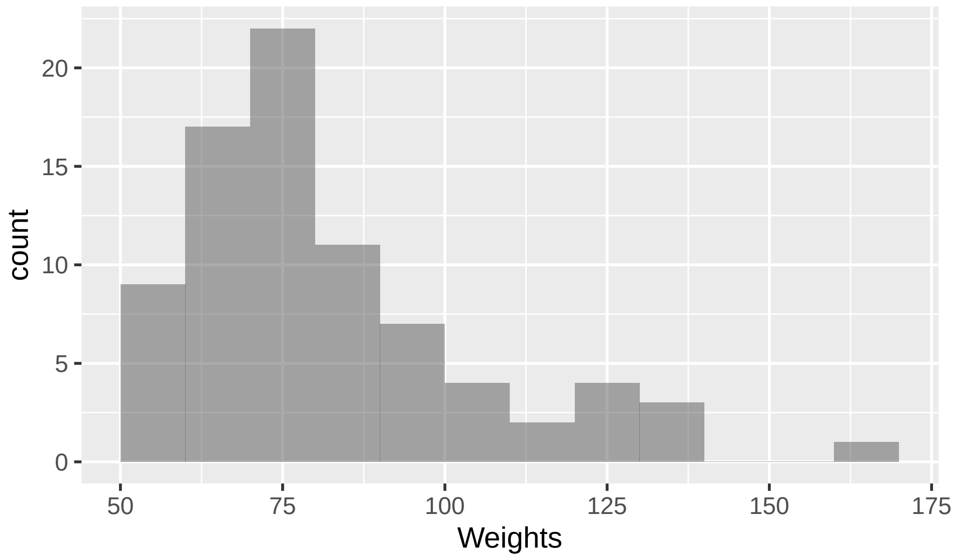
```
# Figure 5.10, page 141
gf_histogram(~mpg, data = Nissan, binwidth = 1, center = .5)
```




```
gf_qq(~mpg, data = Nissan, xlab = "Normal Scores") %>%
  gf_qqline(linetype = "solid", color = "red")
```




```
# Figure 5.11
gf_histogram(~weight_in_kg, data = MenWeight, xlab = "Weights", binwidth = 10, center = 5)
```




```
gf_qq(~weight_in_kg, data = MenWeight, xlab = "Normal Scores") %>%
  gf_qqline(linetype = "solid", color = "red")
```