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> #Doing Maximum Likelihood Estimation by Hand in R     By John Myles White
> #https://www.r-bloggers.com/doing-maximum-likelihood-estimation-by-hand-in-r/
> #Suppose that you've got a sequence of values from an unknown Bernoulli
variable:
>
> set.seed(45312)
>
> p.parameter <- 0.8
> sequence <- rbinom(10, 1, p.parameter)
> sequence
 [1] 0 1 1 1 1 1 1 0 1 1
>
> #Given the sequence, we want to estimate the value of the parameter, p, which
is not known to us.
> #The maximum likelihood approach says that we should select the parameter
> #that makes the data most probable.
> #
> #For a Bernoulli variable, this is simply a search through the space
> #of values for p (i.e [0, 1]) that makes the data most probable to have
observed.
> #
> #How do we find the parameter numerically?
> #First, we want to define a function that specifies the probability
> #of our entire data set. We assume that each observation
> #in the data is INDEPENDENTLY and IDENTICALLY distributed,
> #so that the probability of the sequence is the product of the probabilities of
each value.
> #For the Bernoulli variables, this becomes the following function:
>
> likelihood <- function(sequence, p.parameter)
+
+ {
+   likelihood <- 1
+
+   for (i in 1:length(sequence))
+   {
+     if (sequence[i] == 1)
+     {
+       likelihood <- likelihood * p.parameter
+     }
+     else
+     {
+       likelihood <- likelihood * (1 - p.parameter)
+     }
+   }
+
+   return(likelihood)
+ }
>
> #To do maximum likelihood estimation, we therefore only need
> #to use an optimization function to maximize this function.
>
```

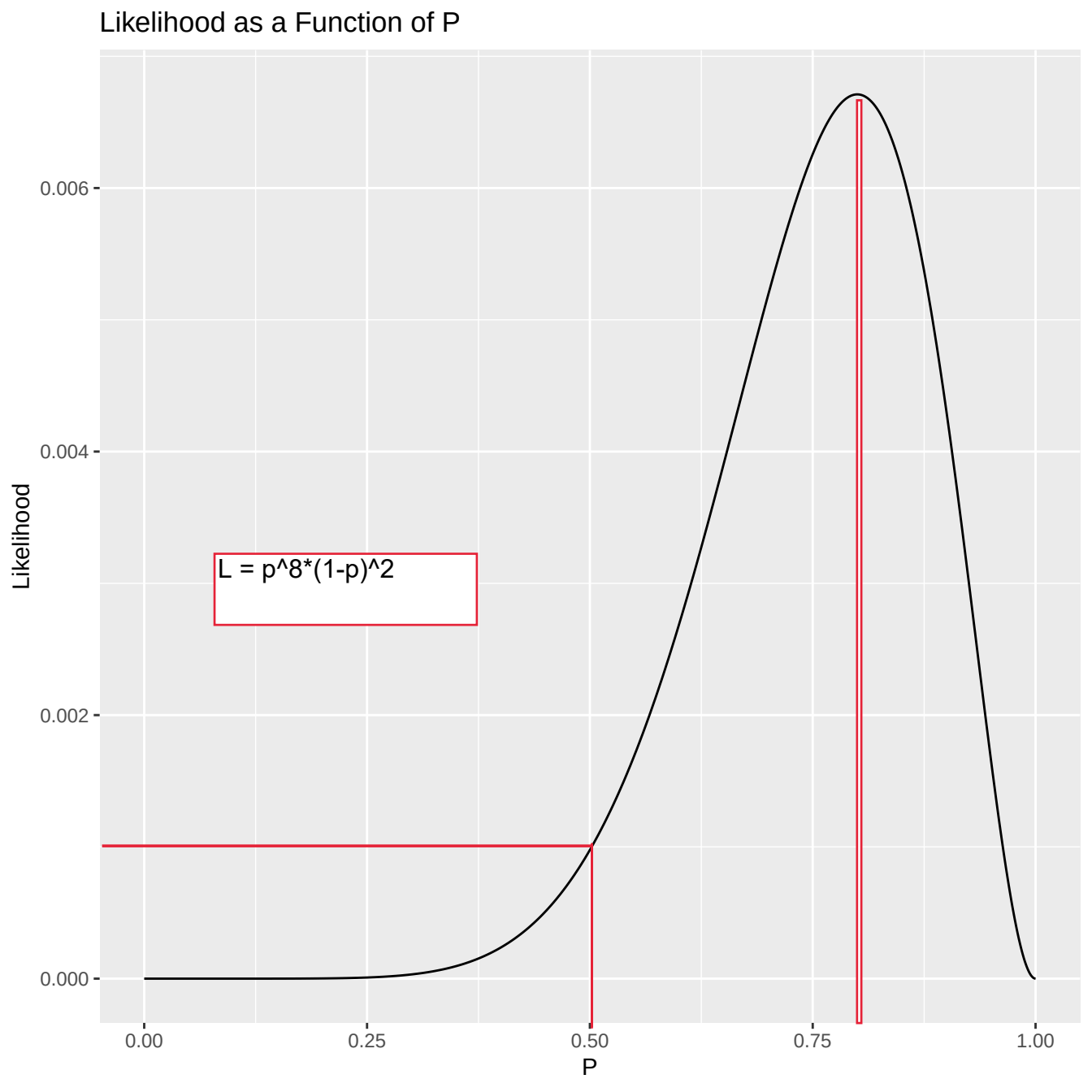
simulation with p=0.8

number of 1's is 8

```
> possible.p <- seq(0, 1, by = 0.001)
>
> library(ggplot2)
>
> windows(7,7)
> #now save the graphs in a pdf file
>  pdf(file="C:/users/jmard/Desktop/RegressionMethodsSpring2020/Lecture 11
07APR2020/MLEexampleR_out.pdf")
>
> qplot(possible.p,
+       sapply(possible.p, function (p) {likelihood(sequence, p)}),
+       geom = 'line',
+       main = 'Likelihood as a Function of P',
+       xlab = 'P',
+       ylab = 'Likelihood')
>
> #Use R's base function optimize to solve the optimization problem:
>
> mle.results <- optimize(function(p) {likelihood(sequence, p)},
+                         interval = c(0, 1),
+                         maximum = TRUE)
>
> mle.results
$maximum
[1] 0.799982

$objective
[1] 0.006710886

>
> objective.atmax <- (mle.results$maximum ^ 8) * ((1-mle.results$maximum)^2)
> objective.atmax
[1] 0.006710886
>
> check <- .5^10  #p=0.5 likelihood=?
> #if p=0.5 then p(S)=P(F) so at .5 likelihood is .5 ^ 10 which = 0.001
> check
[1] 0.0009765625
>
> ##-----------------------------------------##
>
> dev.off()
windows
      2
>
```


Likelihood as a Function of P
0.006
0.004
0.002
0.000
Likelihood
L = p^8*(1-p)^2
0.00
0.25
0.50
0.75
1.00
P