

The likelihood function

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January 12, 2026

See [here](#) for a PDF version of this vignette.

Prerequisites

You should understand the concept of using likelihood ratio for [discrete data](#) and [continuous data](#) to compare support for two fully specified models.

Overview

We have seen how one can use the likelihood ratio to compare the support in the data for two fully-specified models. In practice, we often want to compare more than two models — indeed, we often want to compare a continuum of models. This is where the idea of a *likelihood function* comes from.

Example

In the example [here](#), we assumed that the frequencies of different alleles (genetic types) in forest and savanna elephants were given to us. In practice, these frequencies themselves would have to be estimated from data.

For example, suppose we collect data on 100 savanna elephants, and we see that 30 of them carry allele 1 at marker 1, and 70 carry the allele 0 at marker 1 (again we are treating elephants as haploid to simplify things). Intuitively, we might estimate that the frequency of the 1 allele at that marker is 30/100, or 0.3. But we might think that the data are also consistent with other frequencies near 0.3. For example, maybe the data are also consistent with a frequency of 0.29. Or 0.28? Or...

In this case, we have many more than just two models to compare. Indeed, if we allow that the frequency could, in principle, lie anywhere in the interval $[0,1]$, then we have a continuum of models to compare.

Specifically, for each $q \in [0,1]$, let M_q denote the model that the true frequency of the 1 allele is q . Then, given our observation that 30 of 100 elephants carry allele 1 at marker 1, the likelihood for model M_q is, by the previous definition,

$$L(M_q) = \Pr(D \mid M_q) = q^{30}(1 - q)^{70}.$$

And the LR comparing models M_{q_1} and M_{q_2} is

$$\text{LR}(M_{q_1}, M_{q_2}) = [q_1/q_2]^{30}[(1 - q_1)/(1 - q_2)]^{70}.$$

This is an example of what is called a *parametric model*. A parametric model is collection of models indexed by a parameter vector, often denoted θ , whose values lie in some *parameter space*, usually denoted Θ . The number of parameters included in the vector θ is called the “dimensionality” of the model or parameter space, and often denoted $\dim(\Theta)$.

Here the parameter is q , and the parameter space is $[0, 1]$. The dimensionality of the parameter space is 1.

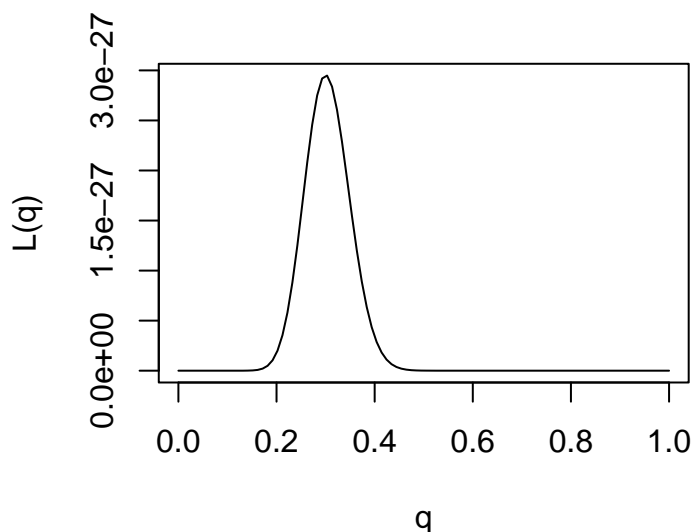
When computing likelihoods for parametric models, we usually dispense with the model notation and simply use the parameter value to denote the model. So instead of referring to the likelihood for M_q we just say the “likelihood for q ”, and write $L(q)$. So the likelihood for q is given by

$$L(q) = q^{30}(1 - q)^{70}.$$

Correspondingly, we can also refer to the “likelihood ratio for q_1 vs. q_2 ”.

We could plot the likelihood function as follows:

```
q <- seq(0,1,length.out = 100)
L <- function (q)
  q^30 * (1-q)^70
plot(q,L(q),ylab = "L(q)",xlab = "q",type = "l")
```



The value of θ that maximizes the likelihood function is referred to as the “maximum likelihood estimate”, and usually denoted $\hat{\theta}$. That is,

$$\hat{\theta} := \operatorname{argmax}_{\theta \in \Theta} L(\theta).$$

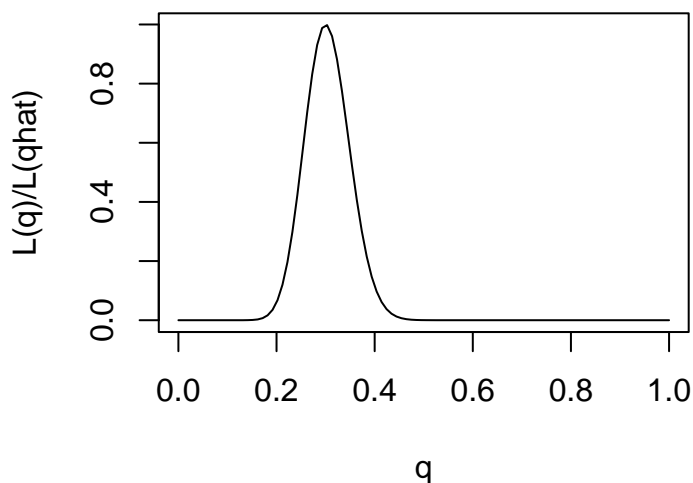
Provided the data are sufficiently informative and the number of parameters is not too large, maximum likelihood estimates tend to be sensible. In this case, we can see that the maximum likelihood estimate is $q = 0.3$, which corresponds to our intuition.

