IPS9 in R: Bootstrap Methods and Permutation Tests (Chapter 16)

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Introduction and background

These documents are intended to help describe how to undertake analyses introduced as examples in the Ninth Edition of *Introduction to the Practice of Statistics* (2017) by Moore, McCabe, and Craig.

More information about the book can be found here. The data used in these documents can be found under Data Sets in the Student Site. This file as well as the associated R Markdown reproducible analysis source file used to create it can be found at https://nhorton.people.amherst.edu/ips9/.

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 1: Looking at data – distributions

This file replicates the analyses from the (online-only) Chapter 16: Bootstrap Methods and Permutation Tests.

First, load the packages that will be needed for this document:

```r
library(mosaic)
library(readr)
```

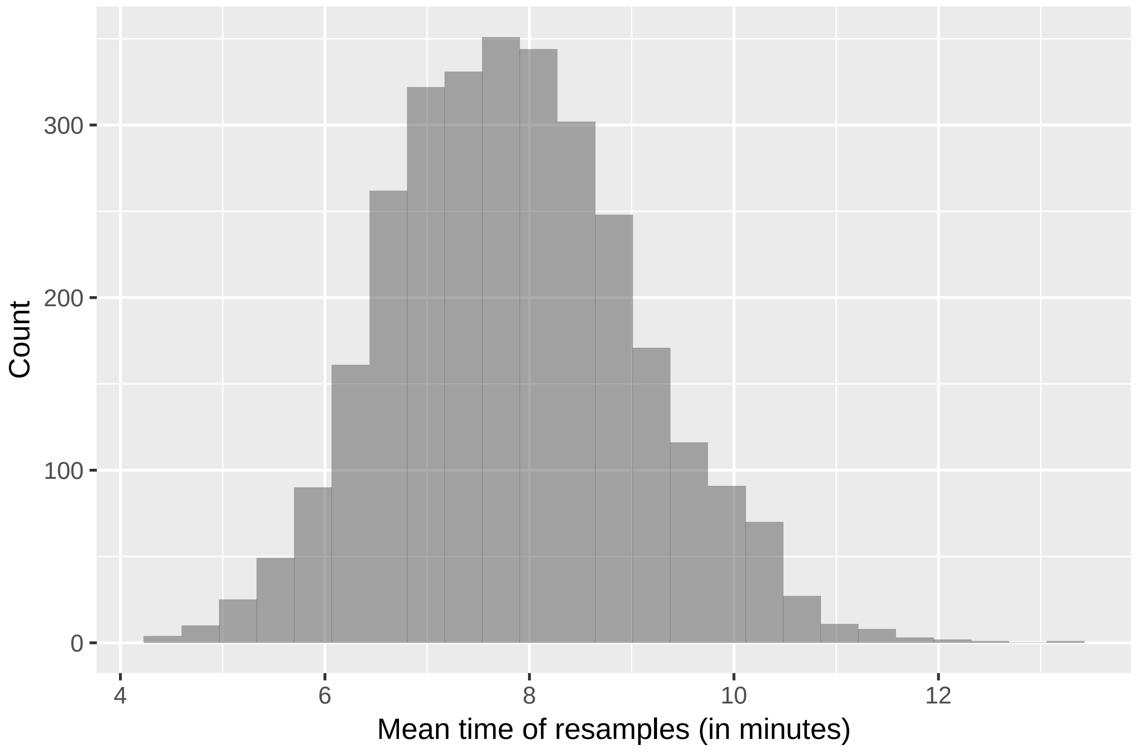
Section 16.1: The bootstrap idea

With the following code, we create many resamples by repeatedly sampling with replacement from the sample of 21 Facebook profiles. Then, we create the bootstrap distribution by finding the mean for the 3,000 resamples. The histogram and qqplots reproduced below can be found on page 5.

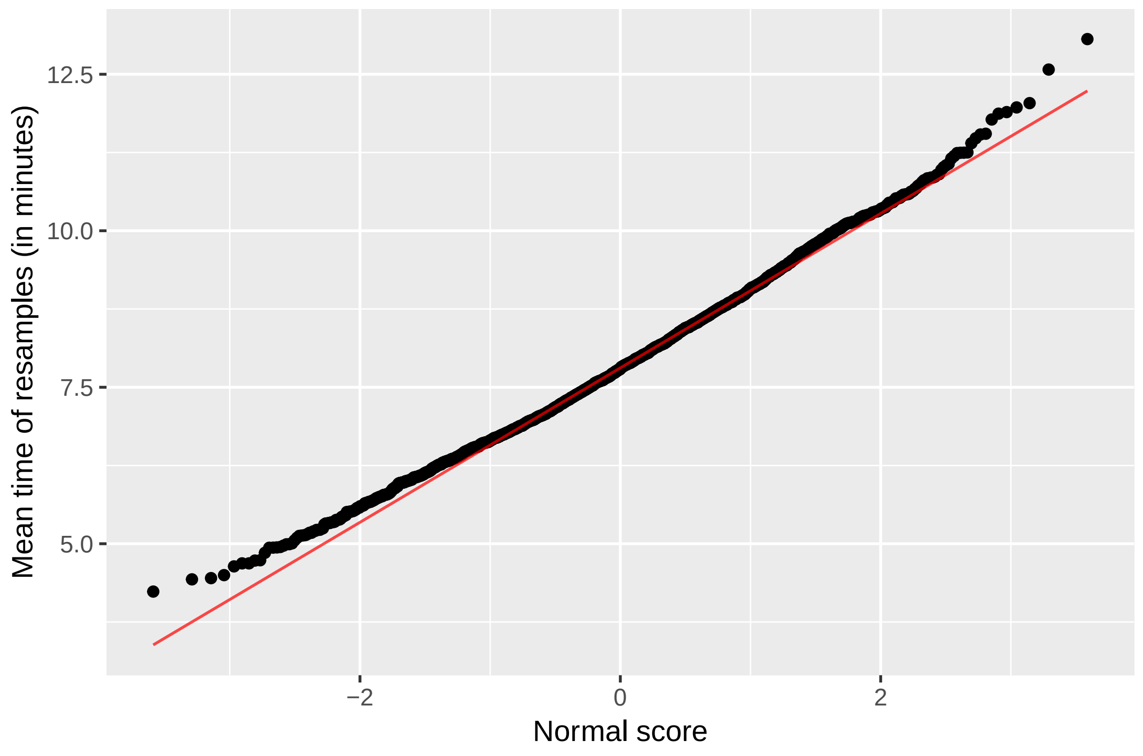
```r
FACE4 <- read_csv("https://nhorton.people.amherst.edu/ips9/data/chapter16/EG16-01FACE4.csv")

set.seed(2018)
numsim <- 3000
Avg_Viewtime <- do(numsim) * mean(~ Time, data = resample(FACE4, 21))

#Figure 16.3(a)
favstats(~ mean, data = Avg_Viewtime)
```

```
##       min       Q1   median       Q3      max     mean       sd    n
##  4.235714 6.977143 7.800714 8.640952 13.06238 7.851172 1.213376 3000
##  missing
##        0
```

```r
gf_histogram(~ mean, data = Avg_Viewtime) %>%
  gf_labs(x = "Mean time of resamples (in minutes)", y = "Count")
```



```r
#Figure 16.3(b)
gf_qq(~ mean, data = Avg_Viewtime) %>%
  gf_qqline(color = "red", linetype = "solid") %>%
  gf_labs(x = "Normal score", y = "Mean time of resamples (in minutes)")
```

