HW 1 #65

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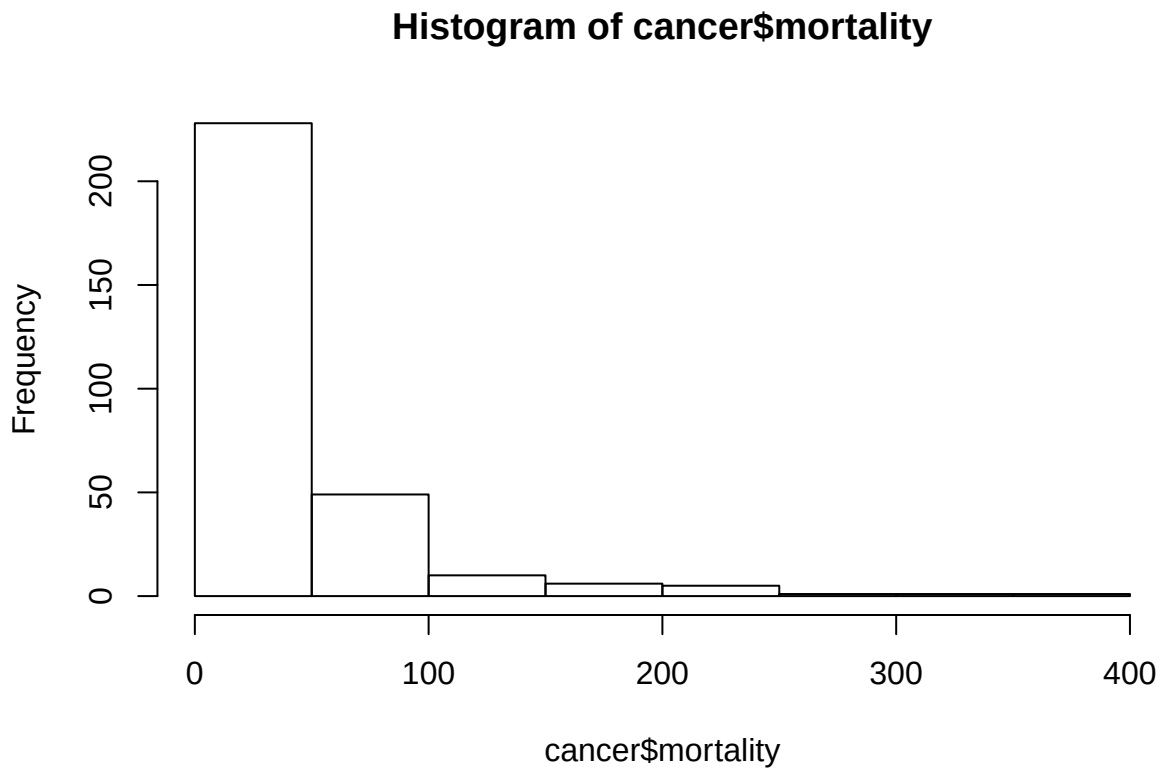
Parts a, b, c, d, f

```
# a.
hist(cancer$mortality, freq = T)
```




```
# b.
mean(cancer$mortality)
```

```
## [1] 39.85714
```

```
sum(cancer$mortality)
```

```
## [1] 11997
```

