Iteration & Likelihood

For Loops!

```
x<-1:100000
#
for (i in x){
  x[i]<-x[i] +1
}
```

For Loops: Costs & Benefits

Benefits:

1. Remove repetitive code
2. Can *m*ap same operation across a vector, matrix, list, etc.

Costs:

1. Slow.
2. Lots of Code.

Speed: Many Operations Faster via *Vectorization*

```
1:10 + 1

#  [1]  2  3  4  5  6  7  8  9 10 11
```

Many Operations Faster via *Vectorization*

```
system.time(1:100000+1)

#    user  system elapsed
#       0       0       0


system.time({
  x<-1:100000
  for(i in x) x[i]<-x[i] +1
})

#    user  system elapsed
#   0.231   0.002   0.233
```

Vectorization Ubiquitos

```
dnorm(5, mean = 1:10, sd = 1)

#  [1] 1.338e-04 4.432e-03 5.399e-02 2.420e-01 3.989e-01
#  [6] 2.420e-01 5.399e-02 4.432e-03 1.338e-04 1.487e-06
```

Vectorization Ambiguous in Many Instances...

```
sampMean <- function (vec, size) mean(sample(vec, size))

sampMean(vec=1:5, size=1:5)

# [1] 1
```

How to Vectorize Ambiguous Functions

```
sampMeanV <- Vectorize(sampMean,
                       vectorize.args="size")

sampMeanV(vec=1:5, size=1:5)

# [1] 2.000 2.500 3.333 2.750 3.000
```

The Guts of Vectorize

```
sampMeanV

# function (vec, size)
# {
#     args <- lapply(as.list(match.call())[-1L], eval, parent.frame())
#     names <- if (is.null(names(args)))
#         character(length(args))
#     else names(args)
#     dovec <- names %in% vectorize.args
#     do.call("mapply", c(FUN = FUN, args[dovec], MoreArgs = list(args[!dovec]),
#         SIMPLIFY = SIMPLIFY, USE.NAMES = USE.NAMES))
# }
# <environment: 0x1dc83c0>
```

Minimizing Code for Mapping Functions: the Apply Family

Take an object type - vector, matrix, list, etc., and map a function to every element, cleanly and quickly.

sapply for Vectors

```
f <- function(x) x+1
#
sapply(1:5,f)

# [1] 2 3 4 5 6
```

Anonymous Functions and sapply

```
sapply(1:5, function(x) x+1)

# [1] 2 3 4 5 6
```

Apply Statements Faster than For Loops

```
system.time({
  x<-1:100000
  for(i in x) x[i]<-x[i] +1
})

#    user  system elapsed
#   0.216   0.001   0.217


system.time(sapply(1:100000, f))

#    user  system elapsed
#   0.188   0.002   0.191
```

Lots of Possibilities with sapply

```
sapply(1:5, function(x) sampMean(1:5, x))

# [1] 5.000 2.500 2.667 3.000 3.000
```

Many Output Types with sapply

```
sapply(1:5, function(x) return( c(x+2, x^2) ) )

#      [,1] [,2] [,3] [,4] [,5]
# [1,]    3    4    5    6    7
# [2,]    1    4    9   16   25
```

apply for Matrices

```
m <- matrix( c(1, 2,
               3, 4), ncol=2)
```

apply for Matrices

```
m <- matrix( c(1, 2,
               3, 4), ncol=2)
```

```
apply(m, 1, sum)

# [1] 4 6
```

apply for Matrices

```
m <- matrix( c(1, 2,
               3, 4), ncol=2)
```

```
apply(m, 1, sum)

# [1] 4 6
```

```
apply(m, 2, sum)

# [1] 3 7
```

apply for Matrices

```
apply(m, c(1,2), sum)

#      [,1] [,2]
# [1,]    1    3
# [2,]    2    4
```

lapply for Lists - mclapply to use multiple cores

```
x <- list(a = 1:10,
          beta = exp(-3:3),
          logic = c(TRUE,FALSE,FALSE,TRUE))

# compute the list mean for each list element
lapply(x,mean)

# $a
# [1] 5.5
#
# $beta
# [1] 4.535
#
# $logic
# [1] 0.5
```

