

SOME EXERCISES ABOUT LIKELIHOOD

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/UFPR/DEST/LEG/



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1 Uniform distribution

Let X be a r.v. with uniform distribution $X \sim U(0, \theta)$.

A random sample gave the following values: 5.5; 3.2; 4, 8, 5.3; 3.8 and 5.0. Obtain the likelihood function and one or more appropriate interval(s) specifying the form of obtaining.

```
# <r code> -----  
data <- c(5.5, 3.2, 4.8, 5.3, 3.8, 5)  
# </r code> -----
```

The likelihood of a Uniform($0, \theta$) is

$$\begin{aligned} L(\theta) &= \theta^{-n}, & \text{for } x_i < \theta \text{ for all } i \\ &= \theta^{-n}, & \text{for } \theta > x_{(n)}, \end{aligned}$$

and equal to zero otherwise.

Given the data above, we get $x_{(n)} = 5.5$ and the likelihood is shown in Figure 1, together with some intervals.

```
# <r code> -----  
lkl.unif <- function(theta, data) {  
  n <- length(data) ; xn <- max(data)  
  # this next step, in the way presented, isn't very efficient, since I'll  
  # compute the likelihood for all theta's and then, if necessary, convert to  
  # zero. however, since we have here a very simple likelihood (and this  
  # notation is extremely clear, btw), I keep in this way  
  lkl = theta**(-n)*{theta >= xn}  
  return(lkl)  
}  
theta.seq <- seq(4, 12, length.out = 100)  
lklseq.unif <- lkl.unif(theta.seq, data)  
  
par(mfrow = c(1, 2), mar = c(4, 4, 2, 2) + .1) # cosmetics  
# plotting the normalized likelihood function to have unit maximum  
plot(theta.seq, lklseq.unif/max(lklseq.unif), type = "l",  
      xlab = expression(theta), ylab = "Likelihood")  
# probability-based interval -----  
# cutoff's corresponding to a 95% and 99% confidence interval for the mean  
cuts <- c(.15, .04) * lkl.unif(max(data), data) / max(lklseq.unif)  
abline(h = cuts, lty = 2:3)  
# uniroot.all finds the zeros, so we need to subtract the cutoff point from  
# the likelihood to be able to find the points where the likelihood is cut  
ic.lkl.unif <- function(theta, cut, ...) {  
  lkl.unif(theta, ...)/max(lklseq.unif) - cut  
}
```

```

ic.95.prob <- rootSolve::uniroot.all(ic.lkl.unif, range(theta.seq),
                                   data = data, cut = cuts[1])
ic.99.prob <- rootSolve::uniroot.all(ic.lkl.unif, range(theta.seq),
                                   data = data, cut = cuts[2])
abline(v = ic.95.prob, lty = 2) ; abline(v = ic.99.prob, lty = 3)

plot(theta.seq, lklseq.unif/max(lklseq.unif), type = "l",
     xlab = expression(theta), ylab = "Likelihood")
# pure likelihood interval -----
# cutoff's corresponding to a 95\% and 99\% confidence interval for the mean
cuts <- c(.05, .01) * lkl.unif(max(data), data) / max(lklseq.unif)
abline(h = cuts, lty = 2:3)

ic.95.pure <- rootSolve::uniroot.all(ic.lkl.unif, range(theta.seq),
                                   data = data, cut = cuts[1])
ic.99.pure <- rootSolve::uniroot.all(ic.lkl.unif, range(theta.seq),
                                   data = data, cut = cuts[2])
abline(v = ic.95.pure, lty = 2) ; abline(v = ic.99.pure, lty = 3)
# </r code> -----

```

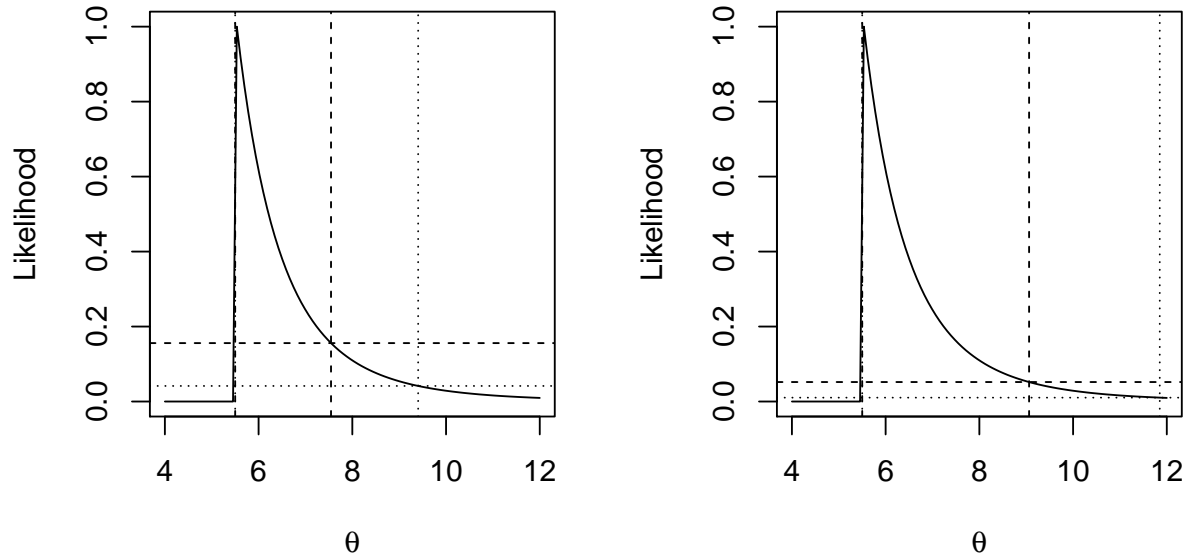


Figure 1: Likelihood function of θ in $\text{Uniform}(0, \theta)$ based on $x_{(6)} = 5.5$. In the left, likelihood intervals at 15% (dashed line) and 4% (dotted line) cutoff. In the right, likelihood intervals at 5% (dashed line) and 1% (dotted line) cutoff. These cutoffs correspond, in both sides, to a 95% and 99% confidence interval, respectively.

