

# STAT641HW1

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## Exercise 1.

```
# non-parametric bootstrap for theta
library(boot)
set.seed(123) # set seed for reproducibility
x <- rgamma(200, shape = 2, scale = 5) # original data

# non-parametric bootstrap
theta_boot <- function(x, indices) {
  mean(x[indices]) / 2
}

boot(data = x, statistic = theta_boot, R = 999)
```

## ORDINARY NONPARAMETRIC BOOTSTRAP

Call:

```
boot(data = x, statistic = theta_boot, R = 999)
```

Bootstrap Statistics :

	original	bias	std. error
t1*	4.578726	0.007596511	0.2201269

```
# parametric bootstrap for theta
library(boot)
set.seed(123) # set seed for reproducibility
x <- rgamma(200, shape = 2, scale = 5) # original data
```

```
boot_theta <- function(x) mean(x) / 2

gamma_boot <- function(x, mle){
  rgamma(length(x), shape = 2, scale = mle)
}

(b <- boot(x, boot_theta, R = 1000, sim = "parametric", ran.gen = gamma_boot,
          mle = mean(x) / 2))
```

## PARAMETRIC BOOTSTRAP

Call:

```
boot(data = x, statistic = boot_theta, R = 1000, sim = "parametric",
      ran.gen = gamma_boot, mle = mean(x)/2)
```

Bootstrap Statistics :

	original	bias	std. error
t1*	4.578726	0.005143687	0.2135533

```
# mean(b$t) # bootstrap estimate of theta

# mean(b$t) - b$t0 # bootstrap bias estimate

# sd(b$t) # parametric bootstrap SE
```

## Exercise 2.

```
library(resampledData)
library(dplyr)
data("Bangladesh")
head(Bangladesh)
```

	Arsenic	Chlorine	Cobalt
1	2400	6.2	0.42
2	6	116.0	0.45
3	904	14.8	0.63

4	321	35.9	0.68
5	1280	18.9	0.58
6	151	7.8	0.35

```
chl <- with(Bangladesh, Chlorine[!is.na(Chlorine)])
```

(a)

```
# 95% confidence interval for mean chlorine level mu
library(bootstrap)
set.seed(123)

bsample <- bootstrap(chl, 5000, mean)
quantile(bsample$thetastar, probs = c(0.025, 0.975))
```

2.5%	97.5%
54.24833	104.65179

(b)

```
boot.bangladesh <- function(data, indices){
  mean(data[indices])
}
set.seed(123)
(bangladesh.boot <- boot(chl, boot.bangladesh, 5000))
```

ORDINARY NONPARAMETRIC BOOTSTRAP

Call:

```
boot(data = chl, statistic = boot.bangladesh, R = 5000)
```

Bootstrap Statistics :

	original	bias	std. error
t1*	78.08401	0.04634684	12.9565

```
boot.ci(bangladesh.boot, index = 1, type = c("perc", "bca"))
```

#### BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS

Based on 5000 bootstrap replicates

CALL :

```
boot.ci(boot.out = bangladesh.boot, type = c("perc", "bca"),
        index = 1)
```

Intervals :

Level	Percentile	BCa
95%	( 54.23, 104.66 )	( 56.79, 109.13 )

Calculations and Intervals on Original Scale

```
# bootstrap-t
pacman::p_load(boot, bootstrap)
# Statistic: mean + SE
mean_stat <- function(data, idx){
  d <- data[idx]
  est <- mean(d)
  se <- sd(d) / sqrt(length(d))
  c(est, se)
}

set.seed(123)
boot_bangladesh <- boot(chl, statistic = mean_stat, R = 5000)
boot.ci(boot_bangladesh, type = "stud")
```

#### BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS

Based on 5000 bootstrap replicates

CALL :

```
boot.ci(boot.out = boot_bangladesh, type = "stud")
```

Intervals :

Level	Studentized
95%	( 54.46, 106.96 )

Calculations and Intervals on Original Scale

All four intervals are similar towards the lower end. However, inspecting the BCa interval is shifted upward and has a larger endpoint compared to the other intervals. I would report the

BCa interval because it has second order accuracy and corrects for both bias and skewness in the bootstrap distribution.