

EEB 581, Problem Set Eight

Solutions

Consider the following 25 data points (to save retyping, this list is also on the website as a text link)

8.26 6.33 10.4 5.27 5.35 5.61 6.12 6.19 5.2 7.01 8.74 7.78 7.02
6 6.5 5.8 5.12 7.41 6.52 6.21 12.28 5.6 5.38 6.6 8.74

Using this data

- 1: Using a randomization test, what is the p value for a test that the mean = 8?

Assuming the distribution is symmetric about the mean, we expected equal numbers above and below the mean, while we have 5 above the mean and 20 below. Recall that since we really don't care which number is in excess, this is a two-sided test, and we need to compute the probability of seeing 5 (or fewer) above the mean and 5 (or fewer) below the mean. Under the null hypothesis, the expected number k is distribution as a binomial with $n = 25$ and $p = 1/2$. In R, `> pbinom(5, 25, 0.5)` returns the probability that $k \leq 5$, or 0.002038658. Likewise, the chance of seeing 5 or fewer below the mean (i.e. $k \geq 20$) is `> 1 - pbinom(20, 25, 0.5)`, or 0.0004552603. Hence, the probability of seeing something this extreme is 0.002493918, or 0.25%.

- 2: What is the jackknife estimate, its standard error, and the approximate confidence intervals for the estimated skew,

$$\widehat{S}_3 = \frac{1}{n} \sum_i^n (x_i - \bar{x})^3$$

Using the R code from the the R bootstrap notes, we first need to define the skew. Let \mathbf{x} be the data vector, then define the skew with the function `SK`,

```
> SK <- function(x) sum((x-mean(x))^3) /length(x)
```

Here (from the notes) is the R code to bootstrap this data.

```
jack <- numeric(length(x)-1)
```

```
pseudo <- numeric(length(x))
```

```
for (i in 1:length(x))
```

```
{ for (j in 1:length(x))
```

```
{if(j < i) jack[j] <- x[j] else if(j > i) jack[j-1] <- x[j]}
```

```
pseudo[i] <- length(x)*SK(x) -(length(x)-1)*SK(jack)}
```

The jackknife estimator is the mean of the pseudovalues,

```
> mean(pseudo)
```

```
[1] 8.735525
```

The standard error is the square root of the variance of the pseudovalues,

```
> sqrt(var(pseudo)/length(x))
```

```
[1] 5.3032
```

The approximate 95% confidence interval is given by $\text{mean}(\text{pseudo}) \pm t_{0.975, n-1} \sqrt{\text{var}(\text{pseudo})/n}$

Using R, the upper and lower limits become

```
> mean(pseudo) + qt(0.975, length(x)-1)*sqrt(var(pseudo)/length(x))
```

```
[1] 19.68079
```

```
> mean(pseudo) - qt(0.975, length(x)-1)*sqrt(var(pseudo)/length(x))
```

```
[1]-2.209743
```

3: Using 1000 bootstrap samples, consider an estimate of the scaled kurtosis,

$$\hat{K} = \frac{1}{n} \sum_i^n (x_i - \bar{x})^4 - 3 \left(\frac{1}{n} \sum_i^n (x_i - \bar{x})^2 \right)^2$$

Again, letting \mathbf{x} be the data vector, then the estimated kurtosis is given by the function `kur`,

```
> kur <- function(x) sum((x-mean(x))^4)/length(x) -
  3*(sum((x-mean(x))^2)/length(x))^2
To generate 1000 bootstrap values the R code from the bootstrap notes is
> boot <- numeric(1000)
for (i in 1:1000) boot[i] <- kur(sample(x,replace=T))
```

(a) Plot the distribution of bootstrap values

```
> hist(boot) yields
The bootstrap estimator becomes
> mean(boot)
[1] 11.53792
```

(b) What is the estimated bias and the standard deviation for \hat{K} ?

```
> bias <- mean(boot) - kur(x)
[1] -7.30799
> sqrt(var(boot))
[1] 13.27730
```

(c) Using the results for (a), what is an approximate 95% (normally-assumption) confidence interval for K ?

Assuming normality, the approximate 95% confidence interval is given by

$$\hat{K} \pm 1.96\sqrt{\text{Var}(\text{bootstrap})}$$

(or adjusting for the bias an lower and upper values of

```
> kur(x) - bias - 1.96*sqrt(var(boot))
[1] 0.1303970
> kur(x) - bias + 1.96*sqrt(var(boot))
[1] 52.1774
```

(d) Compute Efron's 95% confidence limit for this data.

```
> quantile(boot,0.975)
[1] 36.45404
```

and

```
> quantile(boot,0.025)
[1] -8.53793
```

(e) Compute Hall's 95% confidence limit for this data.

```
> 2*kur(x) - quantile(boot,0.025)
[1] 46.22974
```

and

```
> 2*kur(x) - quantile(boot,0.975)
[1] 1.237769
```

Fun R fact. If \mathbf{x} is a vector of data, then the R command `sample(x,replace=T)` returns a sampling with replacement vector of the data in \mathbf{x} , i.e., a bootstrap sample.