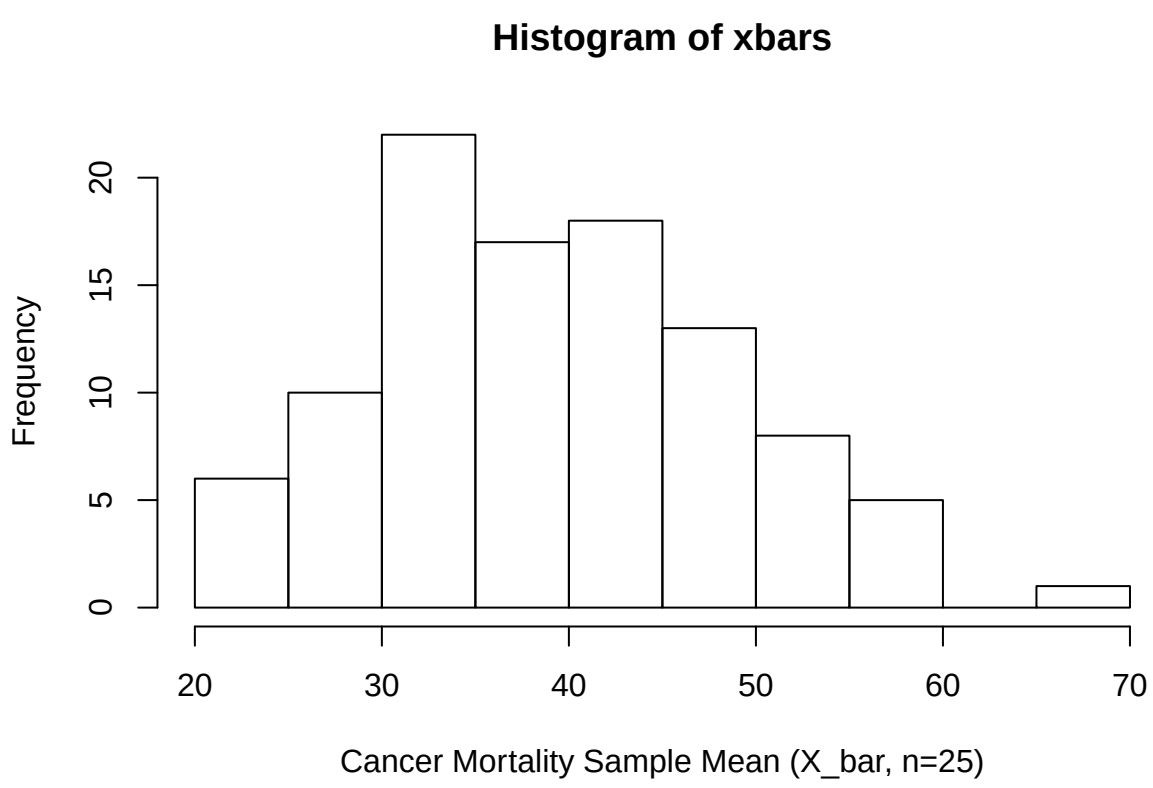
```r
(length(cancer$mortality)-1)/length(cancer$mortality)*var(cancer$mortality) #population var
```

```
## [1] 2590.103
```

```r
(length(cancer$mortality)-1)/length(cancer$mortality)*sd(cancer$mortality) #pop SD
```

```
## [1] 50.80844
```

```r
# Note: Since the variance function in R uses the n-1 in the denominator, I modify
#the result to reflect the actual population variance, not the estimator.

# c. Simulate sampling distribution of x_bar with n=25

xbars <- numeric(100)
for(i in 1:100){
  xbars[i] <- mean(sample(cancer$mortality, 25, replace = F))
}
hist(xbars, freq = T, xlab = "Cancer Mortality Sample Mean (X_bar, n=25)")
```




```r
# d.
x_bar <- mean(sample(cancer$mortality, 25, replace = F)) #n=25
x_bar #mean cancer mortality estimator
```

```
## [1] 37.96
```

```r
total <- x_bar*301 #total cancer mortality estimator
total
```

```
## [1] 11425.96
```

```r
# e.
popvar <- (1-(1/301))*var(cancer$mortality)
sqrt(popvar) # pop SD
```

```
## [1] 50.89305
```

```r
# f.
var_xbar <- (var(cancer$mortality)/25)*(1-(25/301))
lower_lim <- x_bar - (1.96*sqrt(var_xbar))
upper_lim <- x_bar + (1.96*sqrt(var_xbar))
c(lower_lim, upper_lim) # 95% CI for X_bar
```

```
## [1] 18.82456 57.09544
```

```r
#I am 95% confident that the average cancer mortality per county
#in the three states is contained within the values above

var_total <- (301^2)*var_xbar
lower_lim <- total - 1.96*sqrt(var_total)
upper_lim <- total + 1.96*sqrt(var_total)
c(lower_lim, upper_lim) # 95% CI for T
```

```
## [1]  5666.192 17185.728
```

```r
#I am 95% confident that the total cancer for all counties
#in the three states is contained within the values above

#Conclusion: Yes, the intervals cover the population values.
```