In both graphs of Figure 1 we have two confidence intervals for θ , one corresponding to a 95% confidence interval (dashed line) and one corresponding to a 99% confidence interval for the mean (dotted line). In the left we have a probability-based likelihood interval, in the right we have a pure likelihood interval.

The left ones are bad intervals, since they're based in a large-sample theory that results in an exact interval for the Gaussian case, in a good approximation for a reasonably regular case, and as we can see by the figure... here we doesn't have a regular likelihood (the likelihood isn't well approximated by a quadratic function), thus, here this interval should not be so good.

Explaining better how we arrived in these intervals:

For a normalized likelihood, $L(\theta)/L(\hat{\theta})$, we have the following Wilk's likelihood ratio statistic, defined as W

$$W \equiv 2 \log \frac{L(\hat{\theta})}{L(\theta)} \sim \chi_1^2.$$

Its χ^2 distribution is exact only in the normal mean model, and approximately true when the likelihood is reasonably regular.

Based in this Wilk's statistic we are able to find the probability that the likelihood interval covers θ ,

$$\Pr \left\{ \frac{L(\theta)}{L(\hat{\theta})} > c \right\} = \Pr \left\{ 2 \log \frac{L(\theta)}{L(\hat{\theta})} < -2 \log c \right\} = \Pr \{ \chi_1^2 < -2 \log c \}.$$

So, if for some $0 < \alpha < 1$ we choose a cutoff

$$c = e^{-\frac{1}{2} \chi_{1,(1-\alpha)}^2},$$

where $\chi_{1,(1-\alpha)}^2$ is the $100(1 - \alpha)$ percentile of χ_1^2 .

For $\alpha = 0.05$ and 0.01 we have a cutoff $c = 0.15$ and 0.04 , that corresponds to a 95% and 99% confidence interval, respectively. \square

Having the cutoff values we need now to find the interval values, i.e., in which points the cutoff horizontal line cuts the likelihood.

For this purpose we use the function `rootSolve::uniroot.all`.

A likelihood interval at 15% and 4% cutoff for θ are (5.5, 7.545) and (5.5, 9.405).

Already on the right side of Figure 1 we have a more coherent, let's say, confidence interval for the Uniform likelihood. While the likelihood isn't regular, it is still possible to provide an exact theoretical justification for a confidence interval interpretation. Now

$$\Pr \left\{ \frac{L(\theta)}{L(\hat{\theta})} > c \right\} = \Pr \left\{ \frac{X_{(n)}}{\theta} > c^{1/n} \right\} = 1 - \Pr \left\{ \frac{X_{(n)}}{\theta} < c^{1/n} \right\} = 1 - (c^{1/n})^n = 1 - c.$$

So the likelihood interval with cutoff c is a $100(1 - c)\%$ confidence interval.

A likelihood interval at 15% and 4% cutoff for θ are (5.5, 9.062) and (5.5, 11.849).

Comparing the obtained intervals we see a broader range with the pure likelihood intervals. In other words, with the pure likelihood intervals we see a higher uncertainty than with the (not so recommended here) probability-based likelihood intervals.

For doing this exercise I read and used it Pawitan's book:

```
@book{pawitan,  
  author    = {Yudi Pawitan},  
  title     = {In All Likelihood:  
              Statistical Modelling and Inference Using Likelihood},  
  year      = {1991},  
  publisher = {Oxford University Press},  
  address   = {Great Clarendon Street, Oxford OX2 6DP},  
}
```

2 Poisson distribution

Let X be a r.v. of a Poisson distribution ($X \sim P(\lambda)$) for which the following random sample was obtained: (3, 1, 0, 2, 1, 1, 0, 0).

```
# <r code> -----  
data <- c(3, 1, 0, 2, 1, 1, 0, 0)  
# </r code> -----
```

- (a) Obtain the likelihood function, its quadratic approximation and intervals for λ .

The likelihood and the log-likelihood of a $\text{Poisson}(\lambda)$ is

$$L(\lambda) = \prod_{i=1}^n \frac{e^{-\lambda} \lambda^{x_i}}{x_i!} \quad \text{and} \quad \log L(\lambda) = l(\lambda) = -n\lambda + \log \lambda \sum_{i=1}^n x_i - \sum_{i=1}^n \log x_i!.$$

We work here with the log-likelihood to make our life easier, since the computations are much simpler in the log scale.

By computing the Score (derivative of $l(\lambda)$ wrt to λ) and making it equal to zero, we find the MLE $\hat{\lambda} = \bar{x}$. Computing the second derivative we find the observed information

$$I_O(\lambda) = \frac{n\bar{x}}{\lambda^2} \quad \rightarrow \quad I_O(\hat{\lambda}) = \frac{n}{\bar{x}}.$$

A graph of the Poisson log-likelihood is provided in black in Figure 2.