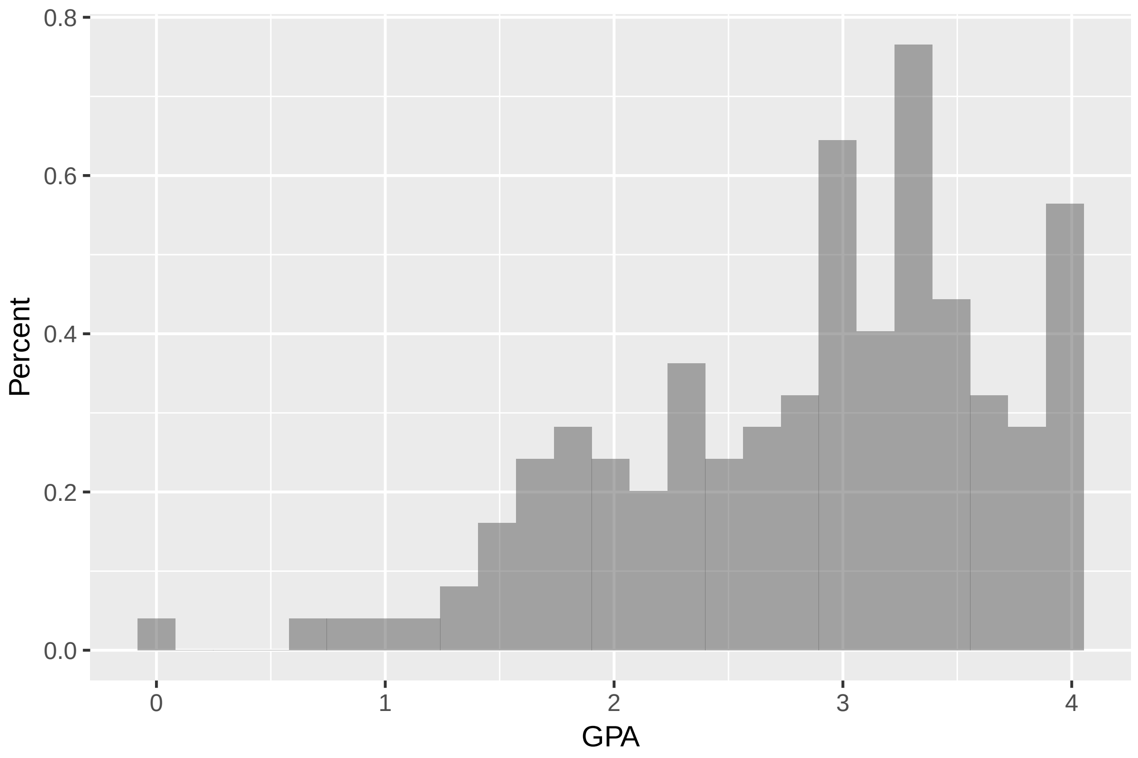


The pseudorandom number used to set the seed enables the reproduction of results. The `do()` function in the `mosaic` package simplifies the iteration and resampling
processes by allowing us to set the number of repetitions and specify what to repeat.

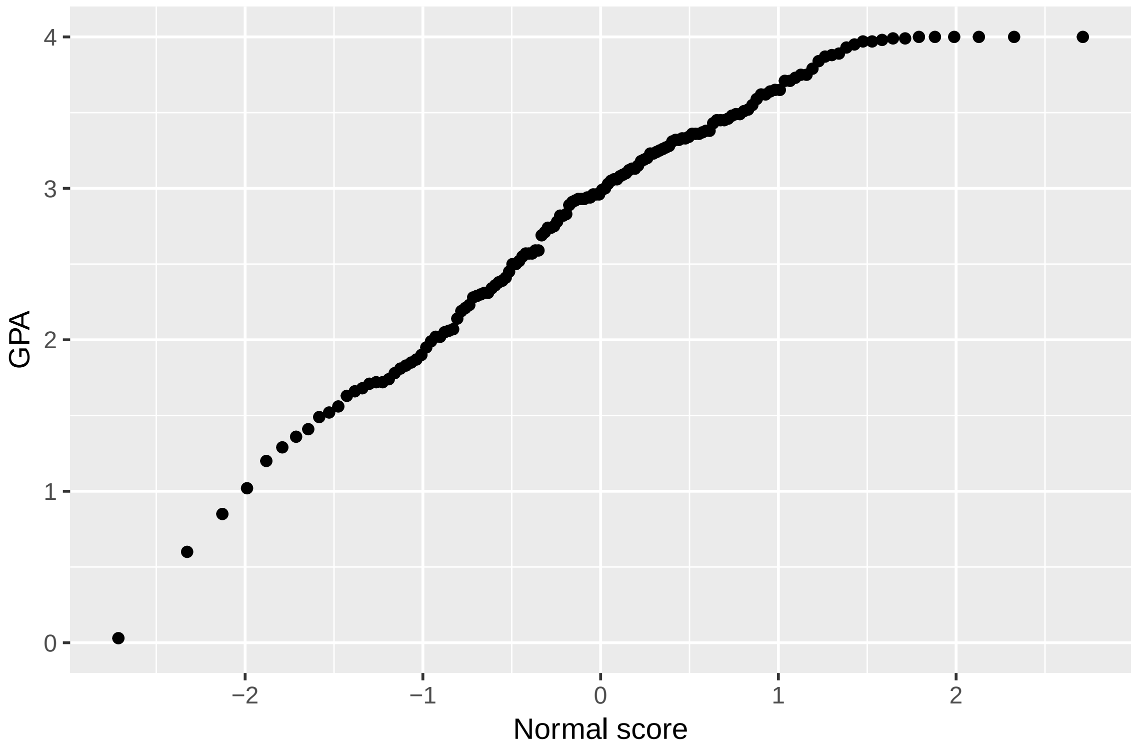
Section 16.2: First steps in using the bootstrap