Part g. (repeat for n=100)

```r
# d.
x_bar <- mean(sample(cancer$mortality, 100, replace = F)) #n=100
x_bar #mean cancer mortality estimator
```

```
## [1] 43.32
```

```r
total <- x_bar*301 #total cancer mortality estimator
total
```

```
## [1] 13039.32
```

```r
# e.
popvar <- (1-(1/301))*var(cancer$mortality)
sqrt(popvar) # pop SD
```

```
## [1] 50.89305
```

```r
# f.
var_xbar <- (var(cancer$mortality)/100)*(1-(100/301))
lower_lim <- x_bar - (1.96*sqrt(var_xbar))
upper_lim <- x_bar + (1.96*sqrt(var_xbar))
c(lower_lim, upper_lim) # 95% CI for X_bar
```

```
## [1] 35.15508 51.48492
```

```r
#I am 95% confident that the average cancer mortality per county
#in the three states is contained within the values above

var_total <- (301^2)*var_xbar
lower_lim <- total - 1.96*sqrt(var_total)
upper_lim <- total + 1.96*sqrt(var_total)
c(lower_lim, upper_lim) # 95% CI for T
```

```
## [1] 10581.68 15496.96
```

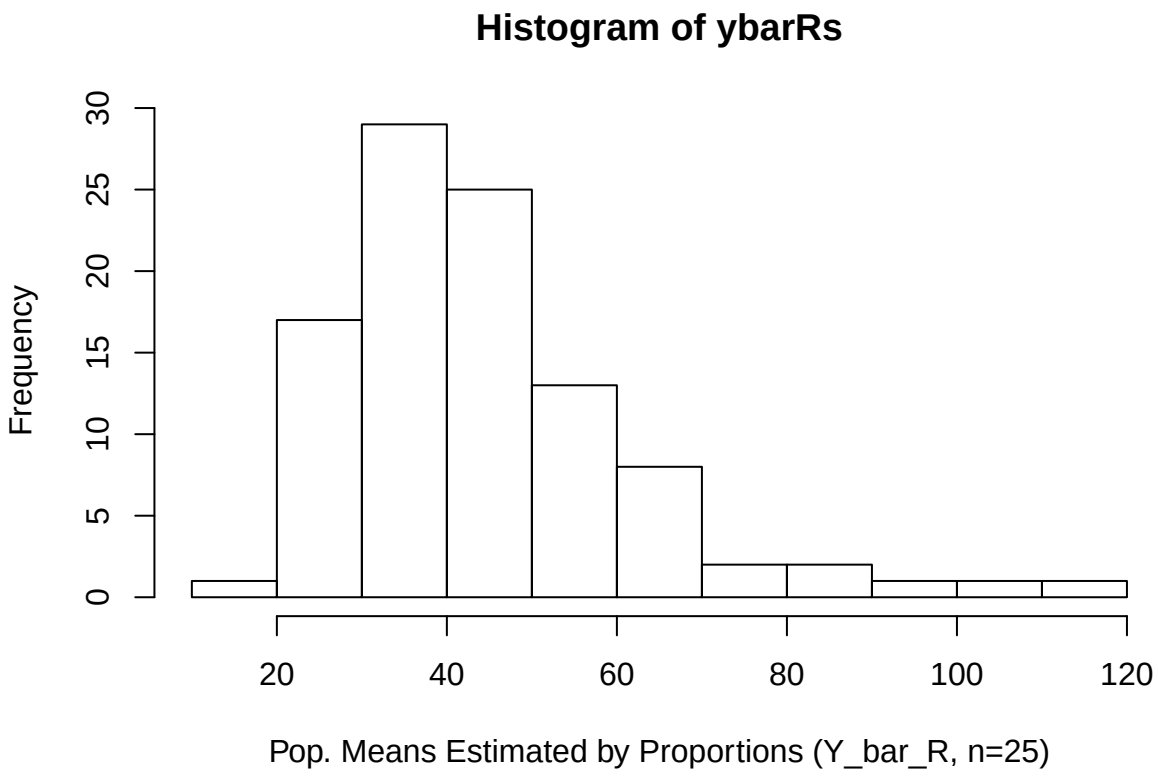
```r
#I am 95% confident that the total cancer mortality for all counties
#in the three states is contained within the values above

#Conclusion: Yes, the intervals cover the population values.
```

Part h.

This is effective because the ratio estimates achieve comparable precision with a much smaller sample.