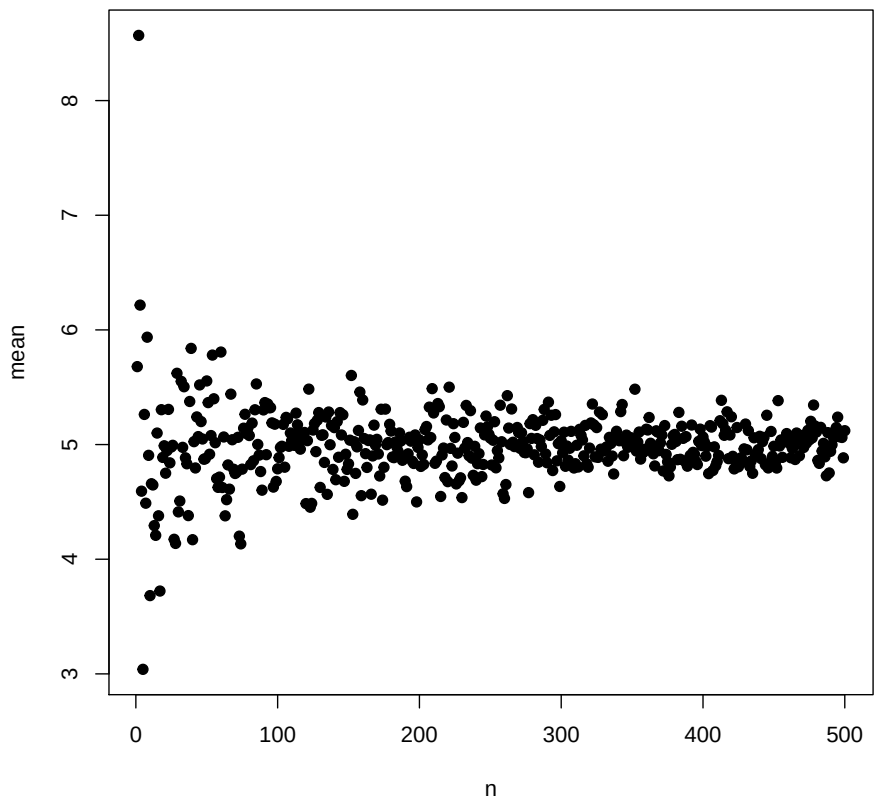
Exercise: Apply Yourself!

1. Using sapply, write a short script to show the relationship between n and estimated mean for a normally distributed population with a mean of 5 and SD of 3.
2. Challenge: What is the bootstrapped SE at each sample size? 50 boots!

   hint: 2 lines with bootstrap, 3-4 with nested sapply

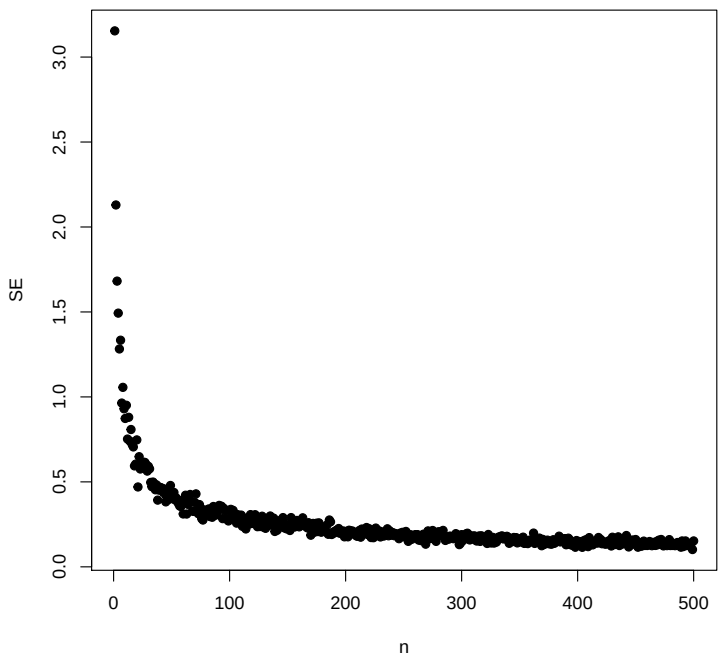
Exercise: Apply Yourself!

```
set.seed(697)
vec <- sapply(1:500, function(x) mean(rnorm(x, mean=5, sd=3)))
```