Doing a quadratic approximation (Taylor expansion of second order) in $l(\lambda)$ around $\hat{\lambda}$ we have

$$\begin{aligned} l(\lambda) &\approx l(\hat{\lambda}) + (\lambda - \hat{\lambda})l'(\hat{\lambda}) + \frac{1}{2}(\lambda - \hat{\lambda})^2 l''(\hat{\lambda}) \\ &\quad \text{(the Score is zero at the MLE)} \\ &= l(\hat{\lambda}) + \frac{1}{2}(\lambda - \hat{\lambda})^2 l''(\hat{\lambda}) = l(\hat{\lambda}) + \frac{1}{2}(\lambda - \hat{\lambda})^2 I_O(\hat{\lambda}). \end{aligned}$$

A graph of the quadratic approximation of the Poisson log-likelihood is provided in red in Figure 2. There we can see how good is the approximation around the maximum likelihood estimator (MLE). Here the sample size is very small, the idea is that as the sample size increase the quality, in this case the range, of the approximation also increase. This should happen because as the sample size increase the Poisson likelihood should be more symmetric.

In the topright graph of Figure 2 we have two intervals for λ .

```
# <r code> -----
# likelihood -----
lkl.poi <- function(lambda, data) {
  n <- length(data)
  # log-likelihood ignoring irrelevant constant terms
  lkl = -n * lambda + sum(data) * log(lambda)
  return(lkl)
}
lambda.seq <- seq(0, 4.5, length.out = 100)
lklseq.poi <- lkl.poi(lambda.seq, data)
par(mar = c(4, 4, 2, 2) + .1) # cosmetics
layout(matrix(c(1, 3, 2, 3), 2, 2), heights = c(1.5, 1)) # more cosmetics
plot(lambda.seq, lklseq.poi, type = "l",
      xlab = expression(lambda), ylab = "log-likelihood")
lambda.est <- mean(data) # MLE
abline(v = lambda.est, lty = 3, col = 4)
# quadratic approximation -----
quadprox.poi <- function(lambda, lambda.est, data) {
  n <- length(data)
  obs.info <- n / lambda.est # observed information
  lkl.poi(lambda.est, data) - .5 * obs.info * (lambda - lambda.est)**2
}
curve(quadprox.poi(x, lambda.est, data), col = 2, add = TRUE)
legend(2.4, -6.25, c("log-like", "Quadratic\napprox.", "MLE"),
      col = c(1, 2, 4), lty = c(1, 1, 3), bty = "n")
# intervals for lambda -----
plot(lambda.seq, lklseq.poi, type = "l",
      xlab = expression(lambda), ylab = "log-likelihood")
curve(quadprox.poi(x, lambda.est, data), col = 2, add = TRUE)
abline(v = lambda.est, col = 4, lty = 3)
## probability-based interval -----
# cutoff's corresponding to a 95\% confidence interval for the mean
cut <- log(.15) + lkl.poi(lambda.est, data) ; abline(h = cut, lty = 2)
ic.lkl.poi <- function(lambda, cut, ...) { lkl.poi(lambda, ...) - cut }
ic.95.prob <- rootSolve::uniroot.all(ic.lkl.poi, range(lambda.seq),
                                   data = data, cut = cut)
arrows(x0 = ic.95.prob, y0 = rep(cut, 2),
       x1 = ic.95.prob, y1 = rep(-25, 2), lty = 2, length = .1)
## wald confidence interval -----
```

```

cut <- log(.15) + quadprox.poi(lambda.est, lambda.est, data)
abline(h = cut, lty = 2, col = 2)
se.lambda.est <- sqrt(lambda.est / length(data))
wald.95 <- lambda.est + qnorm(c(.025, .975)) * se.lambda.est
arrows(x0 = wald.95, y0 = rep(cut, 2),
       x1 = wald.95, y1 = rep(-25, 2), lty = 2, length = .1, col = 2)
# a better look in the approximation around the MLE -----
lambda.seq <- seq(.8, 1.2, length.out = 25)
plot(lambda.seq, lkl.poi(lambda.seq, data), type = "l",
     xlab = expression(lambda), ylab = "log-likelihood")
curve(quadprox.poi(x, lambda.est, data), col = 2, add = TRUE)
abline(v = lambda.est, lty = 3, col = 4)
# </r code> -----

