# Error in Estimates & Probability Distributions

## For loops in the Wild

```
# Create a counter to keep track of data clusters
ext$cluster <- rep(NA, nrow(ext))
ext$cluster[1] <- 1
# iterate over the whole column
for (i in 2:nrow(ext)) {

    # If we've moved on to the next cluster, change the counter
    ext$cluster[i] <- ifelse(ext$effect..[i] < ext$effect..[i -
        1], ext$cluster[i - 1] + 1, ext$cluster[i - 1])
}
```

## 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
- $\sigma^2$ if describing the population
- Units in square of measurement...

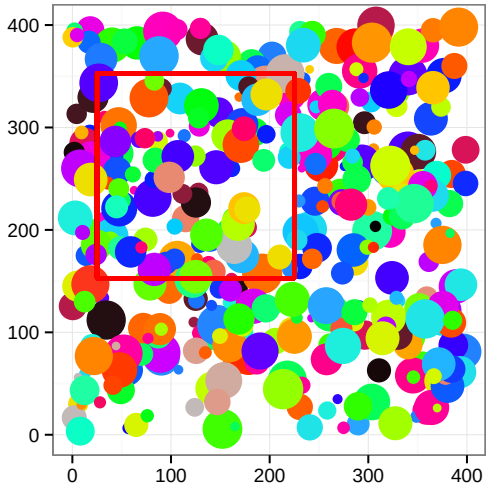
## Sample Properties: Standard Deviation

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

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

## 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

What does that variation look like?

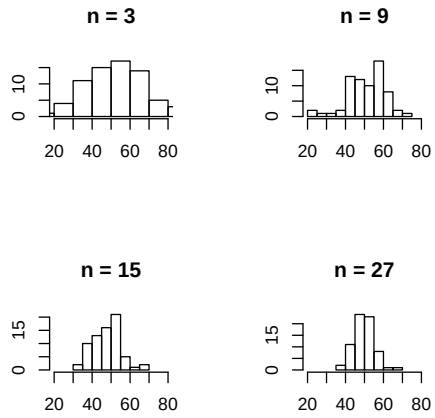
## Exercise: Variation in Estimation

- 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

```
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*

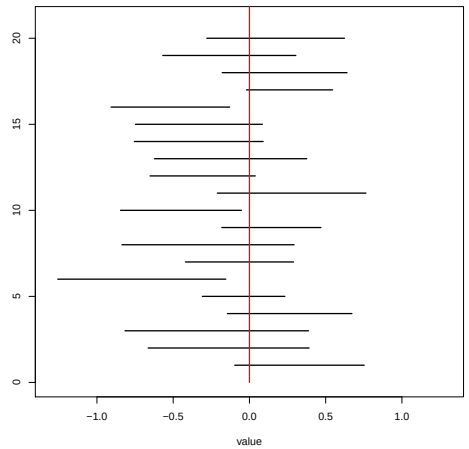
## Exercise: 95% Confidence Interval