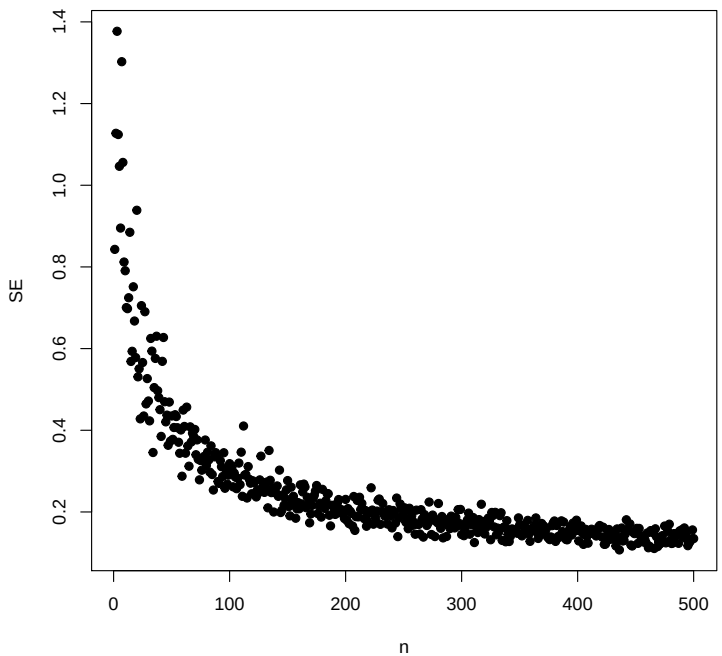
Exercise: Apply Yourself!

```
seVec <- sapply(1:500, function(x){
    mvec<- sapply(1:50, function (i) mean(rnorm(x, mean=5, sd=3)))
    return(sd(mvec))
})
```



Exercise: Apply Yourself!

```
library(bootstrap)
seVec2 <- sapply(1:500, function(x)
  sd(bootstrap(rnorm(x, mean=5, sd=3), 50, mean)$thetastar))
```



Application of Iterative Solutions: Likelihood

Likelihood: how well data support a given hypothesis.

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Note: Each and every parameter choice IS a hypothesis

Likelihood Defined

$$L(\theta|D) = p(D|\theta)$$

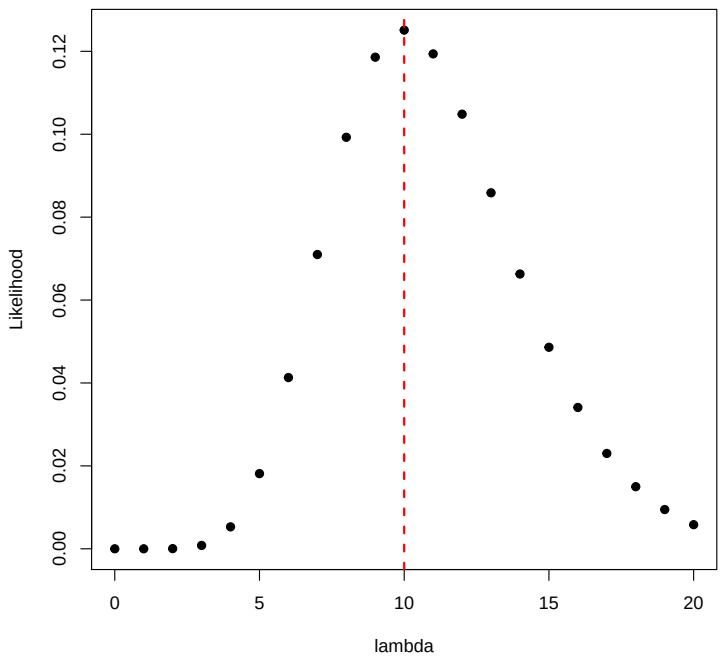
Where D is the data and θ is some choice of parameter values

Maximum Likelihood

The Maximum Likelihood Estimate is the value at which $p(D|\theta)$ is highest.

Example of Maximum Likelihood

Let's say we have counted 10 individuals in a plot. Given that the population is Poisson distributed, what is the value of λ?



