Math 3070 § 1. **Parametric Bootstrapping Example:** Name: Example
Treibergs **Find Standard Error and Bias of s.** June 27, 2011

This is an example of Parametric Bootstrapping to find the approximate standard error and bias of a statistic. We use the Bar Soap data encountered before. A QQ-Plot shows that the sample is reasonably normal, so we assume it is taken from the distribution $N(\mu, sigma)$. The sample mean $\bar{x}$ and standard deviation s are estimators for μ and σ. We are interested in the standard error of the sample standard deviation. We know that the sample variance s^2 is an unbiased estimator for σ^2, but because we make a nonlinear transformation, s is not necessarily an unbiased estimator for σ. In principle, we could derive the theoretical standard error knowing that it is the square root of the sample variance which satisfies a chi-squared distribution.

But, now with availability of computing power, it is easier just to simulate and measure! The idea is to take a random sample of size n from $N(\bar{x}, s)$, call it $x_1^*, \ldots, x_n^*$, take its standard deviation and call that the first bootstrapped estimate s_1^*. We repeat B times to get simulated sd's $s_1^*, s_2^*, \ldots, s_B^*$ and then the mean and standard deviations give the bootstrapped estimates

$$\overline{s^*} = \frac{1}{B}\sum_{i=1}^{B} s_i^*; \qquad S_{s^*} = \sqrt{\frac{1}{B-1}\sum_{i=1}^{B}\left(s_i^* - \overline{s^*}\right)^2}.$$

S_{s^*} is an estimate for the standard error σ_s. However, ve have to correct for bias. Denote bias of the sample standard deviation by

$$b_s = \mathrm{E}(s) - \sigma.$$

An estimate for the bias is given by

$$\widehat{b_s} = \overline{s^*} - s$$

which is the difference of the performance of the sample standard deviations against the bootstrap population standard deviation s. If $\widehat{b_s}$ is negative then the sample standard deviation is underestimating the population sd. Since we are simulating a population whose parameters are close to the background $N(\mu, \sigma)$, the bias in the bootstrap sample will be close to the background sample. Thus the bias corrected estimate of the background sd is

$$s^{**} \approx s - \widehat{b_s}.$$

The bias also influences the standard error. Indeed, the square of the standard error is

$$\begin{aligned}
\sigma_s^2 &= \mathrm{E}\left([S-\sigma]^2\right)\\
&= \mathrm{E}\left([S - \mathrm{E}(S) + \mathrm{E}(S) - \sigma]^2\right)\\
&= \mathrm{E}\left([S - \mathrm{E}(S)]^2 + 2[S - \mathrm{E}(S)][\mathrm{E}(S) - \sigma] + [\mathrm{E}(S) - \sigma]^2\right)\\
&= \mathrm{E}\left([S - \mathrm{E}(S)]^2\right) + 2\mathrm{E}\left(S - \mathrm{E}(S)\right)[\mathrm{E}(S) - \sigma] + \mathrm{E}\left([\mathrm{E}(S) - \sigma]^2\right)\\
&= \mathrm{E}\left([S - \mathrm{E}(S)]^2\right) + 0 + b_s^2\\
&\approx S_{s^*}^2 + (\overline{s^*} - s)^2.
\end{aligned}$$

