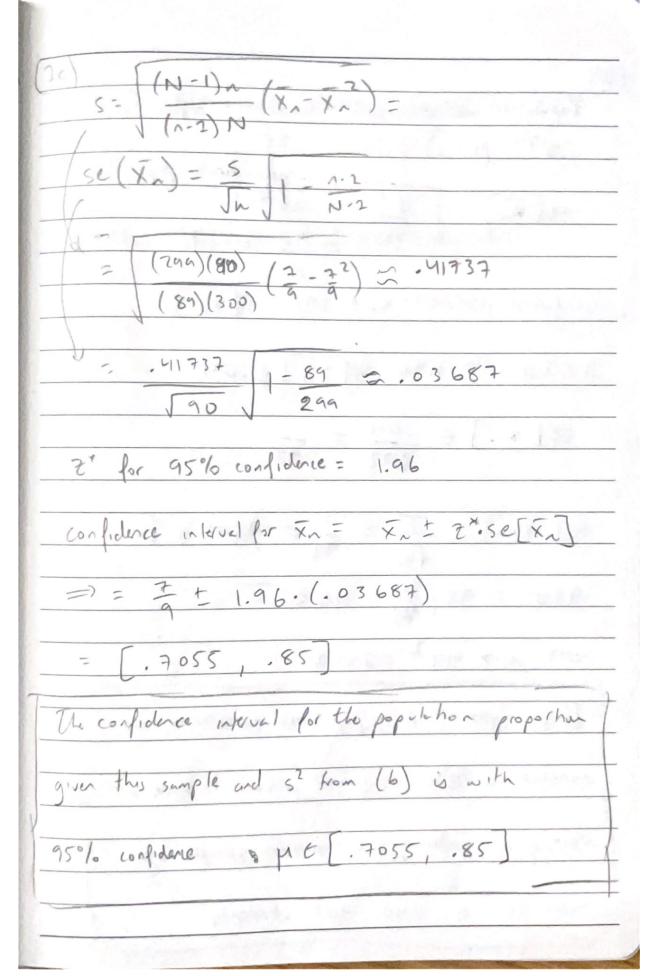
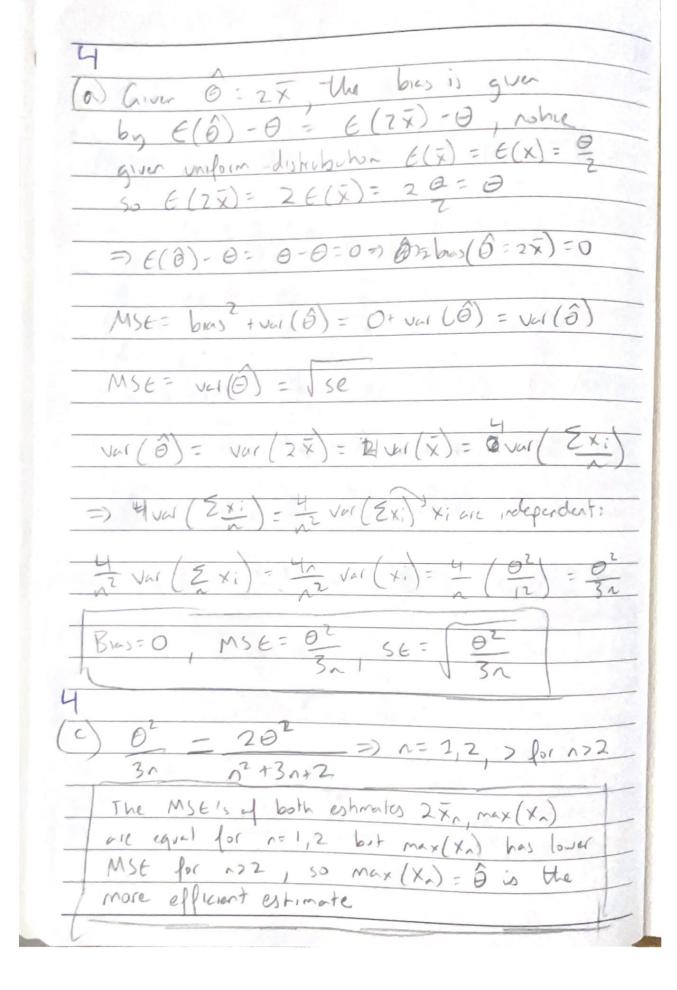
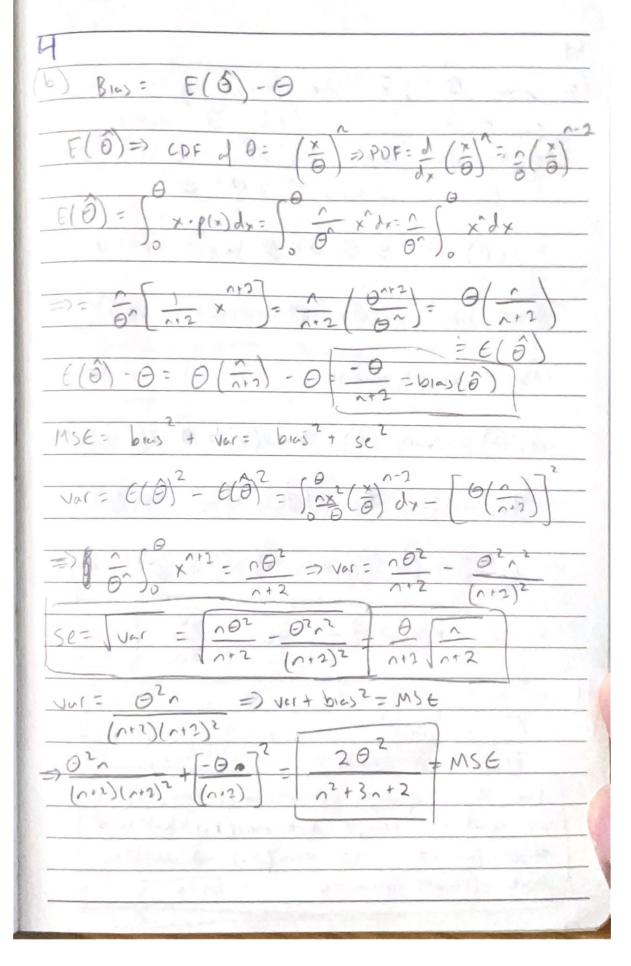
02 = E(Xi-M) = Z Xi2 - ZMX; + = 2x12 - 22 pxi + 2p2 Existra ours M - 5 M(h) + h = M - 5h 5 + h = M - h = M(1-h) this Qz = M(1-h) b) For unbiased estimate E(32)-52=0 (1-N) 1-2 Z (x;-X (1-1) 1 (2 x; 2-2x, 5 x; + 5 x, 2)) -2 (1×2-2×x2+1×x (N-2) ~ (x - x ~



