

# STAT 403 Spring 2018

## HW06

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### Q1

#### Q1-1

Since bootstrap samples are taken with replacement from sample  $X_1, X_2, \dots, X_n$ , for each value  $X_i$  in bootstrap sample,

$$P(X_i = X_1) = P(X_i = X_2) \dots = P(X_i = X_n) = \frac{1}{n}$$

The CDF of  $X_i$  can be written as

$$\begin{aligned} F_{X_i}(x) &= P(X_i \leq x) \\ &= \sum_{k=1}^n P(X_i = x_k), \text{ where } x_k \leq x, \text{ and } x_k \in x_1, x_2, \dots, x_n \\ &= \frac{1}{n} \sum_{k=1}^n I(x_k \leq x) \end{aligned}$$

The CDF of  $X_i$  is same as  $\widehat{F}_n(x)$ , the EDF of original data set. Therefore we can conclude that the bootstrap sample is an IID from EDF of original data set.

## Q1-2

$$\begin{aligned} \text{Var}(\bar{X}^*) &= \text{Var}\left(\frac{1}{n} \sum_{i=1}^n X_i\right), \text{ since } \bar{X}^* = \frac{1}{n} \sum_{i=1}^n X_i \\ &= \frac{\text{Var}(\sum_{i=1}^n X_i)}{n^2}, \text{ by property of variance} \\ &= \frac{\sum_{i=1}^n \text{Var}(X_i)}{n^2} \\ &= \frac{\text{Var}(X)}{n} \end{aligned}$$

$$\text{Note that } \text{Var}(X) = \frac{1}{n} \sum_{i=1}^n (X_i - \bar{X})^2$$

$$\text{Var}(\bar{X}^*) = \frac{\sum_{i=1}^n (X_i - \bar{X})^2}{n^2}$$

$$S_n^2 = \frac{1}{n-1} \sum_{i=1}^n (X_i - \bar{X})^2$$

$$(n-1)S_n^2 = \sum_{i=1}^n (X_i - \bar{X})^2$$

$$\text{Var}(\bar{X}^*) = \frac{(n-1)S_n^2}{n^2}$$

As  $n \rightarrow \infty$ ,  $\frac{n-1}{n^2} \rightarrow \frac{1}{n}$ . Therefore, when bootstrap sample size is large enough, variance of bootstrap sample mean is equal to  $\frac{S_n^2}{n}$ .