Thus the bias corrected approximate standard error is

$$se^{**} = \sqrt{S_{s^*}^2 + \widehat{b_s}^{\,2}}.$$

R Session:

```
R version 2.11.1 (2010-05-31)
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[R.app GUI 1.34 (5589) i386-apple-darwin9.8.0]

[Workspace restored from /home/1004/ma/treibergs/.RData]

> tt <- read.table("M3073BarSoapData.txt",header=TRUE)
> attach (tt)
> tt
   Weights
1     11.6
2     12.6
3     12.7
4     12.8
5     13.1
6     13.3
7     13.6
8     13.7
9     13.8
10    14.1
11    14.3
12    14.3
13    14.6
14    14.8
15    15.1
16    15.2
17    15.6
18    15.6
19    15.7
20    15.8
21    15.8
22    15.9
```
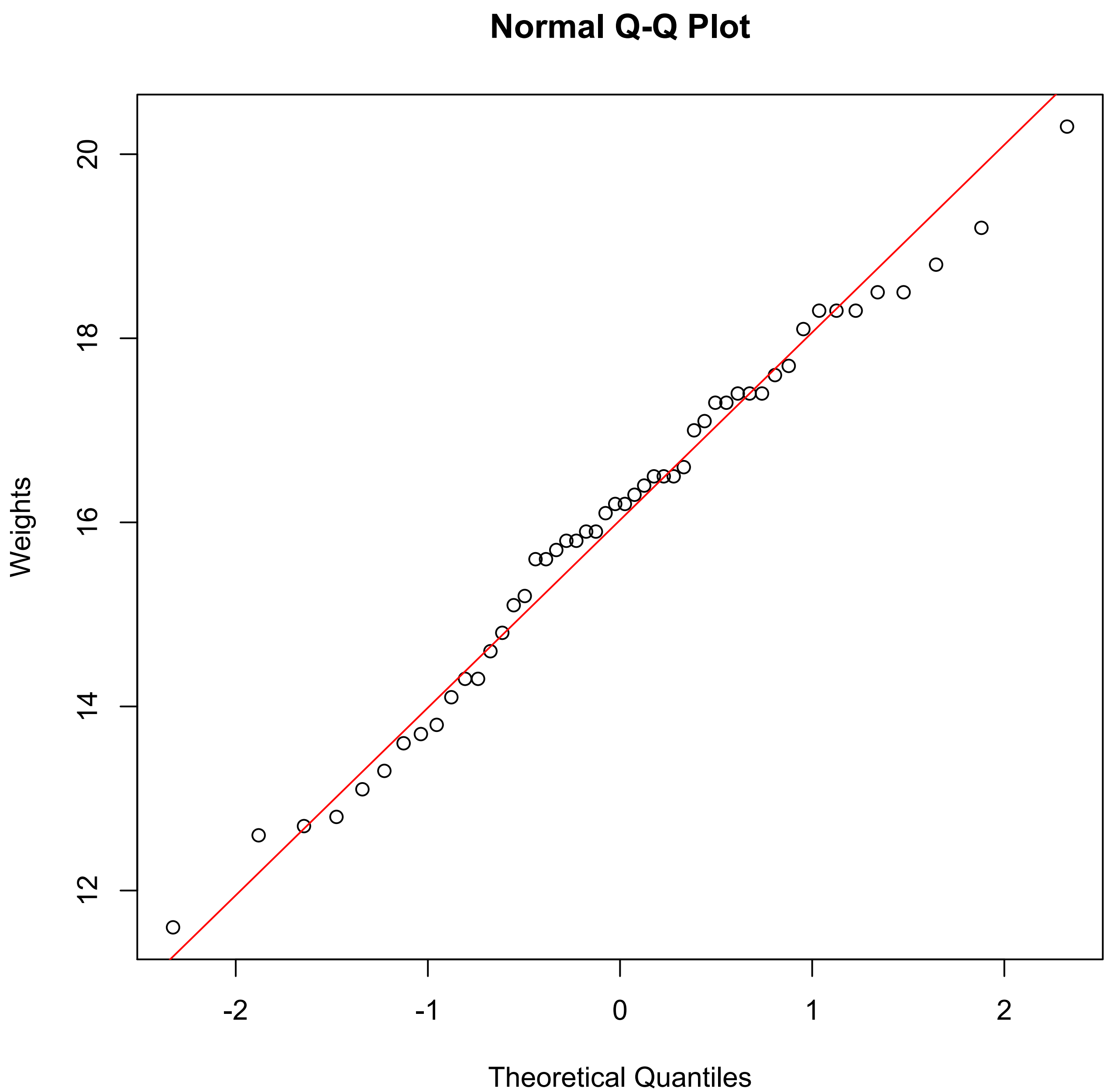
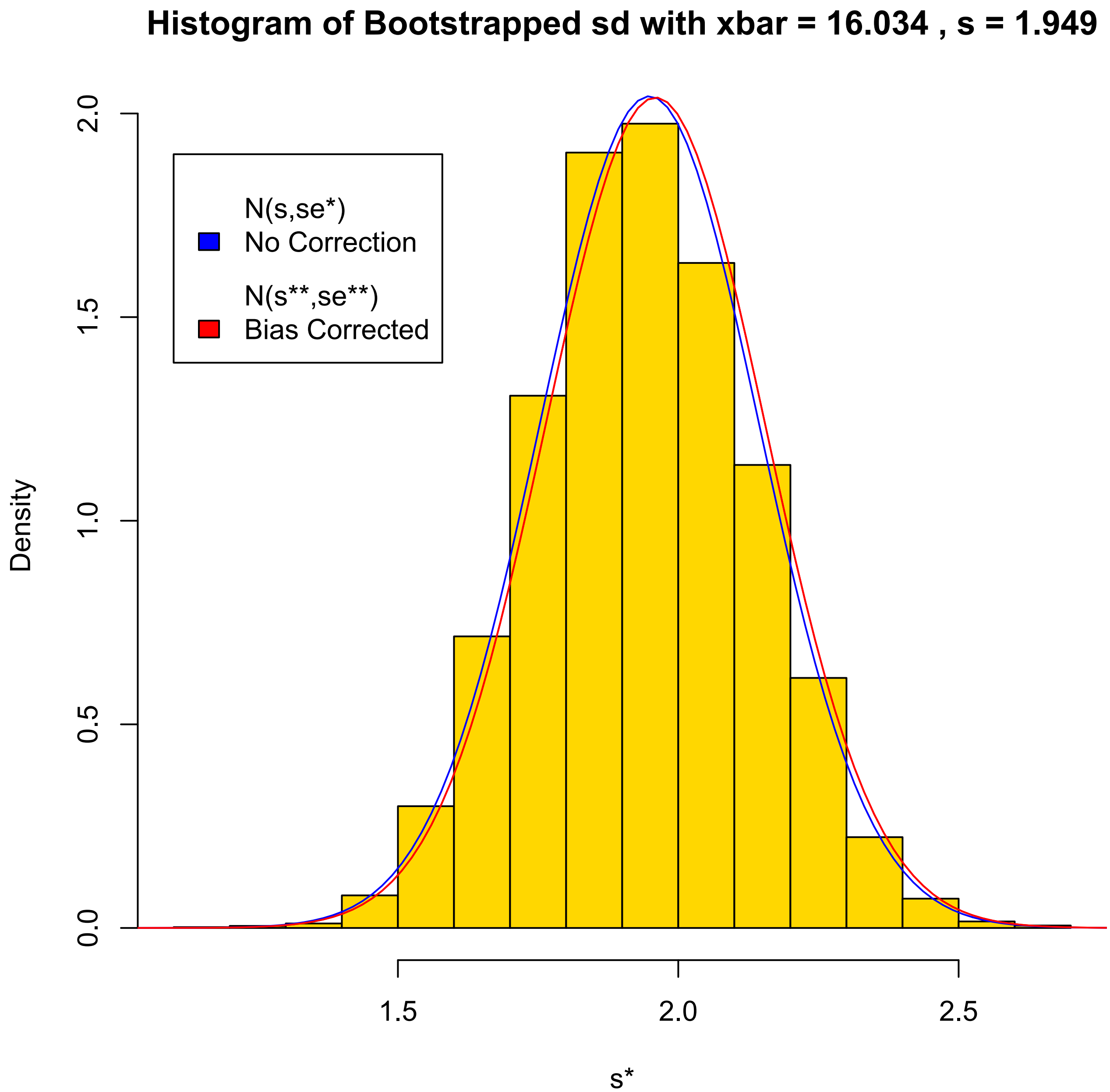