```

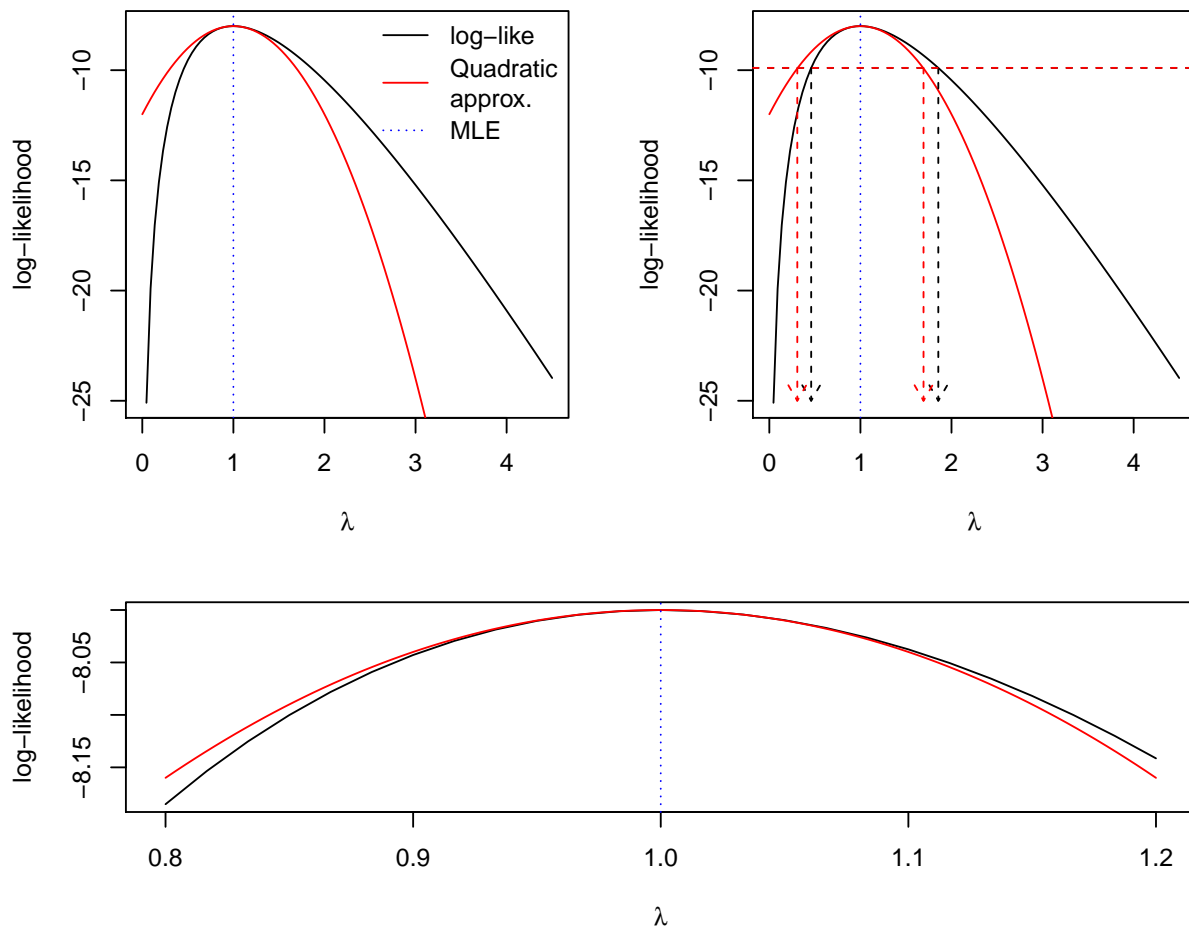


Figure 2: log-likelihood function and MLE of λ in $\text{Poisson}(\lambda)$ based on `data`. In the topleft, a quadratic approximation in red. In the topright, two intervals for λ - one based in the likelihood (in black) and one based in the quadratic approximation (in red). In the bottom we provide a better look in the quadratic approximation.

In the topright, in black, we have a interval based in the likelihood, $\lambda \in (0.459, 1.855)$, but with a cutoff criterion based in a χ^2 distribution. Thus, to have a nominal 95% confidence interval we use a cutoff $c = 15\%$. As we saw before, this interval is based in a large-sample theory. Since we're dealing here with a reasonable regular case, this interval shows as a good approximation.

Still in the topright of Figure 2, in red we have a interval based in the quadratic approximation of the log-likelihood, $\lambda \in (0.307, 1.693)$. From the quadratic approximation we get

$$\log \frac{L(\lambda)}{L(\hat{\lambda})} \approx -\frac{1}{2} I_O(\hat{\lambda})(\lambda - \hat{\lambda})^2,$$

that also follows a χ^2 distribution, since we have a r.v. $\hat{\lambda}$ normalized (with its expected value subtracted and divided by its variance) and squared. From this we get the following exact (in the normal case) 95% confidence interval

$$\hat{\lambda} \pm 1.96 I_O(\hat{\lambda})^{-1/2} \quad (\hat{\lambda} \pm 1.96 \text{ se}(\hat{\lambda})).$$

In the nonnormal cases this is an approximate 95% CI.

The actual variance is $I_E(\hat{\lambda})^{-1/2}$, but for the Poisson case the Fisher (expected) information is equal to the observed one, $I_O(\hat{\lambda})^{-1/2}$.

A very nice thing that we can see from this intervals is that a Wald interval (a \pm interval) corresponds to a cut in the quadratic approximation exactly in the same point that the probability-based interval cuts the (log-)likelihood. Thus, as more regular the likelihood, better will be the fit of the approximation and more reliable will be the Wald interval.

(b) **Repeat the previous question for reparametrization $\theta = \log(\lambda)$.**

By the invariance property of the MLE we have

$$\hat{\lambda} = \bar{x} \quad \Rightarrow \quad g(\hat{\lambda}) = \log \hat{\lambda} = \hat{\theta} = \log \bar{x} = g(\bar{x}).$$

i.e., the MLE of $\hat{\theta}$ is $\log \bar{x}$.

By the Delta Method we compute the variance of $\hat{\theta}$,

$$V[\theta] = V[g(\lambda)] = \left[\frac{\partial}{\partial \lambda} g(\lambda) \right]^2 V[\lambda] = \left[\frac{1}{\lambda} \right]^2 \frac{\lambda}{n} = \frac{1}{\lambda n} \quad \rightarrow \quad V[\hat{\theta}] = \frac{1}{\bar{x} n}.$$

