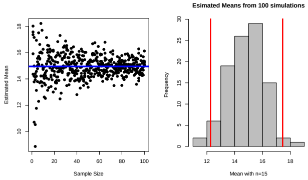
Sample Properties & Simulation



But first, a gratuitous advertisement

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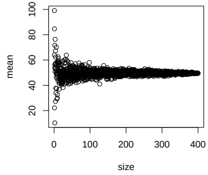
Loops: Simulation to Estimate Precision

Last time...
How does sample size influence precision of our estimate of the mean?



The anatomy of a simulation

1) Create a vector of sample sizes you want to iterate over

```
n <- rep(1:400, times = 4)
```

The anatomy of a simulation

2) Create a blank vector of means

```
m <- rep(NA, times = length(n))
```

length gets length of a vector

The anatomy of a simulation

3) The For Loop

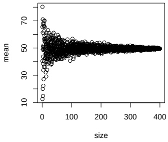
```
for (i in 1:length(n)) {
    m[i] <- mean(sample(population, size = n[i]))
}
```

- i is an index to iterate over
- the values of i are from the vector *1:length(n)*

The anatomy of a simulation

4) Plot it

```
plot(n, m, xlab = "size", ylab = "mean")
```



Precision plateaus around 50.

Exercise

- Write a for loop that calculates the first 15 numbers of the fibonacci sequence

1, 1, 2, 3, 5, 7, 9...
(Challenge: do it with a starting vector of only NA's)

(hint - create a blank vector, but with the first two entries as 1)
(hint - aVec[i+1] is aVec[2] if i=1)

Exercise

```r
# start with a blank vector with some 1's
fibVec <- c(1, 1, rep(NA, 13))

# now loop
for (i in 3:15) {
    fibVec[i] <- fibVec[i - 1] + fibVec[i - 2]
}

fibVec

##  [1]   1   1   2   3   5   8  13  21  34  55  89 144 233 377
## [15] 610
```

Sample Properties: Variance

How variable was that population?

$$s^2 = \frac{\sum_{i=1}^{n} (Y_i - \bar{Y})^2}{n-1}$$

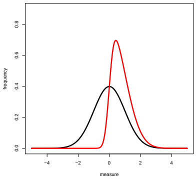
- **Sums of Squares** over n-1
- n-1 corrects for both sample size and sample bias
- σ^2 if describing the population
- Units in square of measurement...

Sample Properties: Standard Deviation

$$s = \sqrt{s^2}$$

- Units the same as the measurement
- If distribution is normal, 67% of data within 1 SD
- 95% within 2 SD
- σ if describing the population

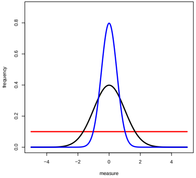
Sample Properties: Skew



Right-Skewed

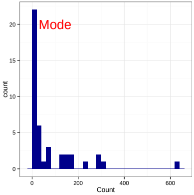
Skew calculated using additional moments (think sums of squares, but cubed)

Sample Properties: Kurtosis



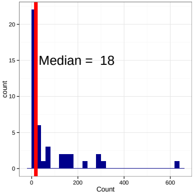
Platukurtic
Leptokurtic
Normal

Sample Properties: Mode



This highest point on a frequency plot.

Sample Properties: Median



This middle value of a dataset.

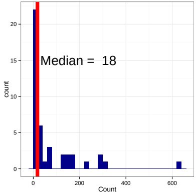
Sample Properties: Median

We obtain the median by sorting and picking the middle value.

```
sort(bird$Count)

##  [1]   1   1   1   1   1   2   2   2   2   3   3   4   5   7
## [15]   7  10  12  13  14  15  16  18  23  23  25  28  33  33
## [29]  59  64  67  77 128 135 148 152 173 173 230 282 297 300
## [43] 625


nrow(bird)  #this is the # of rows in the data frame

## [1] 43


sort(bird$Count)[22]

## [1] 18
```

Sample Properties: Median

The midpoint of the data-set is the 50th percentile!



Percentiles, Quantiles, Quartiles, and all that

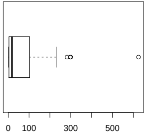
1. Sort a data set
2. The index of the *ith* value minus 0.5 divided by n is its quantile
3. Quantile * 100 is the percentile
4. Quartiles are those points that divide data into 4 equal chunks (25th, 50th, and 75th percentile)

Percentiles, Quantiles, Quartiles, and all that

```
sort(bird$Count)

##  [1]   1   1   1   1   1   2   2   2   2   3   3   4   5   7
## [15]   7  10  12  13  14  15  16  18  23  23  25  28  33  33
## [29]  59  64  67  77 128 135 148 152 173 173 230 282 297 300
## [43] 625
```

Boxplots to Represent Quartile Information

```
boxplot(bird$Count, horizontal = T)
```

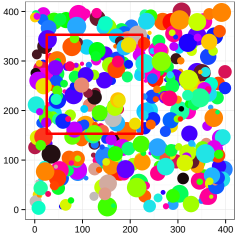


Whiskers show 1.5 * interquartile range, Points show outliers

Variation in Sample Estimates

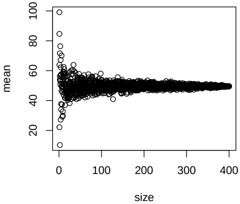
Remember Samples and Populations?

