Bootstrap In-class assignment

Example 1: F_n and bootstrap samples

Suppose that we have observed the sample

$$x = \{2, 2, 1, 1, 5, 4, 4, 3, 1, 2\}.$$

Resampling from x we select 1,2,3,4, or 5 with probabilities 0.3,0.3,0.1,0.2, and 0.1, respectively, What is the cdf F_{X^*} of a randomly selected replicate, which is exactly the eddf $F_n(x)$?

$$F_{X^*}(x) = F_n(x) = \begin{cases} 0, & x < 1; \\ 0.3, & 1 \le x < 2; \\ 0.6, & 2 \le x < 3; \\ 0.7, & 3 \le x < 4; \\ 0.9, & 4 \le x < 5; \\ 1, & x \ge 5 \end{cases}.$$

Example 2: Bootstrap estimate of standard error

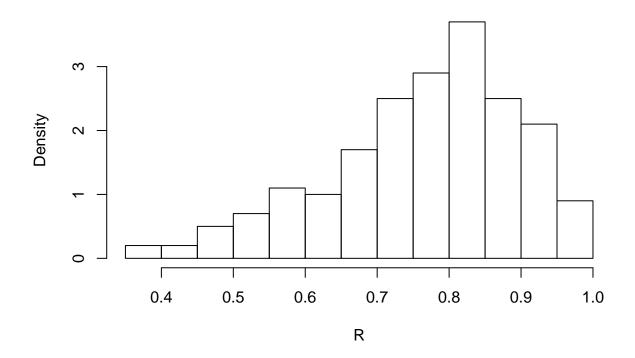
The law school data set law is available in the bootstrap package. The data frame contains LSAT (average score on law school admission test score) and GPA (average undergraduate grade-point average) for 15 law schools.

This data set is a random sample from the universe of 82 law schools in law82 (bootstrap). Estimate the correlation between LSAT and GPA scores, and compute the bootstrap estimate of the standard error of the sample correlation.

```
#library(bootstrap) #for the law data
LSAT<-c(576, 635, 558, 578, 666, 580, 555, 661, 651, 605, 653, 575, 545, 572, 594)
GPA<-c(339, 330, 281, 303, 344, 307, 300, 343, 336, 313, 312, 274, 276, 288, 296)
law=data.frame(LSAT=LSAT, GPA=GPA)
print(cor(law$LSAT, law$GPA))
```

[1] 0.7763745

Histogram of R



Example 3: Bootstrap estimate of bias

Estimate the correlation between LSAT and GPA scores, and compute the bootstrap estimate of bias in the sample correlation.

```
#sample estimate for n=15
theta.hat <- cor(law$LSAT, law$GPA)

#bootstrap estimate of bias
B <- 2000  #larger for estimating bias
n <- nrow(law)
theta.b <- numeric(B)

for (b in 1:B) {
i <- sample(1:n, size = n, replace = TRUE)
LSAT <- law$LSAT[i]
GPA <- law$GPA[i]
theta.b[b] <- cor(LSAT, GPA)
}
bias <- mean(theta.b - theta.hat)
bias</pre>
```

[1] -0.002323304

Example 4: Boostrap estimate of bias of a ratio estimate

The patch(bootstrap) data contains measurements of a certain hormone in the bloodstream of eight subjects after wearing a medical patch. The parameter of interest is

$$\theta = \frac{E(new) - E(old)}{E(old) - E(placebo)}.$$

If $|\theta| \le 0.20$, this indicates bioequivalence of the old and new batches. The statistic is \bar{Y}/\bar{Z} . Compute a bootstrap estimate of bias in the bioequivalence ratio statistic.

```
#data(patch, package="bootstrap")
#patch
#if you can't install
patch=read.csv("patch.csv")
n<-nrow(patch)</pre>
B<-2000
theta.b<-numeric (B)
theta.hat<-mean(patch$y)/mean(patch$z)</pre>
for (b in 1:B){
  i<-sample(1:n, size=n, replace=T)</pre>
  y<- patch$y[i]
  z<-patch$z[i]
  theta.b[b] <-mean(y)/mean(z)
}
bias <-mean(theta.b)-theta.hat
print(list(theta.hat=theta.hat,bias=bias))
## $theta.hat
## [1] -0.0713061
##
## $bias
## [1] 0.008551326
```