From this we can take the observed information for the reparametrization

$$V[\hat{\theta}] = I_O^{-1}(\hat{\theta}) = (\bar{x} n)^{-1}.$$

Now we do, in the same manner, everything that we did in the previous letter.


```

# <r code> -----
# likelihood -----
## we can still use the lkl.poi function, but now we do
## lambda = exp(theta),
## with theta being a real rate (positive or negative)
theta.seq <- seq(-2, 2, length.out = 100)
lklseq.poi <- lkl.poi(exp(theta.seq), data)
par(mar = c(4, 4, 2, 2) + .1) # cosmetics
layout(matrix(c(1, 3, 2, 3), 2, 2), heights = c(1.5, 1)) # more cosmetics
plot(theta.seq, lklseq.poi, type = "l",
      xlab = expression(theta), ylab = "log-likelihood")
theta.est <- log(mean(data)) # MLE
abline(v = theta.est, lty = 3, col = 4)
# quadratic approximation for the reparametrization -----
quadprox.poi.repa <- function(theta, theta.est, data) {
  obs.info <- sum(data) # observed information
  lkl.poi(exp(theta.est), data) - .5 * obs.info * (theta - theta.est)**2
}
curve(quadprox.poi.repa(x, theta.est, data), col = 2, add = TRUE)

legend(-2.15, -27.5, c("log-like", "Quadratic\\napprox.", "MLE"),
      col = c(1, 2, 4), lty = c(1, 1, 3), bty = "n")
# intervals for lambda -----
plot(theta.seq, lklseq.poi, type = "l",
      xlab = expression(theta), ylab = "log-likelihood")
curve(quadprox.poi.repa(x, theta.est, data), col = 2, add = TRUE)
abline(v = theta.est, col = 4, lty = 3)
## probability-based interval -----
# cutoff's corresponding to a 95% confidence interval for the mean
cut <- log(.15) + lkl.poi(exp(theta.est), data) ; abline(h = cut, lty = 2)
ic.lkl.poi <- function(theta, cut, ...) {
  lambda <- exp(theta)
  lkl.poi(lambda, ...) - cut
}
ic.95.prob <- rootSolve::uniroot.all(ic.lkl.poi, range(theta.seq),
                                   data = data, cut = cut)
arrows(x0 = ic.95.prob, y0 = rep(cut, 2),
       x1 = ic.95.prob, y1 = rep(-43, 2), lty = 2, length = .1)
## wald confidence interval -----
cut <- log(.15) + quadprox.poi.repa(theta.est, theta.est, data)
abline(h = cut, lty = 2, col = 2)

se.theta.est <- sqrt(1 / sum(data))
wald.95 <- theta.est + qnorm(c(.025, .975)) * se.theta.est

arrows(x0 = wald.95, y0 = rep(cut, 2),
       x1 = wald.95, y1 = rep(-43, 2), lty = 2, length = .1, col = 2)

```

```

# a better look in the approximation around the MLE -----
theta.seq <- seq(-.75, .75, length.out = 25)
plot(theta.seq, lkl.poi(exp(theta.seq), data), type = "l",
      xlab = expression(theta), ylab = "log-likelihood")
curve(quadprox.poi.repa(x, theta.est, data), col = 2, add = TRUE)
abline(v = theta.est, lty = 3, col = 4)
# </r code> -----