```
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

```
# 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

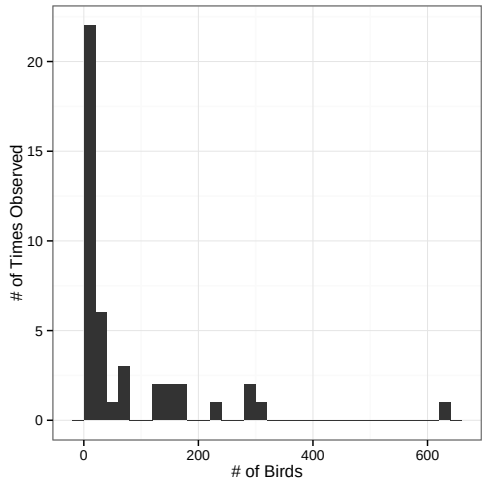



## Variation in Other Estimates

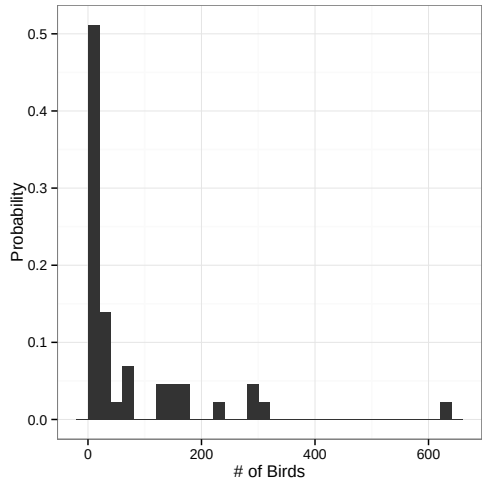
- Many SEs and CIs of estimates have formulae and well understood properties
- For those that do not, we can bootstrap the SE of any estimate - e.g., the median
- Bootstrapped estimates (mean of simulated replicates) can be used to assess bias
- Bootstrapping is not a panacea - requires a good sample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

## Distributions!

## Frequency Distributions Make Intuitive Sense

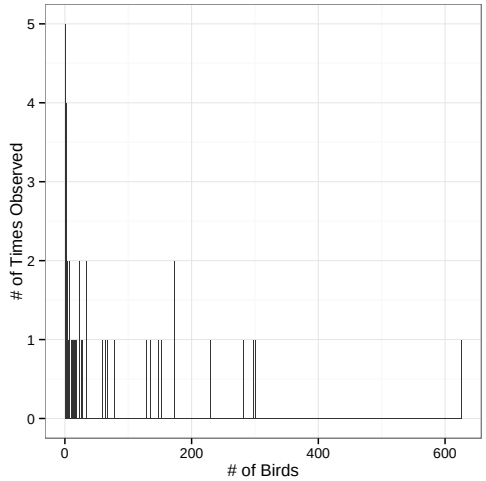



## Frequencies Can be Turned Into Probabilities



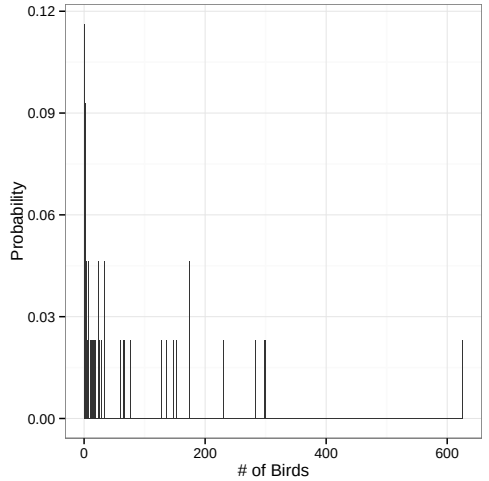

Just divide by total # of observations
But - we have binned observations...

## Frequencies of Individual Observations



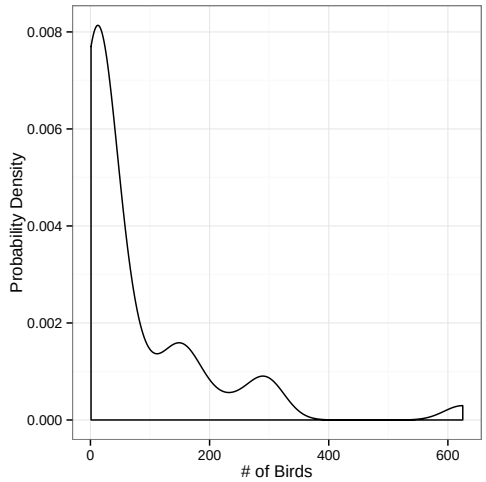