The strongly right skewed distribution is shown on the histogram and Normal quantile plot for the original 150 grade points (page 14):

```
College_GPA <- read_csv("https://nhorton.people.amherst.edu/ips9/data/chapter16/EG16-04GPA.csv")

## Figure 16.8(a)
gf_dhistogram(~ GPA, data = College_GPA) %>%
  gf_labs(x = "GPA", y = "Percent")
```

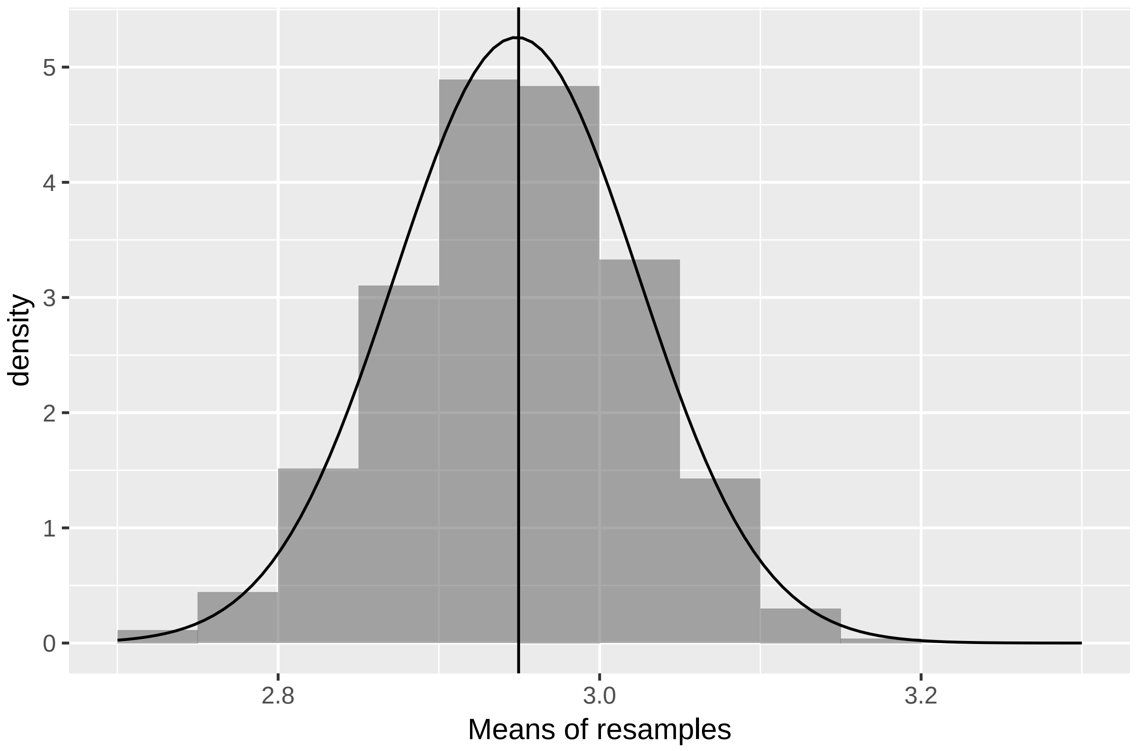


```
## Figure 16.8(b)
gf_qq(~ GPA, data = College_GPA) %>%
  gf_lims(y = c(0, 4)) %>%
  gf_labs(x = "Normal score", y = "GPA")
```