```

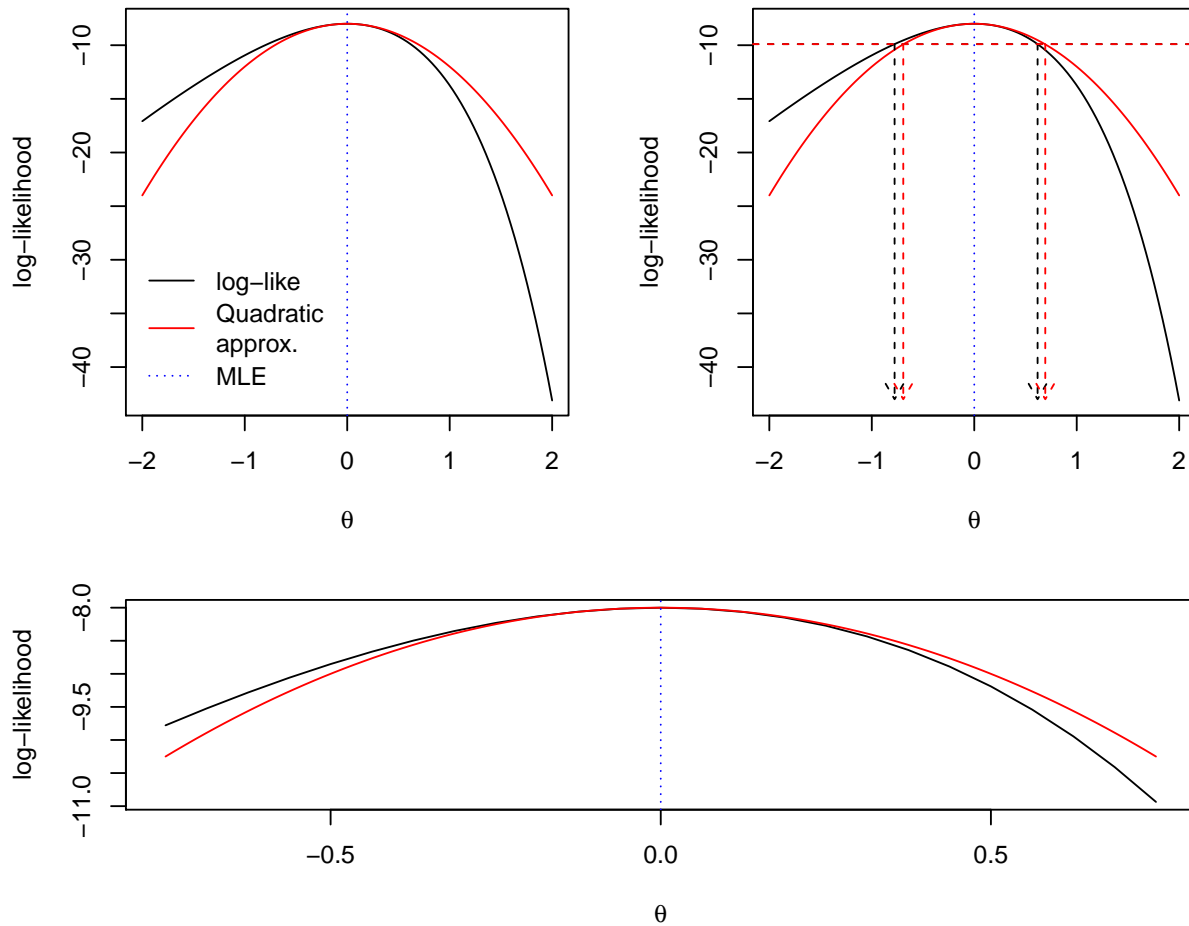


Figure 3: log-likelihood function and MLE of θ in $\text{Poisson}(\lambda = e^\theta)$ based on **data**. In the topleft, a quadratic approximation in red. In the topright, two intervals for θ - one based in the likelihood (in black) and one based in the quadratic approximation (in red). In the bottom we provide a better look in the quadratic approximation.

We obtained here two intervals for θ . One based in a cut in the likelihood, $\theta \in (-0.778, 0.618)$ - in black on the topright of Figure 3, and one based in a cut in the quadratic approximation of the likelihood, $\theta \in (-0.693, 0.693)$ - in red on the topright of Figure 3.

With the parametrization $\theta = \log \lambda$ the two intervals are closer than the ones obtained for λ . i.e., for θ (with the use of the log) we get a more regular likelihood.

- (c) Also obtain (by at least two different methods) confidence intervals for the parameter λ from the likelihood function (approximate or not) of θ .

```
# <r code> -----
# likelihood -----
theta.seq <- seq(-2, 2, length.out = 100)
lklseq.poi <- lkl.poi(exp(theta.seq), data)
par(mar = c(4, 4, 2, 2) + .1) # cosmetics
plot(theta.seq, lklseq.poi, type = "l",
      xlab = expression(theta), ylab = "log-likelihood")
abline(v = lambda.est, lty = 3, col = 4)
# quadratic approximation for the reparametrization -----
curve(quadprox.poi.repa(x, theta.est, data), col = 2, add = TRUE)
legend(-2.15, -22.5, c("log-like", "Quadratic\napprox.", "MLE"),
      col = c(1, 2, 4), lty = c(1, 1, 3), bty = "n")
# intervals for lambda -----
## probability-based interval -----
arrows(x0 = exp(ic.95.prob), y0 = c(-9, -36.5),
      x1 = exp(ic.95.prob), y1 = rep(-43, 2), lty = 2, length = .1)
## wald confidence interval -----
arrows(x0 = exp(wald.95), y0 = c(-9, -24),
      x1 = exp(wald.95), y1 = rep(-43, 2), lty = 2, length = .1, col = 2)
# </r code> -----
```

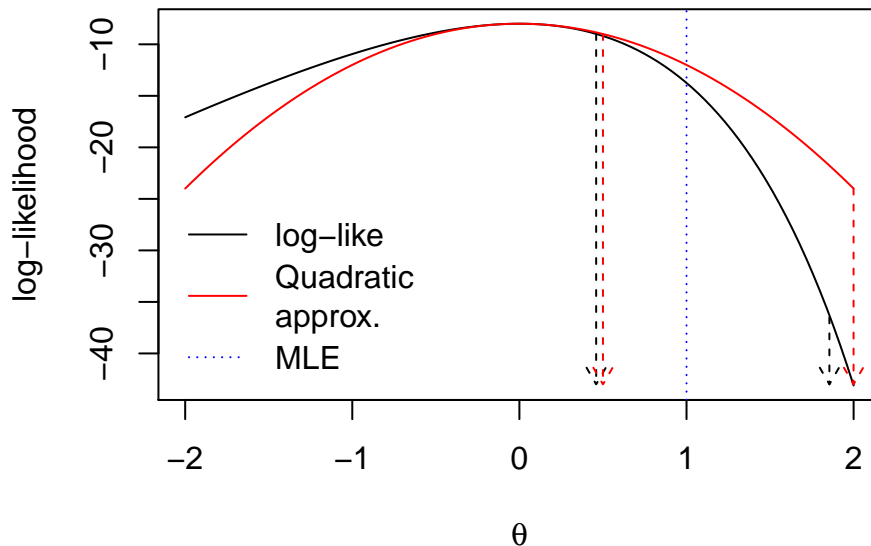


Figure 4: log-likelihood function and quadratic approximation of θ , and MLE of λ in $\text{Poisson}(\lambda = e^\theta)$ based on `data`. In dashed, 95% confidence intervals for λ .

Since the MLE has the invariance property, a very simple idea is: take the obtained interval for θ and apply a transformation, $\lambda = e^\theta$. This simple idea is true for the interval obtained via likelihood function, as we can see in Figure 4. The obtained interval is the same that the one in letter a). However, this idea doesn't work for the interval based in the quadratic approximation.

n the letter a), via the quadratic approximation we got $\lambda \in (0.307, 1.693)$. Here, applying the relation $\lambda = e^\theta$ we get $\lambda \in (0.5, 2)$. i.e., this shows that the invariance property applies to the likelihood, not to the quadratic approximation of the likelihood.

3 Hypergeometric distribution

In order to obtain an audience estimate of a game without using ticket sales data or stadium roulette records, special shirts were distributed to 300 supporters on condition that they were used during a game. During the game 250 fans were randomly selected and 12 of them had the shirt.

a) Obtain the likelihood function for the total number of supporters.

We have here a random variable, let's say, X , representing the number of observed successes, k . Here an observed success is select a fan using a special shirt. So, we have

$$X \sim \text{Hypergeometric}(N, K = 300, n = 250),$$

with probability $p = K/N$.