23	15.9
24	16.1
25	16.2
26	16.2
27	16.3
28	16.4
29	16.5
30	16.5
31	16.5
32	16.6
33	17.0
34	17.1
35	17.3
36	17.3
37	17.4
38	17.4
39	17.4
40	17.6
41	17.7
42	18.1
43	18.3
44	18.3
45	18.3
46	18.5
47	18.5
48	18.8
49	19.2
50	20.3

```
> ################ CHECK NORMALITY OF THE BACKGROUND POPULATION #################
> qqnorm(Weights, ylab="Weights")
> qqline(Weights, col=2)
> # M3074SoapBoot1.pdf
> # Looks Pretty normal
```



```
> ############# FIND DISTRIBUTION PARAMETERS ####################################
> xbar <- mean(Weights); xbar
[1] 16.034
> s <- sd(Weights); s
[1] 1.948585
>
> ############## BOOTSTRAP SIMULATION FROM APPROXIMATE BACKGROUND POP. ##########
>
> # Sample size  n = 50,   No. Bootstrap Samples  B = 10,000
>
> sstar <- replicate(10000,sd(rnorm(50,xbar,s)))
>
> # The bootstrap sample mean gives biased samples.
> sstarbar <- mean(sstar); sstarbar
[1] 1.937850
>
> # The bootstrap sd gives the biased approximate se
> sestar <- sd(sstar); sestar
[1] 0.1953213
>
> # The approximate bias from the bootstrap sample.
> bias <- sstarbar-s; bias
[1] -0.01073481
>
> # Correct the estimated sd of the background population
> s-bias
[1] 1.95932
>
> # Correct the estimated se of the bootstrapped sample
>
> sestarstar <- sqrt(sestar^2 + bias^2); sestarstar
[1] 0.1956161
>
>
> ss <- seq(.7,3.8,1/57)
> sigmahathat <- s-bias
> lines(ss, dnorm(ss,xbar,s),col=4)
> lines(ss, dnorm(ss,s,sestar),col=4)
> lines(ss, dnorm(ss,sigmahathat,sestarstar),col=3)
>
> ######## HISTOGRAM OF BOOTSTRAPPED SAMPLE s* WITH NORMAL SUPERIMPOSED ##########
>
> hist(sstar, xlab= "s*", main = paste("Histogram of Bootstrapped sd with xbar =",
+ xb, ", s =", sb), col = "gold", freq = F)
> # Plot normals with bootstrapped mean and sd
> # Uncorrected N(s,sestar)   Corrected N(sigmahathat,sestarstar)
> lines(ss, dnorm(ss,s,sestar),col=4)
> lines(ss, dnorm(ss,sigmahathat,sestarstar),col=2)
> legend(1.1, 1.9, legend = c("N(s,se*)\nNo Correction\n",
+ "N(s**,se**)\nBias Corrected\n"), fill = c(4,2), bg = "white")
> # M3074SoapBoot2.pdf
```


Histogram of Bootstrapped sd with xbar = 16.034 , s = 1.949
N(s,se*)
No Correction
N(s**,se**)
Bias Corrected
Density
0.0
0.5
1.0
1.5
2.0
1.5
2.0
2.5
s*