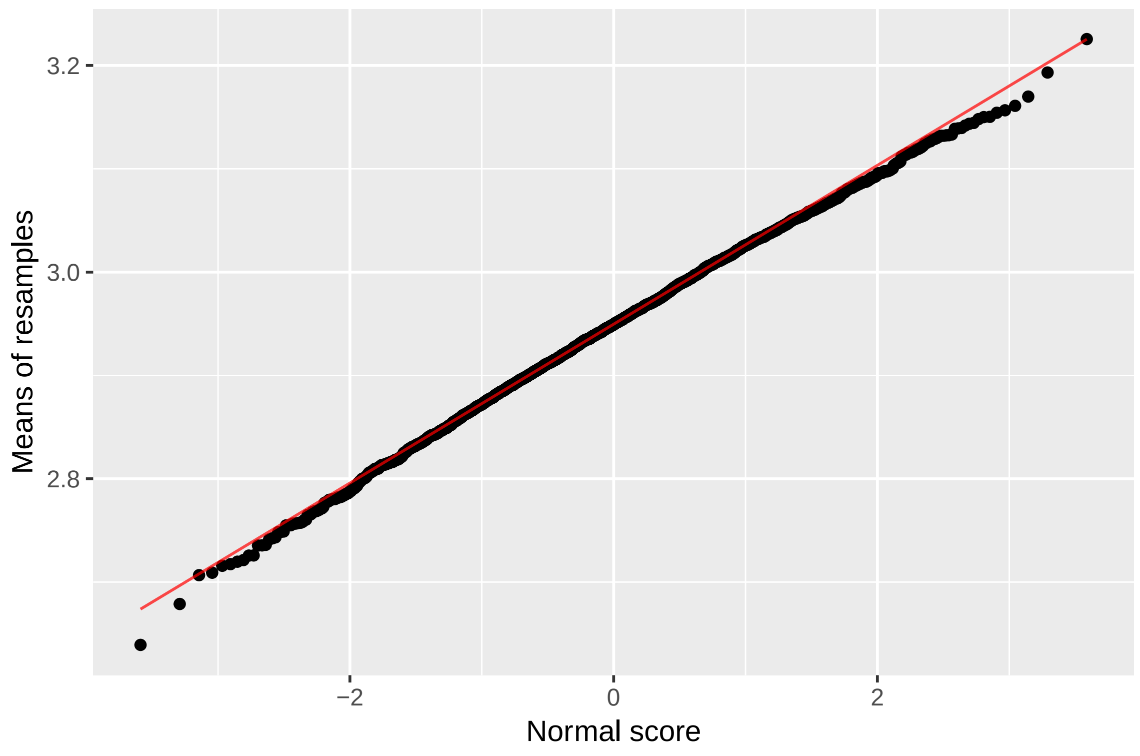


We will now use the 25% trimmed mean as the parameter and use the sample of 150 students to find the statistic that estimates this parameter. The process is similar to the bootstrapping done above, except that we now specify the "trim" argument in the `mean()` function:

```
mean_GPA <- mean(~ GPA, data = College_GPA, trim = 0.25)

numsim <- 3000
GPA_sims <- do(numsim) * mean(~ GPA, data = resample(College_GPA, 150), trim = 0.25)

## Figure 16.9(a)
gf_dhistogram(~ mean, data = GPA_sims, binwidth = 0.05, bins = 12, center = 0.05/2) %>%
  gf_lims(x = c(2.7, 3.3)) %>%
  gf_fitdistr(dist = "dnorm") %>%
  gf_labs(x = "Means of resamples") %>%
  gf_vline(xintercept = as.numeric(mean_GPA))
```



```
## XX Graph doesn't look like the textbook, missing the upstep next to the population trimmed mean

## Figure 16.9(b)
gf_qq(~ mean, data = GPA_sims) %>%
  gf_labs(x = "Normal score", y = "Means of resamples") %>%
  gf_qqline(linetype = "solid", color = "red")
```



```
## XX Graph doesn't look like the textbook one, missing outliers
```

Since the seed has been previously set, we do not need to set the seed in this code chunk again.

To find the 95% confidence interval for the population trimmed mean as the book does on page 16, we can type:

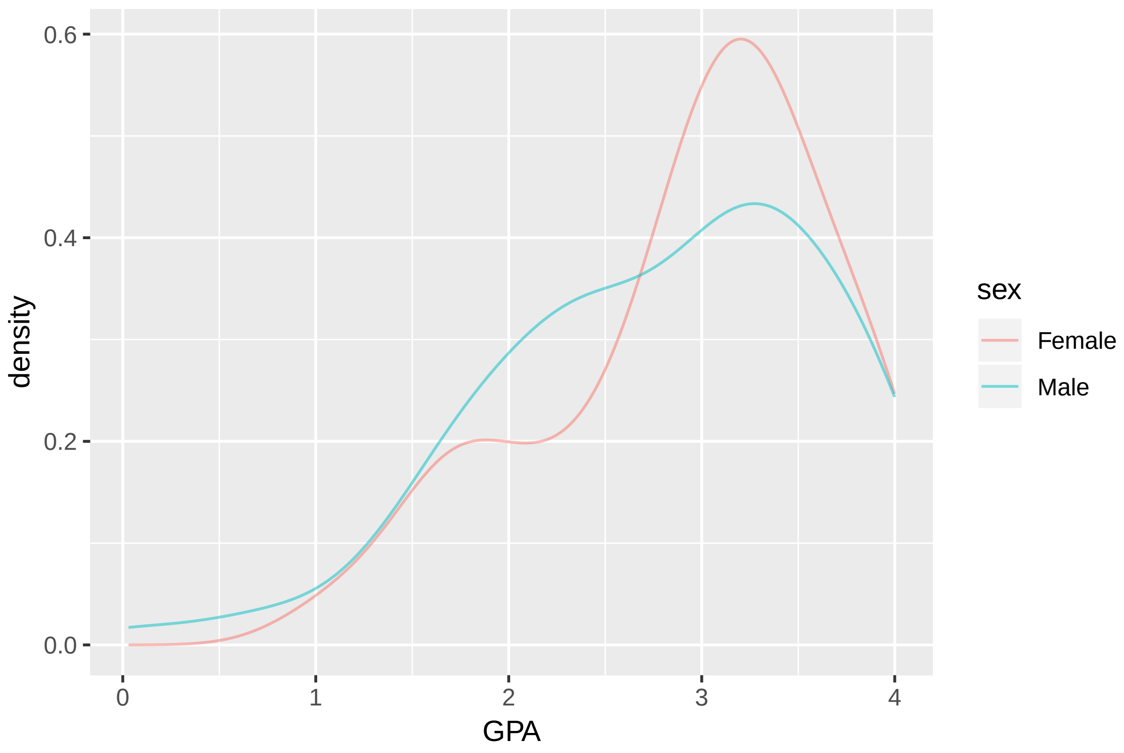
```
confint(GPA_sims, level = 0.95)
```

```
##   name    lower    upper level     method estimate
## 1 mean 2.791954 3.091326  0.95 percentile 2.949605
```