N is the population size, that we want estimate. K is the unknown number of fans using a special shirt, and n is the number of, randomly, selected fans.

$$\begin{aligned} \Pr[X = k] &= \frac{\binom{K}{k} \binom{N-K}{n-k}}{\binom{N}{n}} \\ \Pr[X = 12] &= \frac{\binom{300}{12} \binom{N-300}{250-12}}{\binom{N}{250}} \\ &= \frac{300! 250!}{288! 238! 12!} \frac{(N-300)! (N-250)!}{(N-538)! N!} \\ &= \text{constant} \times \frac{(N-300)! (N-250)!}{(N-538)! N!}. \end{aligned}$$

Since we already have a k , the likelihood is equal to $\Pr[X = k]$.

$$\begin{aligned}
L(N) &= \Pr[X = 12] \\
&= \text{constant} \frac{(N - 300)! (N - 250)!}{(N - 538)! N!} \\
l(N) = \log L(N) &= \log \text{ constant} + \log \frac{(N - 300)! (N - 250)!}{(N - 538)! N!} \\
&\approx \log \frac{(N - 300)! (N - 250)!}{(N - 538)! N!}.
\end{aligned}$$

A plot of the likelihood is provided in Figure 5.

```

# <r code> -----
# likelihood -----
# always starting from N = 539
lkl.hypergeo <- function(N) {
  N.init <- 539
  size <- N - N.init
  n1 <- n2 <- n3 <- n4 <- numeric(size)
  N <- N.init
  for (i in 1:size) {
    n1[i] = log(N - 300)
    n2[i] = log(N - 250)
    n3[i] = log(N - 538)
    n4[i] = log(N)
    N = N + 1
  }
  lkl <- sum(n1) + sum(n2) - sum(n3) - sum(n4)
  return(lkl)
}
compute.lkl <- function(grid, ...) {
  size.grid = length(grid)
  lkl.grid = numeric(size.grid)
  i = 1
  for (j in grid) {
    lkl.grid[i] = lkl.hypergeo(N = j)
    i = i + 1
  }
  return(lkl.grid)
}
# plotting
par(mar = c(4, 4, 2, 2) + .1) # cosmetics
layout(matrix(c(0, 1, 1, 0, # more cosmetics
                2, 2, 3, 3), nrow = 2, byrow = TRUE))
n.grid <- seq(3000, 17000, by = 20)
plot(n.grid, compute.lkl(n.grid), "l", xlab = "N", ylab = "log-like")
abline(v = 6250, lty = 2)

```

```

n.grid <- seq(539, 1e4, by = 20)
plot(n.grid, compute.lkl(n.grid), "l", xlab = "N", ylab = "log-like")
abline(v = 6250, lty = 2)

n.grid <- seq(5000, 8000, by = 10)
plot(n.grid, compute.lkl(n.grid), "l", xlab = "N", ylab = "log-like")
abline(v = 6250, lty = 2)
# </r code> -----