Can we turn these into probabilities?

## Probabilities of Individual Measurements



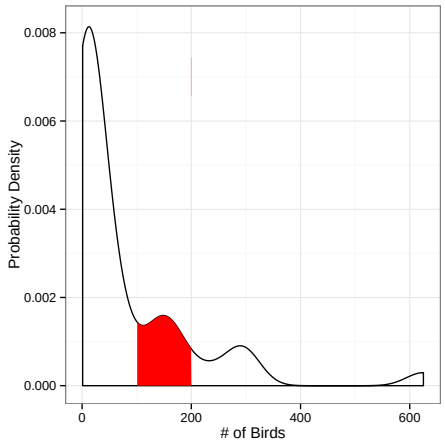

Many probabilities small, and what about the gaps?

## Continuous Probability Distributions



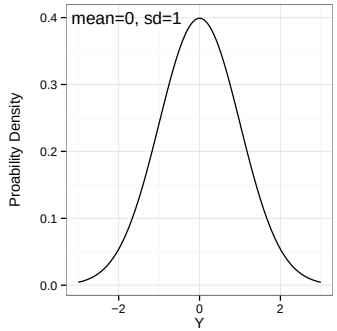

Any individual observation has a *probability density*.

## Probability as Integral Under the Curve



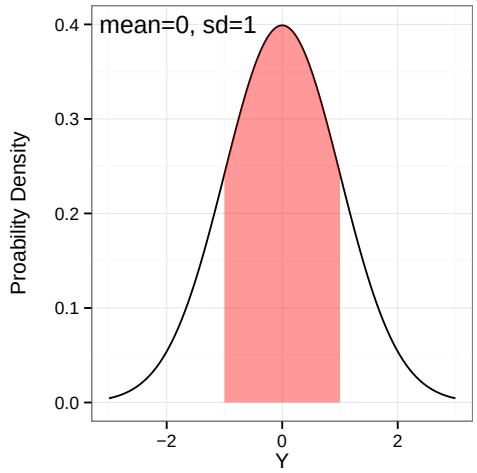

We obtain probabilities of observations between a range of values by integrating the distribution over selected values.

## The Normal Distribution

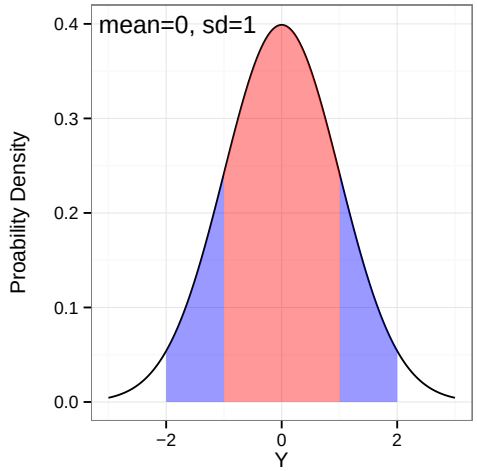



- Defined by it's mean and standard deviation.
- Y $\sim$N($\mu$, $\sigma$)
- Single mode
- Symmetric

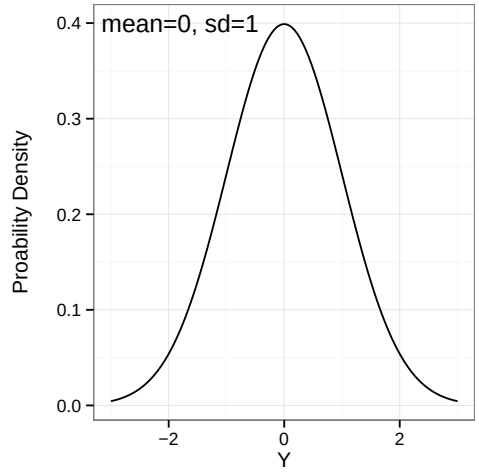
## 67% of Values within 1 SD



## 95% of Values within 2 (1.96) SD

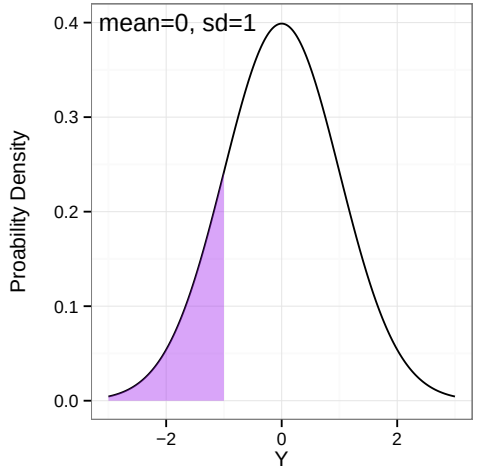



## How to Get A Probability Density in R



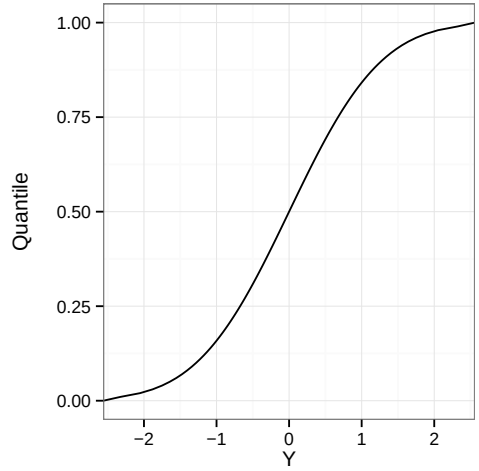