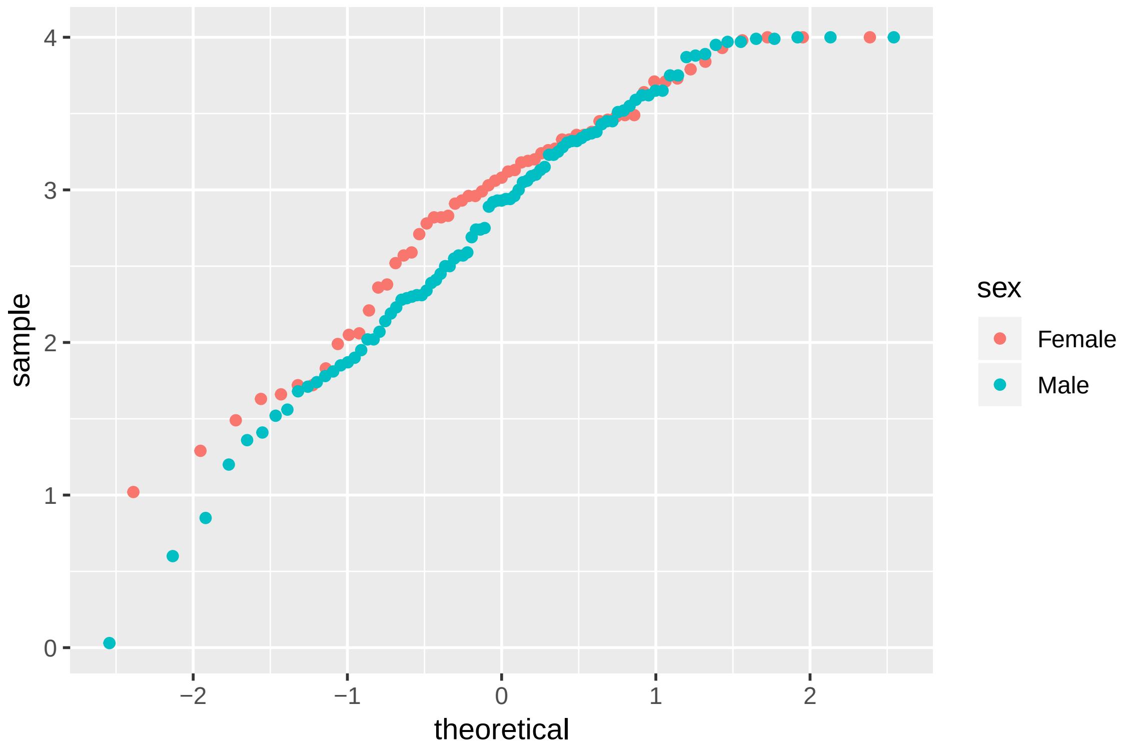
```
## XX The textbook reports 2.794, 3.106 and the standard error is 0.078.
## Now wondering if the GPA_sims is the right data
```

Below we have replicated the Density curves and Normal quantile plots of the distributions of GPA for males and females as well as the summary statistics and the bootstrap standard error for the difference in sample means (page 17-18):

```
College_GPA <- College_GPA %>%
  mutate(sex = dplyr::recode(sex,
        "1" = "Male",
        "2" = "Female"))
## Figure 16.10(a)
gf_dens(~ GPA, data = College_GPA, color = ~ sex)
```



```
## Figure 16.10(b)
gf_qq(~ GPA, data = College_GPA, color = ~ sex)
```

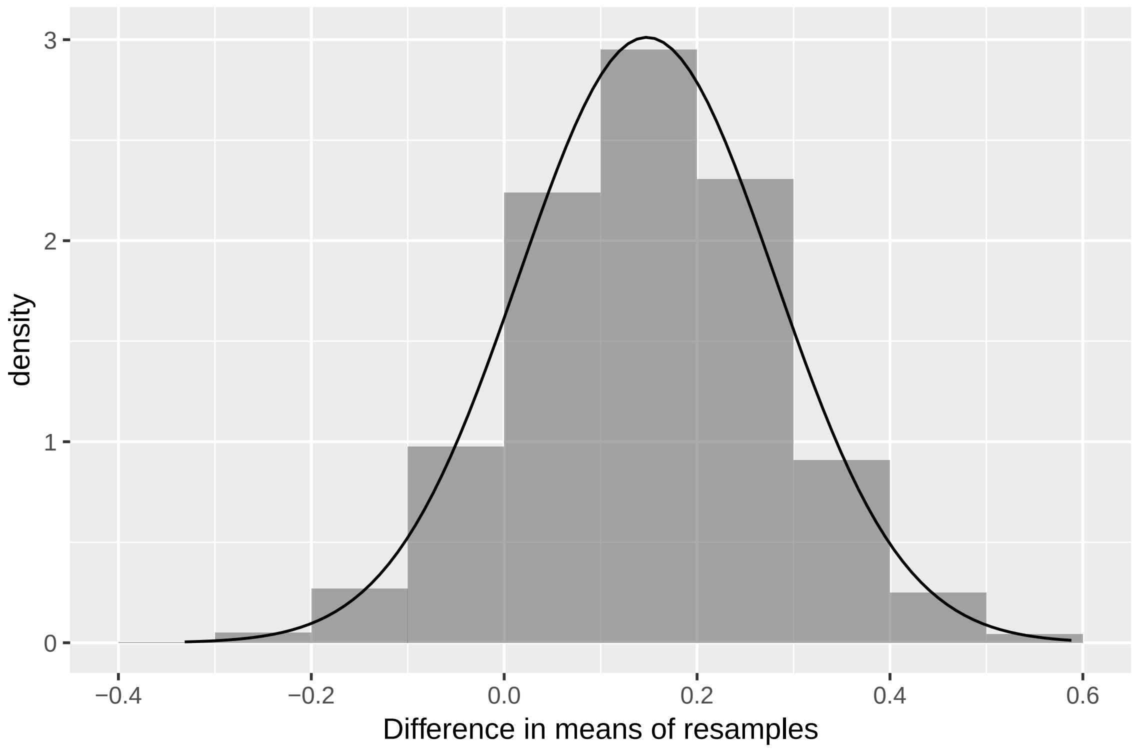


```
Summary_GPA <- cbind(
  tally(~ sex, data = College_GPA),
  mean(GPA ~ sex, data = College_GPA) %>%
    round(digits = 3),
```