Enter Iteration

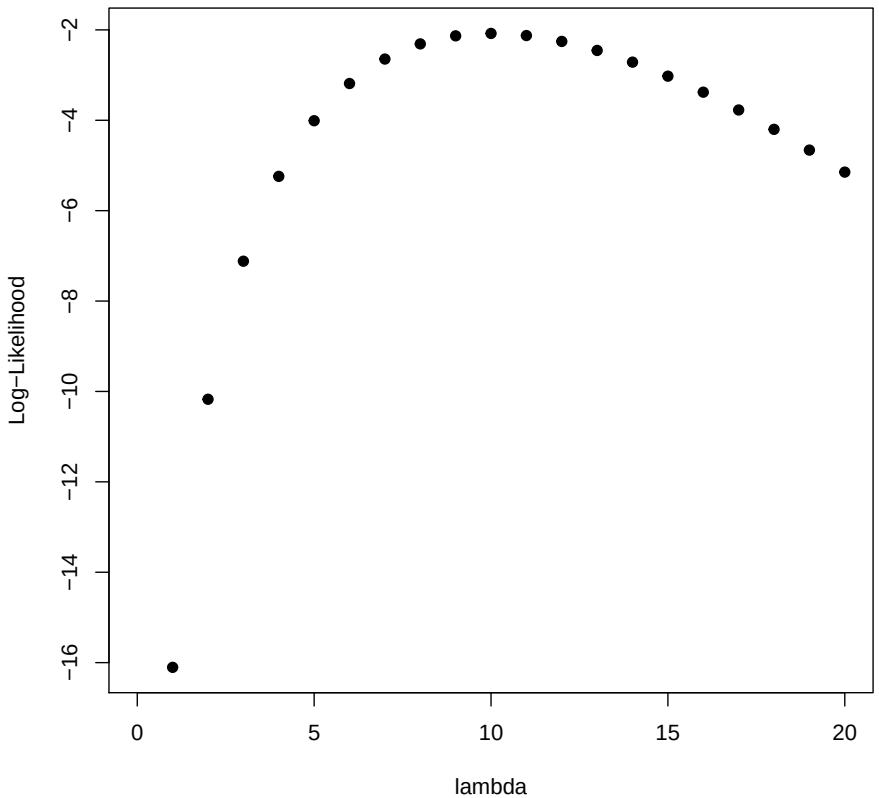
I did this by searching all values of λ using sapply

```
count <- 10
#
l <- sapply(0:20, function(x) dpois(count, lambda=x) )
#
plot(0:20, l, ylab="Likelihood", xlab="lambda", pch=19)
abline(v=10, col="red", lwd=2, lty=2)
```

Maximum Likelihood

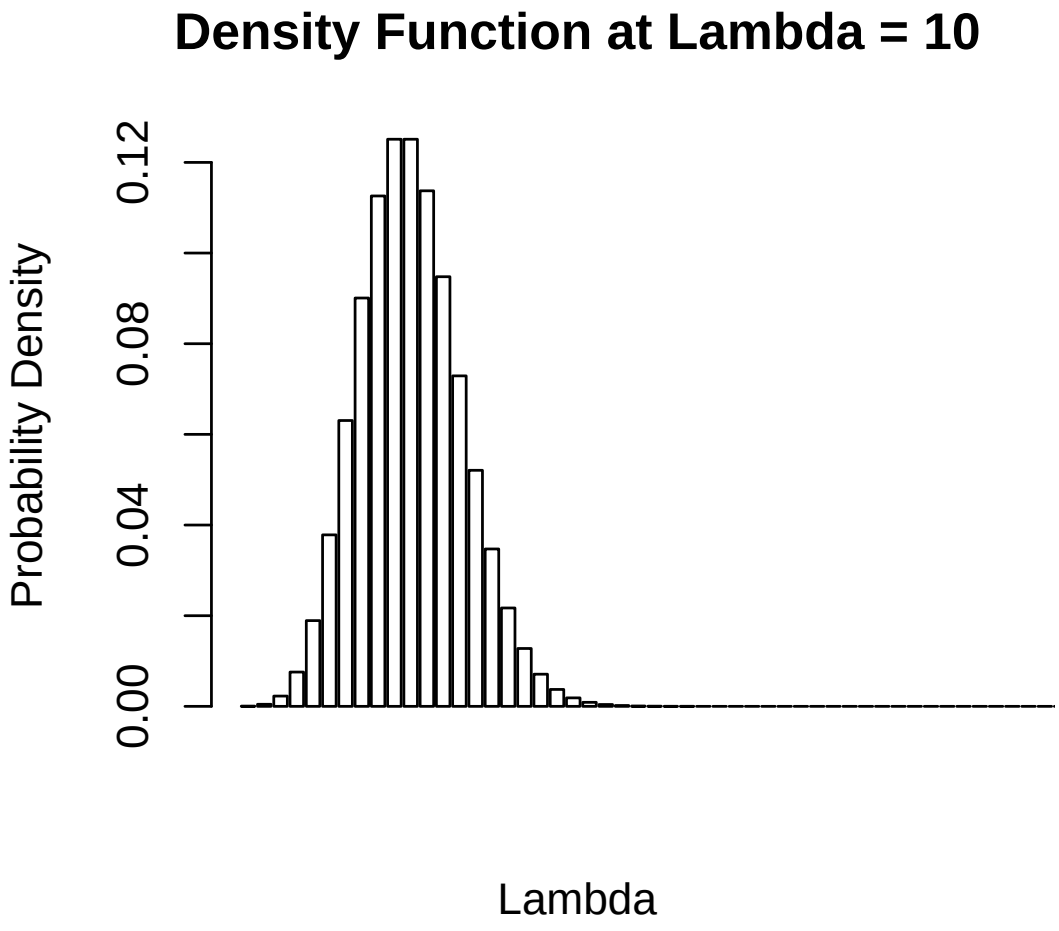
We often maximize log-likelihood because of the more well behaved properties of Log-Likelihood values