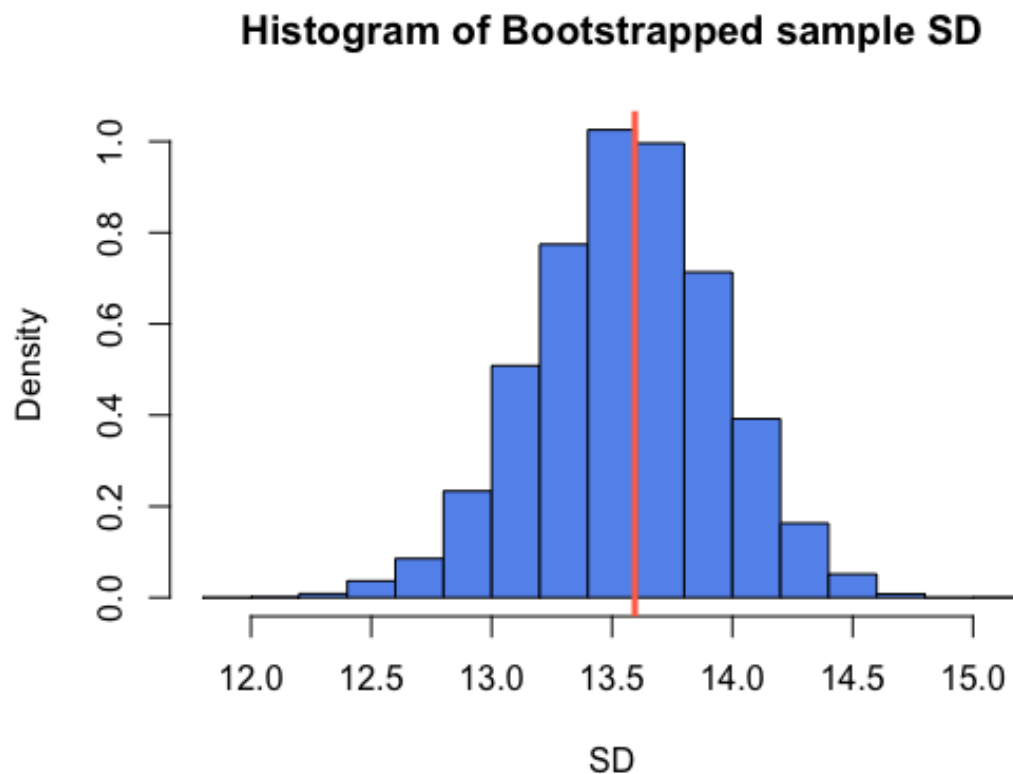
## Q2

### Q2-a

```
origin_sd <- sd(faithful$waiting)
bt_size <- 10000
sample_size <- length(faithful$waiting)
bt_result <- rep(NA, bt_size)

for (ii in 1:bt_size) {
  index <- sample(sample_size, sample_size, replace=T)
  bt_dt <- faithful$waiting[index]
  bt_result[ii] <- sd(bt_dt)
}

hist(bt_result, probability=T, col='cornflowerblue', xlab='SD',
      ylab='Density', main='Histogram of Bootstrapped sample SD')
abline(v=origin_sd, lwd=3, lty=1, col='coral1')
```



## Q2-b

```
bt_var <- sd(bt_result)^2
bt_mse <- mean((bt_result - origin_sd)^2)
> bt_var
[1] 0.147665
> bt_mse
[1] 0.1488451
```

Variance of sample SD is 0.147665, and MSE is 0.1488451.

## Q2-c

```
bt_sd <- sd(bt_result)
lower_bd <- origin_sd + qnorm(0.975) * bt_sd
upper_bd <- origin_sd - qnorm(0.975) * bt_sd
> lower_bd
[1] 14.34813
> upper_bd
[1] 12.84181
```

```
> quantile(bt_result, c(0.025, 0.975))
      2.5%      97.5%
12.78565 14.30731
```

By theorem, the 95% confidence interval is [12.84181, 14.34813]. In bootstrap samples, 95% interquantile is [12.78565, 14.30731].

## Q2-d

$$\text{p-value} = P(\text{getting value more extreme than sample SD} | H_0)$$

Since the bootstrap sample sd follows normal distribution, we may assume the sampling distribution is normal with  $\mu_0 = 15$  and  $\sigma =$  bootstrap standard deviation.

```
bt_sd <- sd(bt_result)
p_value <- 2 * pnorm(origin_sd, 15, bt_sd)

> p_value
[1] 0.0002558503
```

## Q2-e

The variance of bootstrapped samples is  $\frac{\sigma^2}{n}$ , indicating the value will decrease as sample size increases. Larger sample size minimizes the margin of error, of which smaller margin of error makes the estimation more accurate.

## Q3

### Q3-a

Regular bootstrap method to get MSE

```
admission_dt <- UCBAmissions[,1]
origin_or <- (admission_dt[1,1] * admission_dt[2,2]) /
  (admission_dt[2,1] * admission_dt[1,2])

n_male <- admission_dt[1,1] + admission_dt[2,1]
n_female <- admission_dt[1,2] + admission_dt[2,2]
n <- n_male + n_female

male_dt <- c(rep(1, admission_dt[1,1]), rep(0, admission_dt[2,1]))
female_dt <- c(rep(1, admission_dt[1,2]), rep(0, admission_dt[2,2]))

bt_ep_or <- rep(NA, N)
for (ii in 1:N) {
  male_index <- sample(n_male, n_male, replace=T)
  female_index <- sample(n_female, n_female, replace=T)
  sp_male <- male_dt[male_index]
  sp_female <- female_dt[female_index]
  male_adm <- sum(sp_male)
  male_reject <- n_male - male_adm
  female_adm <- sum(sp_female)
  female_reject <- n_female - female_adm
  sp_or <- (male_adm * female_reject) / (male_reject * female_adm)
  bt_ep_or[ii] <- sp_or
}

> bt_ep_mse
[1] 0.008787036
```

The MSE of bootstrap OR is 0.008787036.

### Q3-b

$H_0$ : no gender bias exists ( $OR = 1$ )

$H_1$ : gender bias exists ( $OR \neq 1$ )

$$p\text{-value} = P(\text{getting value more extreme than } 0.3492 | H_0)$$

We may use standard deviation of bootstrap sample as an estimator of sampling distribution standard deviation.

```
bt_ep_sd <- sd(bt_ep_or)
p_value <- 2 * pnorm(origin_or, 1, bt_ep_sd)
```

```
p_value
[1] 3.589365e-12
```

The p-value of this test is  $3.589365 \times 10^{-12}$ .