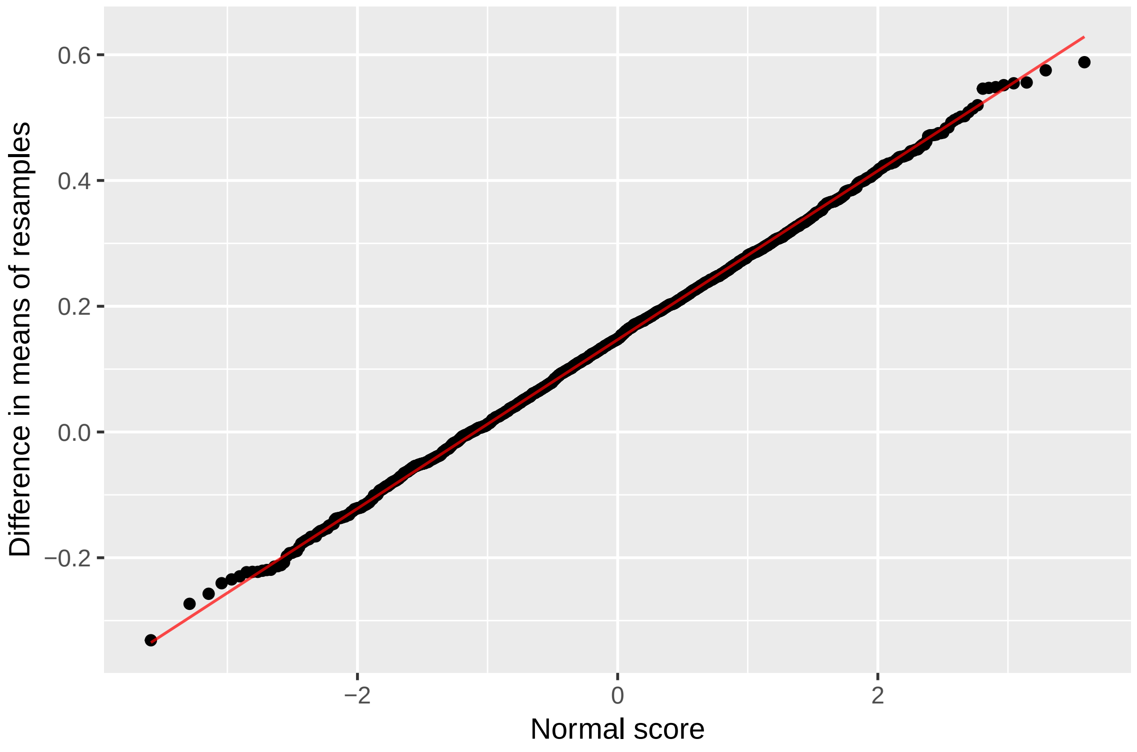
```r
  sd(GPA ~ sex, data = College_GPA) %>%
    round(digits = 3))
colnames(Summary_GPA) = c("n", "Mean", "Standard Error")
Summary_GPA
```

```
##          n  Mean Standard Error
## Female 59 2.933          0.748
## Male   91 2.784          0.859
```

```r
## Bootstrapping
numsim <- 3000
Male <- College_GPA %>%
  filter(sex == "Male")
Female <- College_GPA %>%
  filter(sex == "Female")

diffMeanGPA <- function(Male, Female){
 Sample_Male <- resample(Male)
 Sample_Female<- resample(Female)
 diff(c(mean(~ GPA, data = Sample_Male), mean(~ GPA, data = Sample_Female)))
}

GPA_sex_sims <- do(numsim) * diffMeanGPA(Male, Female)

# Figure 16.11(a)
gf_dhistogram(~ diffMeanGPA, data = GPA_sex_sims, binwidth = 0.1, center = 0.05) %>%
  gf_fitdistr(dist = "norm") %>%
  gf_labs(x = "Difference in means of resamples")
```



```
# Figure 16.11(b)
gf_qq(~ diffMeanGPA, data = GPA_sex_sims) %>%
  gf_labs(x = "Normal score", y = "Difference in means of resamples") %>%
  gf_qqline(linetype = "solid", color = "red")
```



We resample separately from the two samples, so that each of our 3000 resamples consists of two group resamples, one of size 91 drawn with replacement from the male data and one of size 59 drawn with replacement from the female data.

XX No data for Example 16.7 (page 20) “Do all daily numbers have an equal payoff”

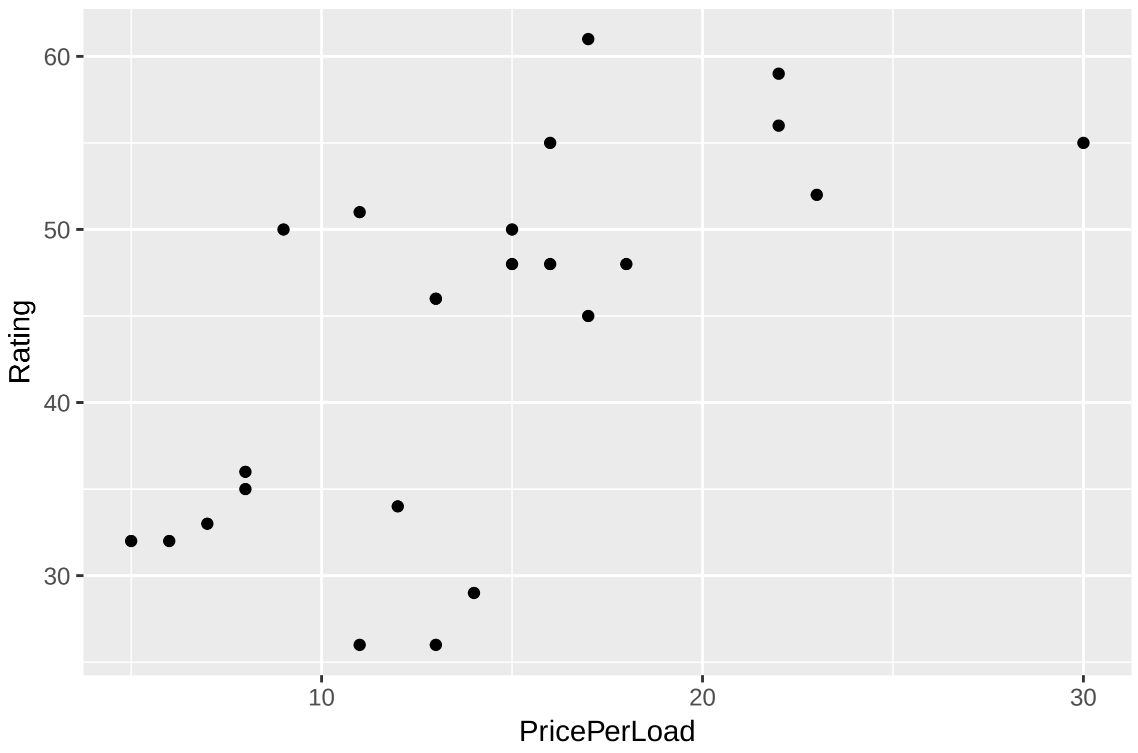
Section 16.3: How accurate is a bootstrap distribution?