Parts i, j, k

```r
# i.
cancer$prop <- cancer$mortality/cancer$pop
ybarRs <- numeric(100)
for(i in 1:100){
  y_bar <- mean(sample(cancer$mortality, 25, replace = F))
  x_bar <- mean(sample(cancer$pop, 25, replace = F))
  ybarRs[i] <- (y_bar/x_bar)*mean(cancer$pop)
}
hist(ybarRs, freq = T, xlab = "Pop. Means Estimated by Proportions (Y_bar_R, n=25)")
```




```
#Compared to part c, the range of the distribution is more constrained.

# j.
y_sample <- sample(cancer$mortality, 25, replace = F)
x_sample <- sample(cancer$pop, 25, replace = F)
y_bar <- mean(y_sample)
x_bar <- mean(x_sample)
R <- y_bar/x_bar #ratio estimator

y_bar_R <- R*mean(cancer$pop)
y_bar_R
```

```
## [1] 21.43712
```

```
T_R <- R*sum(cancer$pop)
T_R
```

```
## [1] 6452.573
```

```
# These estimates are comparable to the values formulated
# in part d.

# k. confidence intervals
```

```
var_ybar_R <- (1/25)*(1-((24)/300))*(((R^2)*var(x_sample)) + var(y_sample)
                                     - 2*R*cov(x_sample,y_sample))
lower <- y_bar_R - (1.96*sqrt(var_ybar_R))
upper <- y_bar_R + (1.96*sqrt(var_ybar_R))
c(lower,upper) # 95% CI for Ybar_R
```

```
## [1]  3.139806 39.734435
```

```
# I am 95% confident that the average number of cancer mortalities in each county
# falls within the above values.

var_T_R <- (301^2)*var_ybar_R
lower <- T_R - (1.96*sqrt(var_T_R))
upper <- T_R + (1.96*sqrt(var_T_R))
c(lower,upper) # 95% CI for T_R
```

```
## [1]   945.0815 11960.0648
```

```
#I am 95% confident that the total cancer mortality for all counties
#in the three states is between the above values.
```

Parts l, m

```
# l. four strata
cancer$group <- ntile(cancer$pop, n=4)
n1 <- mean(sample(cancer$mortality[cancer$group==1], size = 6))
n2 <- mean(sample(cancer$mortality[cancer$group==2], size = 6))
n3 <- mean(sample(cancer$mortality[cancer$group==3], size = 6))
n4 <- mean(sample(cancer$mortality[cancer$group==4], size = 6))
W <- 75/301
xbar_s <- W*(n1+n2+n3+n4)
xbar_s #pop mean mortality estimate
```

```
## [1] 34.2608
```

```
T_s <- 301*xbar_s
T_s #pop total mortality estimate
```

```
## [1] 10312.5
```

```
# m.

#sampling fraction for proportional allocation is simply 1/4th for each strata,
#since each strata is equally sized.

#sampling fraction for optimal allocation:
denom <-
  W*var(cancer$mortality[cancer$group==1]) + W*var(cancer$mortality[cancer$group==2]) +
```

```
  W*var(cancer$mortality[cancer$group==3]) + W*var(cancer$mortality[cancer$group==4])

n_1 <- var(cancer$mortality[cancer$group==1])/denom
n_2 <- var(cancer$mortality[cancer$group==2])/denom
n_3 <- var(cancer$mortality[cancer$group==3])/denom
n_4 <- var(cancer$mortality[cancer$group==4])/denom

c(W*n_1, W*n_2, W*n_3, W*n_4) #optimal allocation sampling fraction
```

```
## [1] 0.003474048 0.009457559 0.032221686 0.954846707
```

```
# Comparing variances.

sig_bar <- W*(sqrt(n_1)) + W*(sqrt(n_2)) + W*(sqrt(n_3)) + W*(sqrt(n_4))

VarXsp_by_VarXso <-
  1 + (W*((sqrt(n_1)-sig_bar)^2 + (sqrt(n_2)-sig_bar)^2 +
            (sqrt(n_3)-sig_bar)^2 + (sqrt(n_4)-sig_bar)^2)
       / ((W*(sqrt(n_1) + sqrt(n_2) + sqrt(n_3) + sqrt(n_4)))^2)
       )

VarXsp_by_VarXso
```

```
## [1] 2.325144
```

Here we conclude that the variance of the mean proportional allocation is 232.5144143 percent of the variance under optimal allocation. Therefore, optimal allocation is clearly preferred.

Part n

The estimates will get better, because as the number of stratifications approach N, Ybar_R will approach the true population mean.