```
dnorm(Y, mean = 0, sd = 1)
```

## The Probability of a Value or More Extreme Value




```
pnorm(Y, mean = 0, sd = 1)
```

## The Cummulative Distribution/Quantile Function



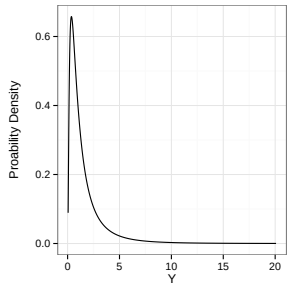

```
qnorm(p, mean = 0, sd = 1)
```

## The Cummulative Distribution/Quantile Function

pnrm an dqnorm are the inverse of one another

```
pnorm(-1)

## [1] 0.1587

qnorm(pnorm(-1))

## [1] -1

qnorm(0.025)

## [1] -1.96
```

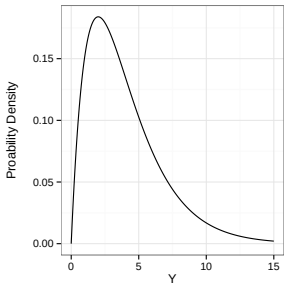
## The Lognormal Distribution




- An exponentiated normal
- Defined by the mean and standard deviation of its log.
- Y ˜LN($\mu_{log}$, $\sigma_{log}$)
- Generated by multiplicative processes

```
dlnorm(Y, meanlog = 0, sdlog = 1)
```

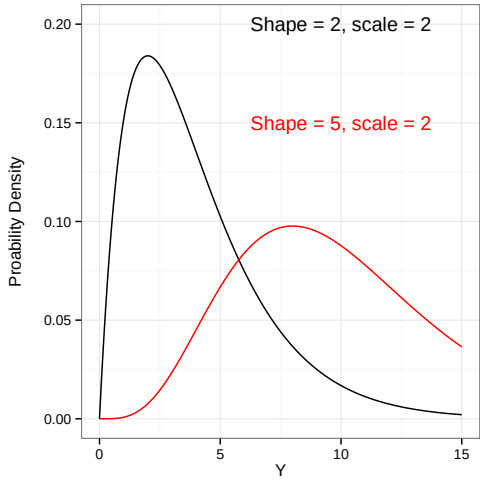
## The Gamma Distribution



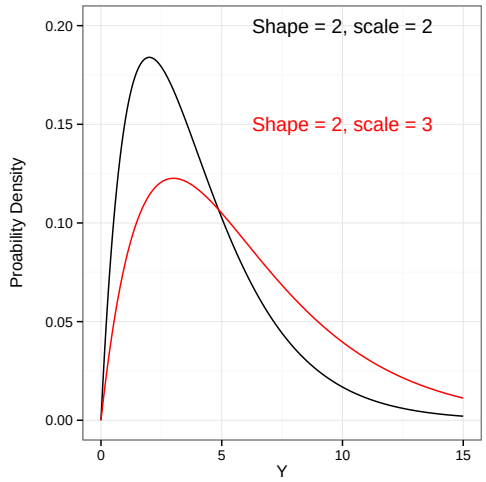

- Defined by number of events(shape) average time to an event (scale)
- Can also use rate (1/scale)
- Y ˜G(shape, scale)
- Think of time spent waiting for a bus to arrive