Section 16.4: Bootstrap confidence intervals

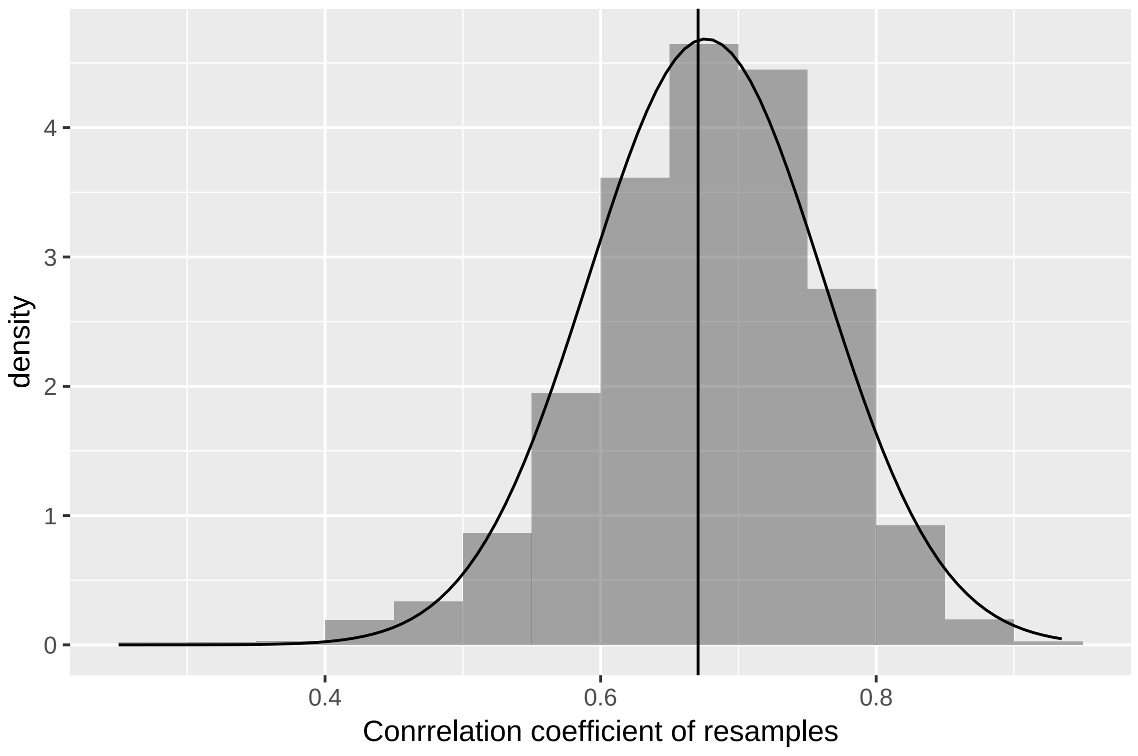
Up to this point, we have demonstrated theh use of the bootstrap to find confidence intervals of the sample mean, trimmed mean, and the difference between two means.

Now we will bootstrap the confidence intervals for the correlation coefficient, as introduced on page 35.