Log-Likelihood



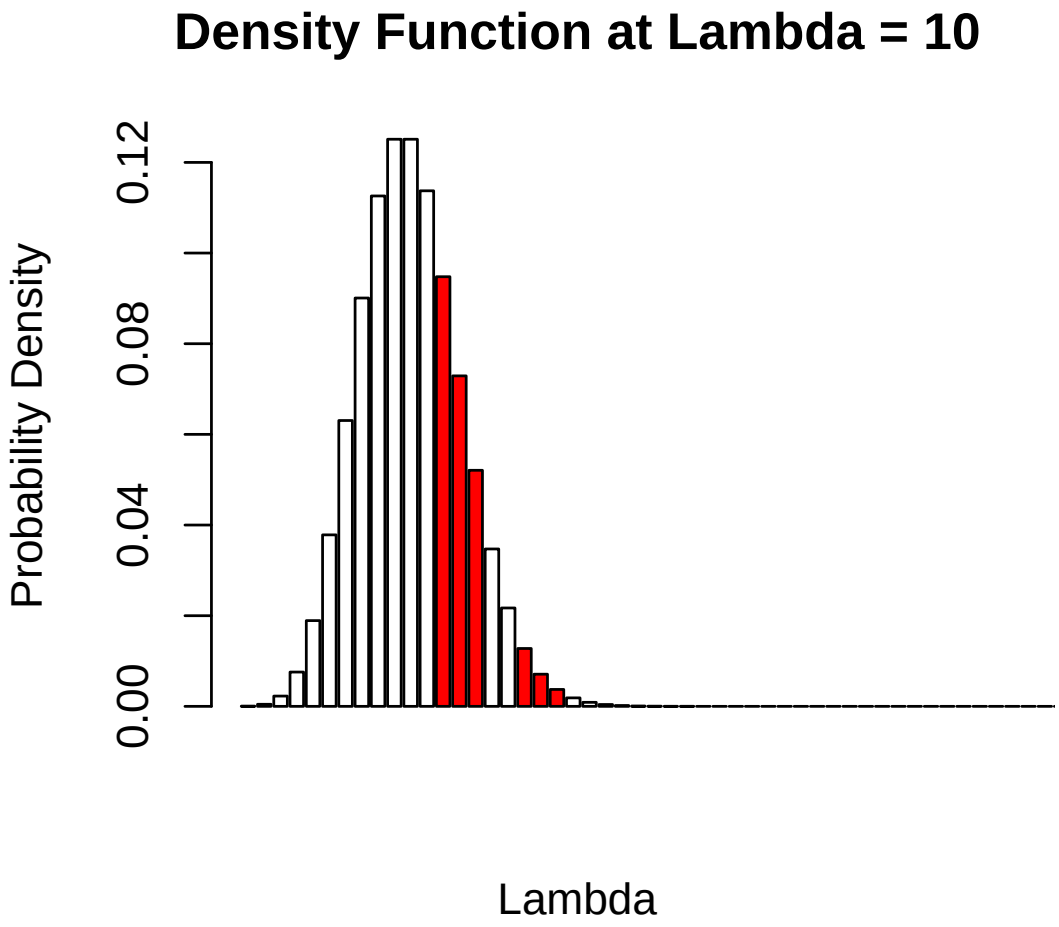
What about Many Data Points?