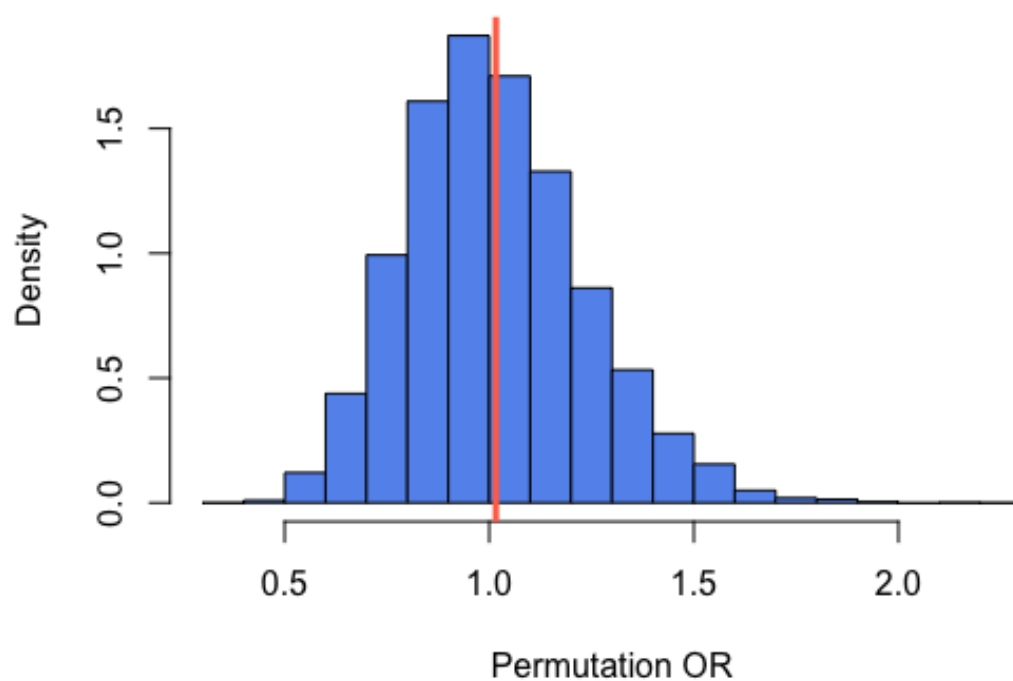
To test this hypothesis, we may also apply permutation test.

```
data_pull <- c(rep(1, admission_dt[1,1] + admission_dt[1,2]),
               rep(0, admission_dt[2,1] + admission_dt[2,2]))
```

```
N <- 10000
bt_per_or <- rep(NA, N)
for (ii in 1:N) {
  sp_index <- sample(n, n, replace=T)
  sp_dt <- data_pull[sp_index]
  sp_male <- sp_dt[1:n_male]
  sp_female <- sp_dt[(n_male+1):n]
  male_admit <- sum(sp_male)
  male_reject <- length(sp_male) - male_admit
  female_admit <- sum(sp_female)
  female_reject <- length(sp_female) - female_admit
  sp_or <- (male_admit * female_reject) / (male_reject * female_admit)
  bt_per_or[ii] <- sp_or
}
```

Since the bootstrap OR follows normal distribution, we may assume the sampling distribution is normal.

## Histogram of Permutation OR



```
bt_per_sd <- sd(bt_per_or)
p_value <- 2 * pnorm(origin_or, 1, bt_per_sd)
```

```
> p_value
[1] 0.002984116
```

The p-value of permutation test is 0.002984116.

### Q3-c

In this problem, we generated data based on parameters: number of male rejected, admitted, and number of female rejected, admitted.

Let  $\theta_1$  denotes male admission rate, and  $\theta_2$  denotes female admission rate.

$$\theta_1 = \frac{\text{\#male admitted}}{\text{\#total male applicants}}$$
$$\theta_2 = \frac{\text{\#female admitted}}{\text{\#total female applicants}}$$

For both empirical and parametric bootstrap approaches, each bootstrap sample has probability of  $\theta_1$  or  $\theta_2$  to be admitted and  $(1 - \theta_1)$  or  $(1 - \theta_2)$  to be rejected, since bootstrap is with replacement. Therefore, both empirical and parametric bootstrap samples should follow same distribution. i.e. empirical and parametric approaches are same procedure in this problem.