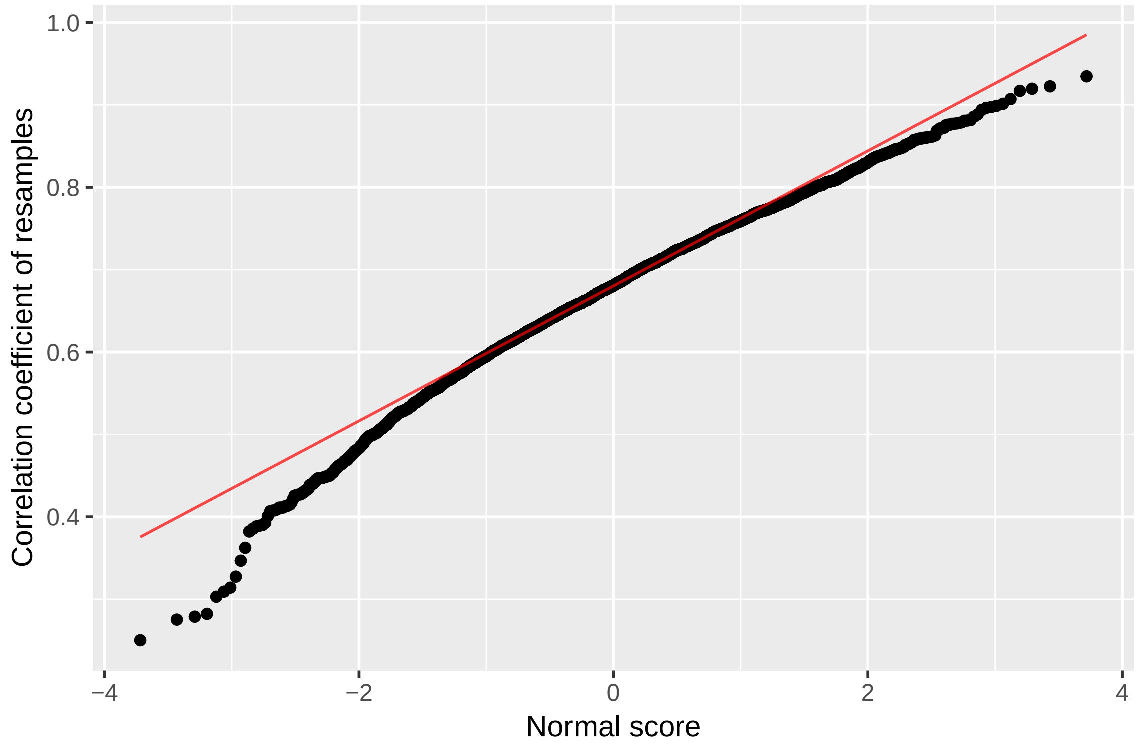
```
LAUND24 <- read_csv("https://nhorton.people.amherst.edu/ips9/data/chapter16/EG16-10LAUND24.csv")

# Figure 16.19
gf_point(Rating ~ PricePerLoad, data = LAUND24)
```



```
# Figure 16.20(a)
numsim <- 5000
cor_LAUND24 <- cor(Rating ~ PricePerLoad, data = LAUND24)
LAUND_sims <- do(numsim) * cor(Rating ~ PricePerLoad, data = resample(LAUND24))
gf_dhistogram( ~ cor, data = LAUND_sims, binwidth = 0.05, center = 0.025) %>%
  gf_fitdistr(dist = "dnorm") %>%
  gf_labs(x = "Conrrelation coefficient of resamples") %>%
  gf_vline(xintercept = cor_LAUND24)
```



```
# Figure 16.20(b)
gf_qq(~ cor, data = LAUND_sims) %>%
  gf_labs(x = "Normal score", y = "Correlation coefficient of resamples") %>%
  gf_qqline(linetype = "solid", color = "red")
```



```r
# Computing the 95% bootstap percentile interval
confint(LAUND_sims, method=c("se", "perc"))
```

```
## Warning: confint: Using df=Inf.
```

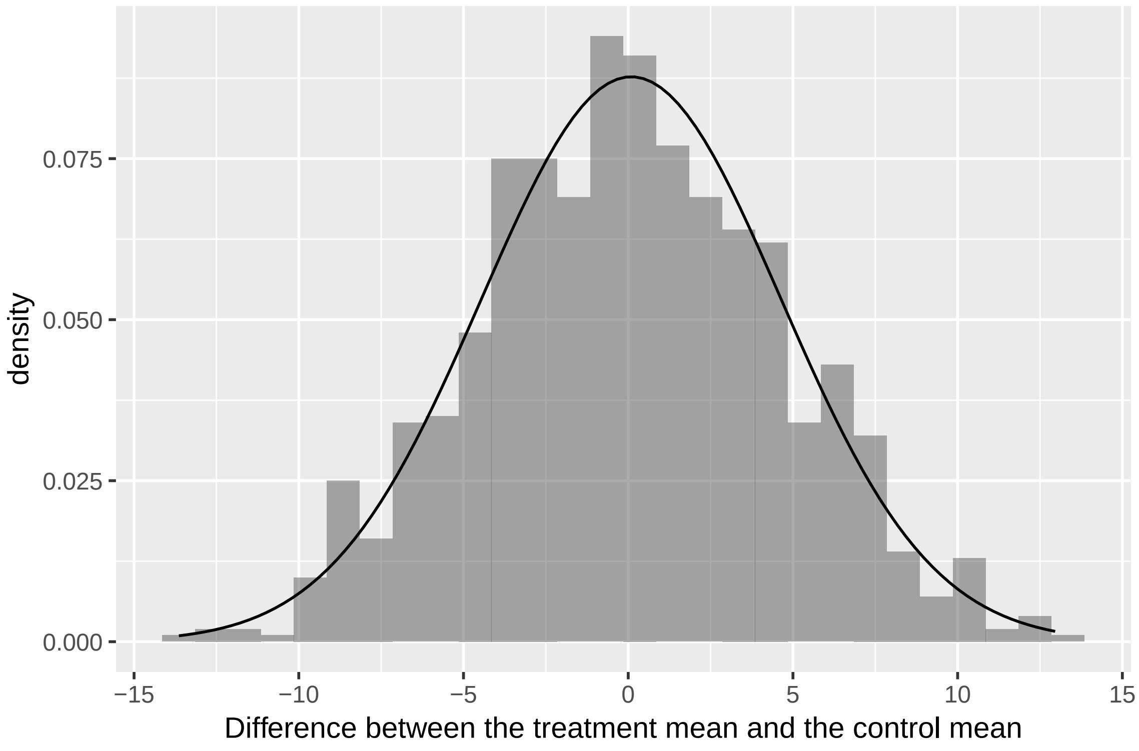
```
##   name     lower     upper level     method  estimate margin.of.error
## 1  cor 0.5095093 0.8432775  0.95     stderr 0.6707535       0.1668841
## 2  cor 0.4914274 0.8263880  0.95 percentile 0.6707535              NA
```

Section 16.5: Significance testing using permutation tests

Permutation tests use resampling to generate a null distribution for a test statistic, with each step randomly resampling without replacement and recalculating the test statistic in each permutation.

In the example provided in the textbook, the permutation test randomimzes the assignment of students to either the treament or control group to test for the effect of the treatment, "directed reading activities" in this case (page 43):

```r
DRP <- read_csv("https://nhorton.people.amherst.edu/ips9/data/chapter16/EG16-11DRP.csv")
numsim <- 1000
DRP_sim <- do(numsim) * diffmean(drp ~ shuffle(group), data = DRP)
gf_dhistogram(~ diffmean, data = DRP_sim, binwidth = 1, center = 0.35) %>%
  gf_fitdistr(dist = "norm") %>%
  gf_labs(x = "Difference between the treatment mean and the control mean")
```


density
Difference between the treatment mean and the control mean