Start with a Probability Distribution



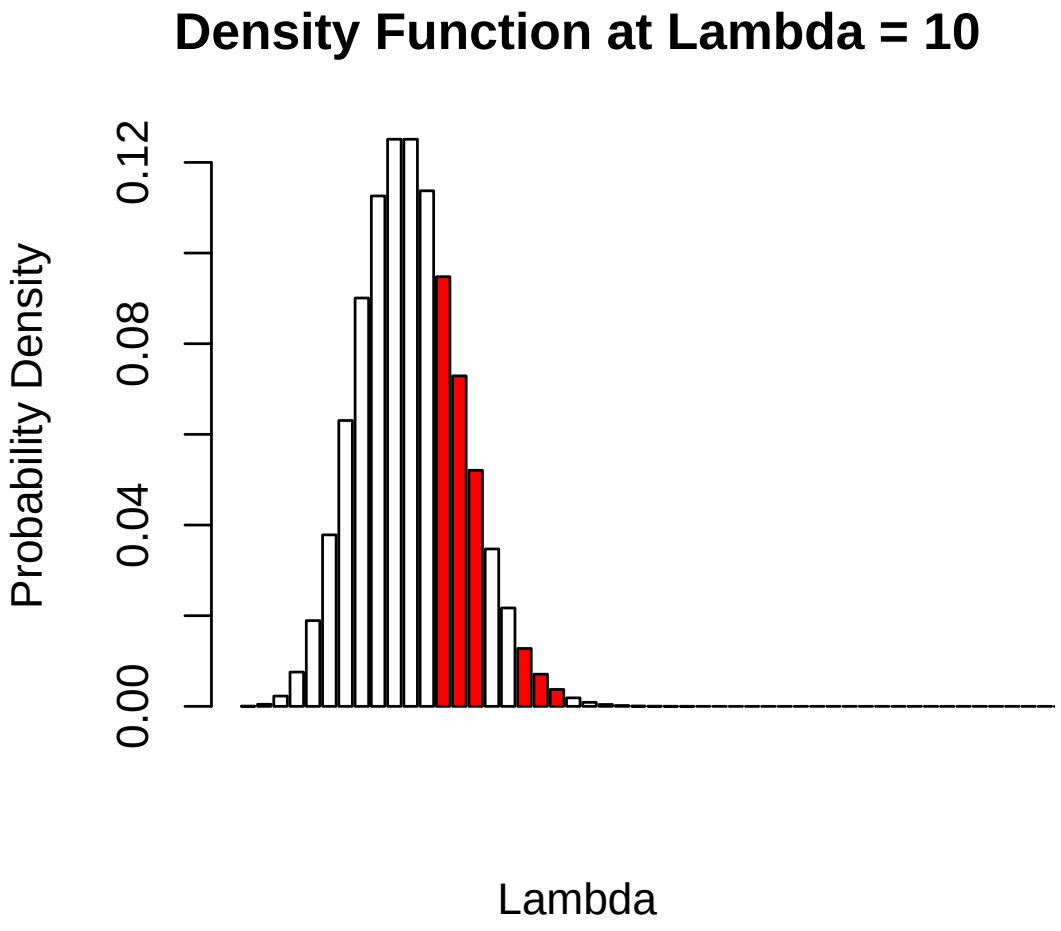
$$p(x) = \frac{\lambda^x e^{-\lambda}}{x!}$$

What is the probability of the data given the parameter?



$$p(x) = \frac{\lambda^x e^{-\lambda}}{x!}$$

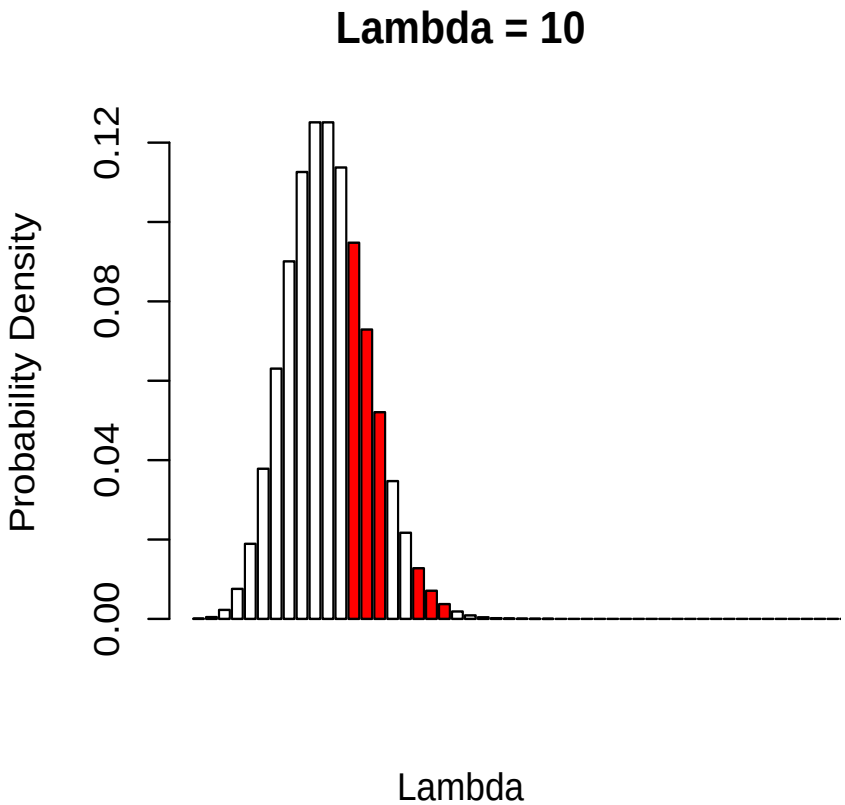
What is the probability of the data given the parameter?