How representative of our population are the estimates from our sample?



Remember Samples and Populations?

We've seen that we get variation in point estimates at any sample size



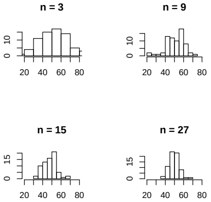
Exercise: Variation in Estimation

- Consider a population with some distribution (rnorm, runif, rgamma)
- Think of the mean of one sample as an individual replicate
- Take many (50) 'replicates' from this population of means
- What does the distribution of means look like? Use *hist*
- How does it depend on sample size (within replicates) or distribution type?

Extra: Show the change in distributions with sample size in one figure.

Central Limit Theorem

The distribution of means converges on normality



Central Limit Theorem Simulation

```r
set.seed(697)
n <- 3
mvec <- rep(NA, times = 100)
# simulate sampling events!
for (i in 1:length(mvec)) {
    mvec[i] <- mean(runif(n, 0, 100))
}
hist(mvec, main = "n=3")
```

Estimating Variation Around a Mean

Great, so, if we can draw many replicated means from a larger population, we can the standard deviation of an estimate!

This standard deviation of the estimate of the mean is the **Standard Error.**

But for a single study, we only have one sample...

A Bootstrap Simulation Approach to Standard Error

- Our sample is representative of the entire population
- Therefore, we can resample it *with replacement* for 1 simulated sample
- We use our sample size as the new sample size as well

We set the replace argument in sample = TRUE
Try sampling from the bird data with replacement.

A Bootstrap Simulation Approach to Standard Error

```
sample(bird$Count, replace = T, size = nrow(bird))
```

```
##  [1]  23 135   1  23  59   4  67  15   3   1 135  13 152 128
## [15]  67 148   7   1   3   2  67   1  23   3 300  64   2 282
## [29] 297  33 297   2  25 128 128 173  14  64   1  33   2 297
## [43] 282
```

```
sample(bird$Count, replace = T, size = nrow(bird))
```

```
##  [1] 297   2 625 230  13  33  25  12   4  28 297   2  12   7
## [15]   3   1  18  28 297   1 282  15 300 148  23   2  33   1
## [29] 625 282  77  23  12  25 297   2   2  33 230 135  67  18
## [43]  77
```

Standard Error

$$SE_{\bar{Y}} = \frac{s}{\sqrt{n}}$$

$\bar{Y}$ - sample mean
s - sample standard deviation
n - sample size

95% Confidence Interval and SE

- Recall that 95% of the data in a sample is within 2SD of its mean
- So, 95% of the times we sample a population, the *true* mean will lie within 2SE of our estimated mean
- This is the 95% **Confidence Interval**

$$\bar{Y} - 2SE \leq \mu \leq \bar{Y} + 2SE$$

Exercise: 95% Confidence Interval

$$\bar{Y} - 2SE \leq \mu \leq \bar{Y} + 2SE$$

- Draw 20 simulated samples with n=10 from a normal distribution of mean 0
- Calculate the upper and lower confidence interval for each
- Compare the 95% CIs to the true value of the mean
- Extra: graph it with segments

Tip: To bind two vectors together as columns, use *cbind*

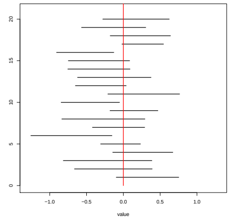
Exercise: 95% Confidence Interval

```r
set.seed(697)
n <- 20
upperCIvec <- rep(NA, n)
lowerCIvec <- rep(NA, n)

# loop and calculate the 95% CI
for (i in 1:n) {
    samp <- rnorm(10)
    upperCIvec[i] <- mean(samp) + 2 * sd(samp)/sqrt(n)
    lowerCIvec[i] <- mean(samp) - 2 * sd(samp)/sqrt(n)
}
```

Exercise: 95% Confidence Interval

```r
# examine the numbers
cbind(upperCIvec, lowerCIvec)[1:10, ]

##       upperCIvec lowerCIvec
##  [1,]    0.75237   -0.09638
##  [2,]    0.39117   -0.66417
##  [3,]    0.38746   -0.81584
##  [4,]    0.67183   -0.14438
##  [5,]    0.23227   -0.30878
##  [6,]   -0.15508   -1.25684
##  [7,]    0.28960   -0.41992
##  [8,]    0.29285   -0.83584
##  [9,]    0.46890   -0.18128
## [10,]   -0.05229   -0.84528
```

Exercise: 95% Confidence Interval



Variation in Other Estimates

- Many SEs and CIs of estimates have formulae and well understood properties
- For those that do not, we can bootstrap the SE of any estimate - e.g., the median
- Bootstrapped estimates (mean of simulated replicates) can be used to assess bias
- Bootstrapping is not a panacea - requires a good sample size to start