Note that from the likelihood function we can easily compute the likelihood ratio for any pair of parameter values! And just as with comparing two models, it is not the likelihoods that matter,

but the likelihood ratios. That is, you can divide the likelihood function by any constant without affecting the likelihood ratios.

One way to emphasize this is to standardize the likelihood function so that its maximum is at 1, by dividing $L(\theta)/L(\hat{\theta})$.

```
q <- seq(0,1,length.out = 100)
L <- function (q)
  q^30 * (1-q)^70
plot(q,L(q)/L(0.3),ylab = "L(q)/L(qhat)",xlab = "q",type = "l")
```

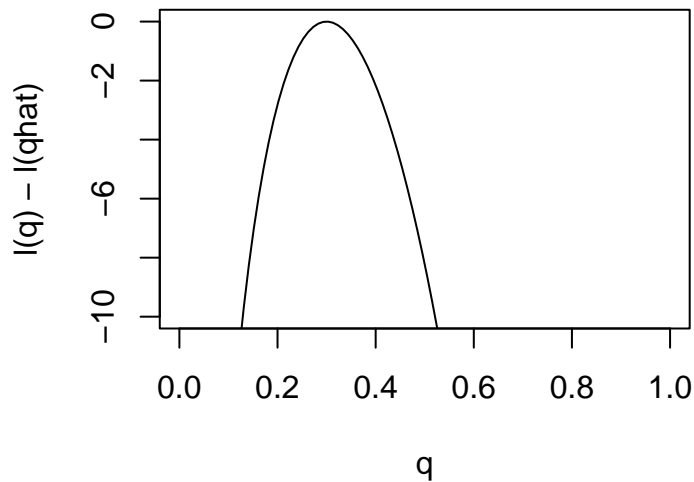


Note that, for some values of q , the likelihood ratio compared with $q = 0.3$ is very close to zero. These values of q are so much less consistent with the data that they are effectively excluded by the data. Just looking at the picture we might say that the values of q less than 0.15 or bigger than 0.5 are pretty much excluded by the data. We will see later how Bayesian analysis methods can be used to make this kind of argument more formal.

The log-likelihood

Just as it can often be convenient to work with the log-likelihood ratio, it can be convenient to work with the log-likelihood function, usually denoted $l(\theta)$ (“lowercase L”). As with log-likelihood ratios, unless otherwise specified, we use the “base e” log. Here is the log-likelihood function:

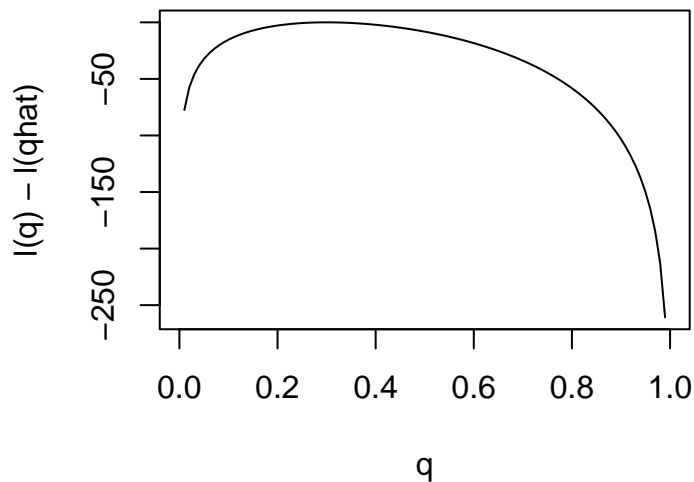
```
q <- seq(0,1,length.out = 100)
l <- function (q)
  30*log(q) + 70 * log(1-q)
plot(q,l(q) - l(0.3),ylab = "l(q) - l(qhat)",xlab = "q",type = "l",
  ylim = c(-10,0))
```



Changes in the log-likelihood function are referred to as “log-likelihood units”. For example, the difference in the support for $q = 0.3$ and $q = 0.35$ is $l(0.3) - l(0.35)$ which is 0.563 log-likelihood units. Again, remember that it is *differences* in l that matter.

Notice that the scale of the Y axis in this plot was set to span 10 log-likelihood units. Setting the scale in this way makes sure the plot focuses on the parts of the parameter space that have more than minuscule support from the data (in this case, LR no smaller than $1/e^{10}$). Without this, the plot can be much harder to read. For example, here is the plot using the default scale selected by R:

```
plot(q,l(q) - l(0.3),ylab = "l(q) - l(qhat)",xlab = "q",type = "l")
```



Notice how different this plot looks to the eye even though it is exactly the same curve being plotted (just different Y axis scale). It is worth thinking about what scale you use when plotting log-likelihoods (and, of course, figures in general!).