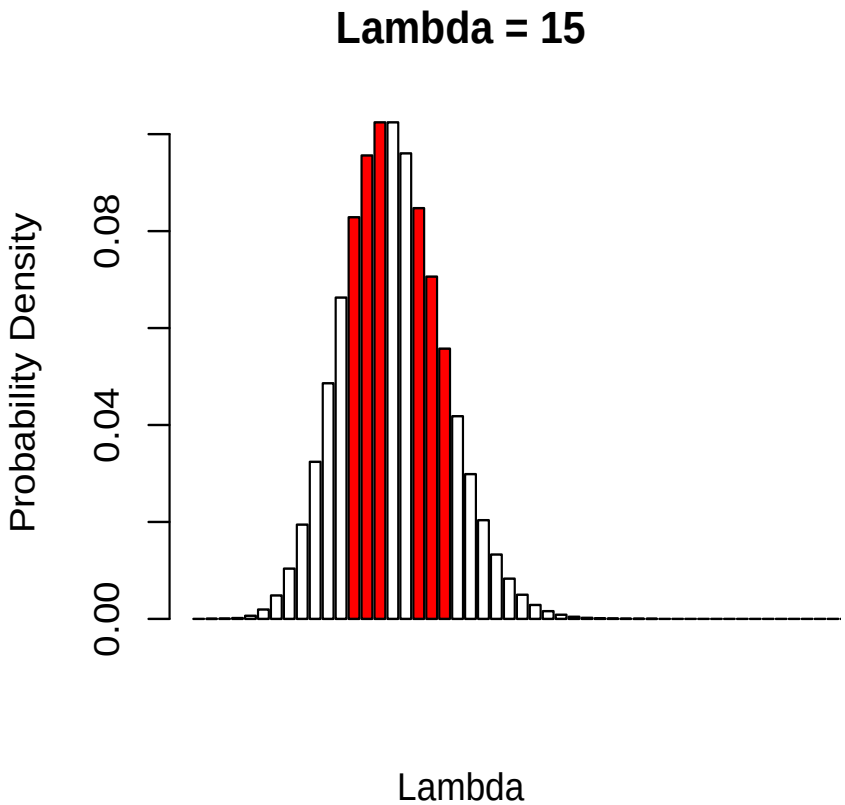


$$\text{p(a and b)} = \text{p(a)p(b)}$$

$$p(D|\theta) = \prod_{i=1}^{n} p(d_i|\theta)$$

Can Compare p(data — H) for alternate H





Compare $p(D|\theta_1)$ versus $p(D|\theta_2)$

Calculating Likelihood and Log-Likelihood for a Data Set

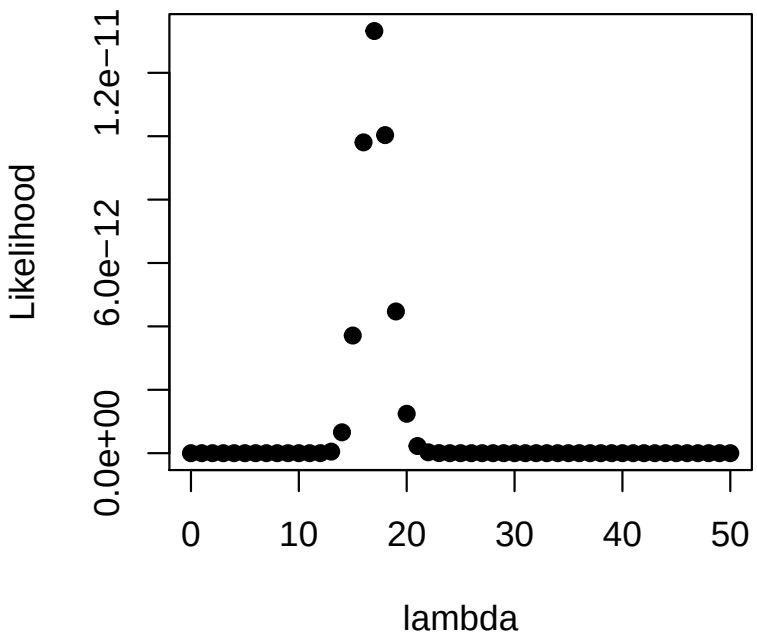
```
lik <- sapply(lambdaVals,
              function(x) prod( dpois(counts, lambda=x) ) )
#
ll <- sapply(lambdaVals,
              function(x) sum( dpois(counts, lambda=x, log=TRUE) ) )
```