(2) Population valuate worst case sceners > p=.5
Population valiance was = .25 52 = p(1-p)=(.5)2 = .25 Signore finite population
$52 = p(1-p) = (.5)^{2} = .25$ $5e(x_{n}) = 5^{2} $ $correction$ $as^{2}b = 2^{*}$
Confidence interval = \(\tau \tau \) 1.96 . Se(\(\tau \))
CI = 2.1.96. se(x,) <.04
$Se[X_n] \leq \frac{.04}{3.92} = \frac{1}{98}$
Se[Xn] = 5 = 985 = 5n
980 = 98 (1) = 49 = [n
=) NZ 492 = 2402
Thus, ignoring haste population correction, we
Conclude a 95% confidence interval to have at
most a .04 width, the minimum sample size
must be nz zyoi=492 students





```
clc; clear; close all;
```

Problem 3

```
data = textread("C:\Users\sayuj\OneDrive - California Institute of
Technology\ACM_157\birth.txt");
birth_weights = data(:, 1);
birth_weights = birth_weights(birth_weights ~= 999);
birth_weights = birth_weights * 0.0283495;
```

Part A

```
population_mean = mean(birth_weights)

population_mean = 3.3899

n = 100;
sample = datasample(birth_weights, 100, 'Replace', false);
sample_mean = mean(sample)

sample_mean = 3.4357

exact_se = std(birth_weights) / sqrt(n) * sqrt(1 - (n - 1) / (length(birth_weights) - 1))

exact_se = 0.0496
```

From the code above, we have calculated the population mean for the birth weights to be 3.3899, the sample mean for a size n = 100 sample to vary closesly around that value, and the exact standard error of mean estimate for n = 100 samples to be 0.0496

Part B results

```
b_results = bootstrap_algo_b(100, birth_weights, sample)
```

```
b results = 0.0495
```

From the results of running this (B) bootstrapping algorithm multiple times it appears that the standard error of this estimation varies around the true exact value.