```
dgamma(Y, shape = 2, scale = 2)
```

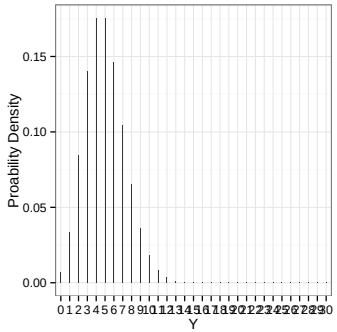
## Waiting for more events



## Longer average time per event



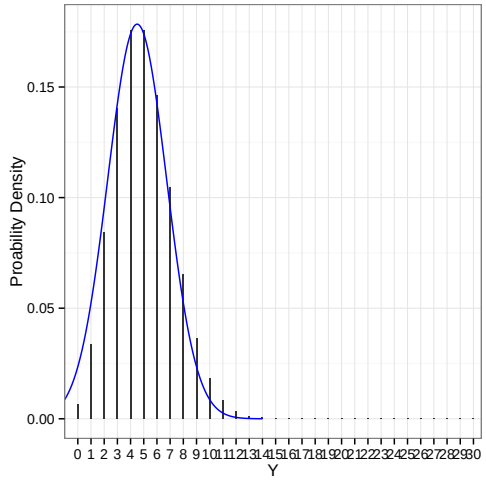

## The Poisson Distribution



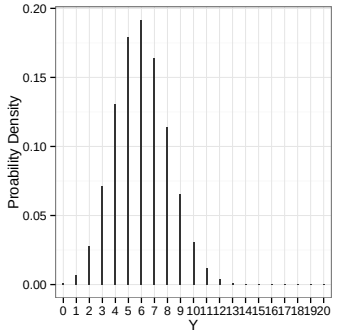

- Defined by $\lambda$ - the mean and variance
- Y ~ P(lambda)

```
dpois(Y, lambda = 5)
```

## When Lambda is Large, Approximately Normal



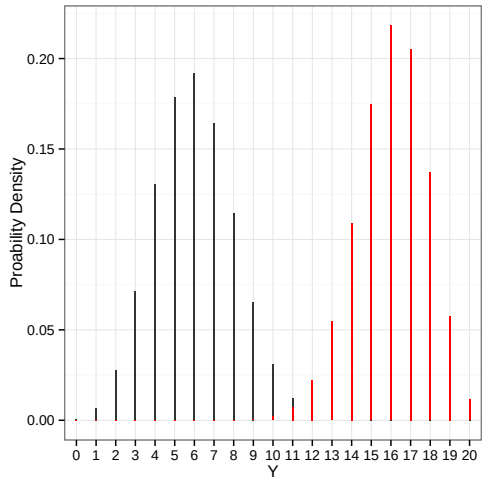

## The Binomial Distribution



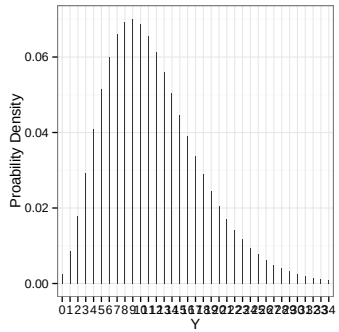

- Results from multiple coin flips
- Defined by size (# of flips) and prob (probability of heads)
- Y ~ B(size, prob)
- bounded by 0 and size

```
dpois(Y, size, prob)
```

## Increasing Probability Shifts Distribution




## The Negative Binomial Distribution




- Distribution of number of failures before n number of successes in k trials
- Or mean # of counts, $\mu$, with an overdispersion parameter, size
- Y ~ NB($\mu$, size)

```
dnbin(Y, mu, size)
```

## Exercise

- Explore the distributions we have discussed
- Examine how changing parameters shifts the output of probability function
- Compare curves generated using density functions (e.g., dnorm) and large number of random draws (e.g. from rnorm)
- Overlay these in plots if you can (hist, lines, etc.)
- Challenge: graphically show integration under the different types of distribution curves