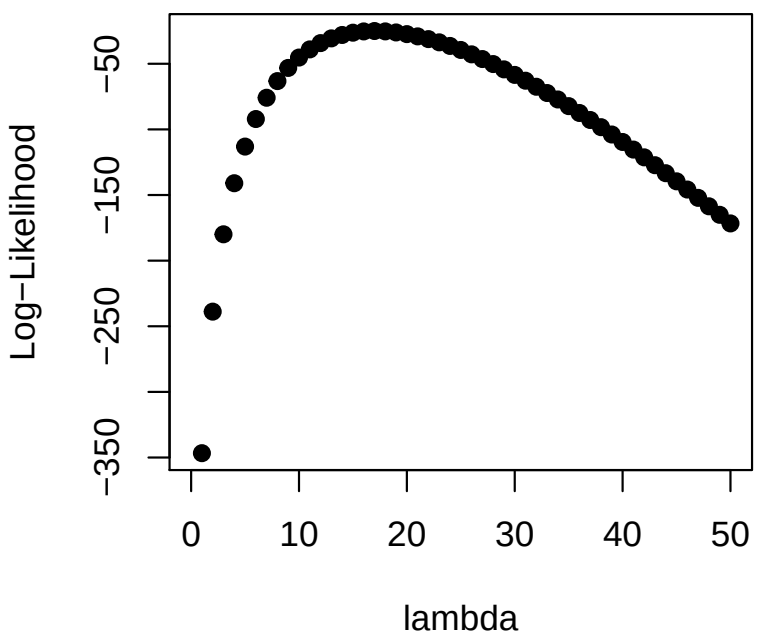
Calculating Likelihood and Log-Likelihood for a Data Set

```
lik <- sapply(lambdaVals,
              function(x) prod( dpois(counts, lambda=x) ) )
#
ll <- sapply(lambdaVals,
              function(x) sum( dpois(counts, lambda=x, log=TRUE) ) )
```

```
max(lik)

# [1] 1.332e-11


lambdaVals[which(lik==max(lik))]

# [1] 17
```

Likelihood and Log-Likelihood of a Data Set

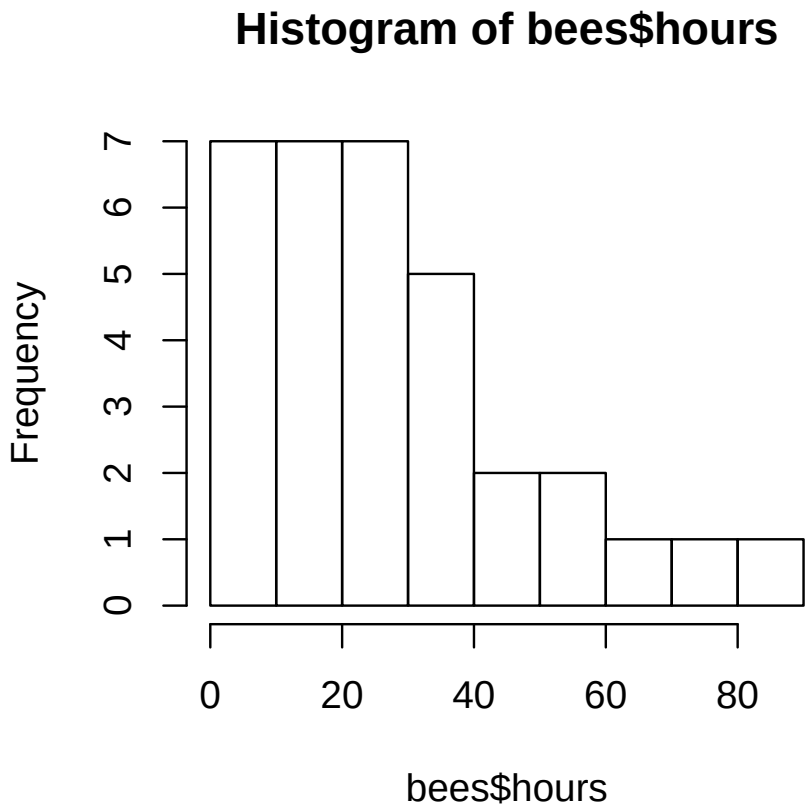




Exercise: Likelihood and Bees!

- Load the Bee Lifespan Data
- Model Bee Lifespans as a Gamma Distribution with shape $= 1$ (1 bee per death)
- What is the ML estimate of a Bee's Lifespan?

Exercise: Likelihood and Bees!



Exercise: Likelihood and Bees!

```
scaleVals <- seq(0.2, 80, 0.2)
#
beeD <- function(x) sum(dgamma(bees$hours, shape=1,
                               scale=x, log=TRUE))
mll <- sapply(scaleVals, beeD)
#
scaleVals[which(mll==max(mll))]

# [1] 27.8
```

Exercise: Likelihood and Bees!