Part C results

```
c_results = bootstrap_algo_c(100, birth_weights, sample)
c_results = 0.0491
```

From the results of running this (C) bootstrapping algorithm multiple times it appears that the standard error of this estimation varies around the true exact value.

Part D results

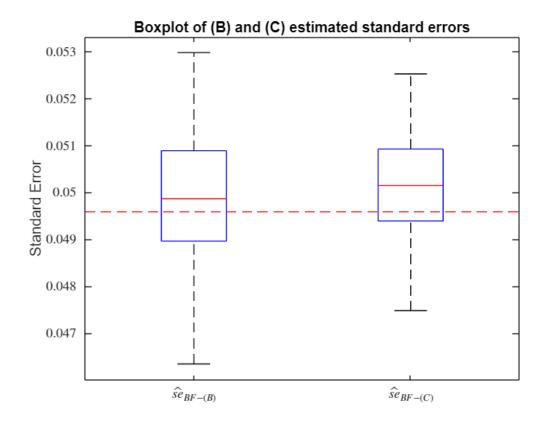
```
algo_b_se = zeros(100, 1);
algo_c_se = zeros(100, 1);
```

```
for s = 1:100
    algo_b_se(s) = bootstrap_algo_b(100, birth_weights, sample);
    algo_c_se(s) = bootstrap_algo_c(100, birth_weights, sample);
end

boxplot([algo_b_se, algo_c_se])

hold on;
line(xlim, [exact_se, exact_se], 'Color', 'r', 'LineStyle', '--');

ylabel('Standard Error');
title('Boxplot of (B) and (C) estimated standard errors');
labels = {'$\hat{se}_{BF-(B)}$', '$\hat{se}_{BF-(C)}$'};
set(gca, 'XTickLabel', labels, 'TickLabelInterpreter', 'latex')
```



From running bootstrapping algorithms B and C 100 times on the same sample and analyzing the boxplot of the results, both estimates seem to accurately estimate the exact standard error pretty well as the true exact standard error (dashed red line) is contained within the mid 50% quartiles of results for both bootstrapping algorithms. Based on the boxplots it also seems possible that the variance of algorithm C's results is a little smaller than algorithm B but there is not conclusive statistically evidence that this is true.

Part B Function Code

```
function bootstrap_se = bootstrap_algo_b(n, birth_weights, sample)
   bootstrap_reps = floor(length(birth_weights) / n);
   bootstrapped_population = repelem(sample, bootstrap_reps);

bootstrap_samples = 1000;
   sample_means = zeros(bootstrap_samples, 1);

for i = 1:bootstrap_samples
        sample_data = datasample(bootstrapped_population, n, 'Replace', false);

   sample_mean = mean(sample_data);

   sample_means(i) = sample_mean;
end

bootstrap_se = sqrt(sum((sample_means - (mean(sample_means))).^2) /
bootstrap_samples);
end
```

Part C Function Code

```
function new bootstrap se = bootstrap algo c(n, birth weights, sample)
    bootstrap_reps = (length(birth_weights) / n);
    bootstrapped population 1 = repelem(sample, floor(bootstrap reps));
    bootstrapped population 2 = repelem(sample, ceil(bootstrap reps));
    r = length(birth_weights) - (floor(bootstrap_reps) * n);
    p = (1 - r / n) * (1 - r / (length(birth_weights) + 1));
    bootstrap samples = 1000;
    sample means = zeros(bootstrap samples, 1);
   for i = 1:bootstrap_samples
        if rand > p
            sample_data = datasample(bootstrapped_population_1, n, 'Replace',
false);
            sample_mean = mean(sample_data);
            sample means(i) = sample mean;
        else
            sample_data = datasample(bootstrapped_population_2, n, 'Replace',
false);
            sample mean = mean(sample data);
            sample_means(i) = sample_mean;
```

```
end
end

% sum((sample_means - (mean(sample_means))).^2)

new_bootstrap_se = sqrt(sum((sample_means - (mean(sample_means))).^2) /
bootstrap_samples);
end
```