```

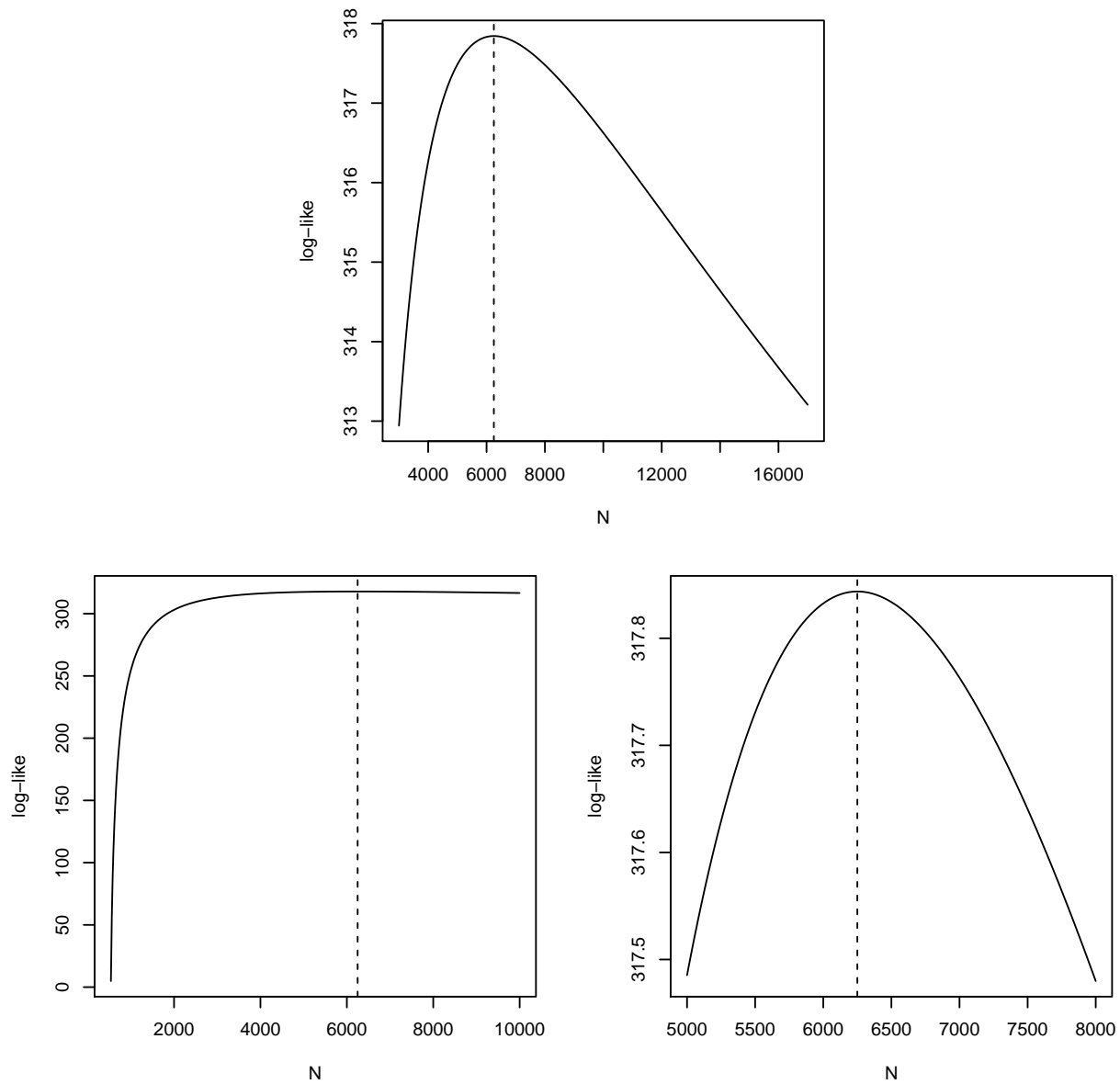


Figure 5: log-likelihood of N in Hypergeometric(N , $K = 300$, $n = 250$) based on $k = 12$. In dashed, the MLE. Different ranges of N to have a better understanding of the likelihood behaviour.

The MLE here is given by $\hat{N} = \lfloor Kn/k \rfloor = 6250$.

Figure 5 present some very interesting behaviours.

In the top, going from $N = 3000$ to $N = 17000$ we can see clearly the likelihood asymmetry. In the bottomleft, starting from the first valid possible value, 539, we see basically nothing. i.e., we don't see any possible curvature in the likelihood. In the bottomright we focus around the MLE to see better the curvature. Around that point we see a very small variation in the likelihood, 0.3, for a range of 3000 in N . This shows how smooth is the curvature around the MLE in a large region.

- b) **Get the point estimate and the interval estimate, the latter by at least two different methods.**

```
# <r code> -----
# point estimate -----
optimize(lkl.hypergeo, lower = 539, upper = 2e4, maximum = TRUE)
# </r code> -----

$maximum
[1] 6251.045

$objective
[1] 317.8437
```

Using the `optimize` routine to do the optimization we obtain $\hat{N} = 6251$, and a log-likelihood of 317.85. This value for \hat{N} is practically equal to what the ML theory says, $\hat{N} = \lfloor Kn/k \rfloor = 6250$.

Next, we compute a quadratic approximation for the hypergeometric (log-)likelihood followed by two intervals, one based in the likelihood, and a wald interval based in the quadratic approximation. All this is presented in Figure 6.

```
# <r code> -----
# quadratic approximation of the likelihood -----
hess <- numDeriv::hessian(lkl.hypergeo, x = 6250)

# quadratic approx.
quadprox.hypergeo <- function(N, N.est = 6250) {
  obs.info <- as.vector(-hess) # observed information
  lkl.hypergeo(N.est) - .5 * obs.info * (N - N.est)**2
}

par(mar = c(4, 4, 2, 2) + .1) # cosmetics
layout(matrix(c(1, 2,
                 3, 3), nrow = 2, byrow = TRUE),
      heights = c(1.5, 1)) # more cosmetics
```

```

# likelihood plot
n.grid <- seq(3000, 17000, by = 20)
plot(n.grid, compute.lkl(n.grid), "l",
     xlab = "N", ylab = "log-likelihood")
abline(v = 6250, lty = 3, col = 4)

# quadratic approximation plot
curve(quadprox.hypergeo(x), col = 2, add = TRUE)

legend(10500, 318.25,
      c("log-like", "Quadratic\napprox.", "MLE"),
      col = c(1, 2, 4), lty = c(1, 1, 3), bty = "n")

# intervals for N -----
# first, we plot again the likelihood and the quadratic approx.
n.grid <- seq(2500, 12000, by = 20)

plot(n.grid, compute.lkl(n.grid), "l",
     xlab = "N", ylab = "log-likelihood")

abline(v = 6250, lty = 3, col = 4)

curve(quadprox.hypergeo(N = x), col = 2, add = TRUE)

## probability-based interval -----
# cutoff's corresponding to a 95% confidence interval for N
cut <- log(.15) + lkl.hypergeo(6250)

abline(h = cut, lty = 2)

ic.lkl.hypergeo <- function(grid) {
  compute.lkl(grid) - cut
}
ic.95.prob <- rootSolve::uniroot.all(ic.lkl.hypergeo, range(n.grid))

arrows(x0 = ic.95.prob, y0 = rep(cut, 2),
      x1 = ic.95.prob, y1 = rep(309.5, 2), lty = 2, length = .1)

## wald confidence interval -----
cut <- log(.15) + quadprox.hypergeo(N = 6250)

abline(h = cut, lty = 2, col = 2)

se.n.est <- sqrt(as.vector(-1 / hess))
wald.95 <- 6250 + qnorm(c(.025, .975)) * se.n.est

arrows(x0 = wald.95, y0 = rep(cut, 2),

```



```

x1 = wald.95, y1 = rep(309.5, 2), lty = 2, length = .1, col = 2)

# a better look in the approximation around the MLE -----
n.grid <- seq(5000, 8000, by = 10)

plot(n.grid, compute.lkl(n.grid), "l",
     xlab = "N", ylab = "log-likelihood")

abline(v = 6250, lty = 3, col = 4)
curve(quadprox.hypergeo(N = x), col = 2, add = TRUE)
# </r code> -----

```

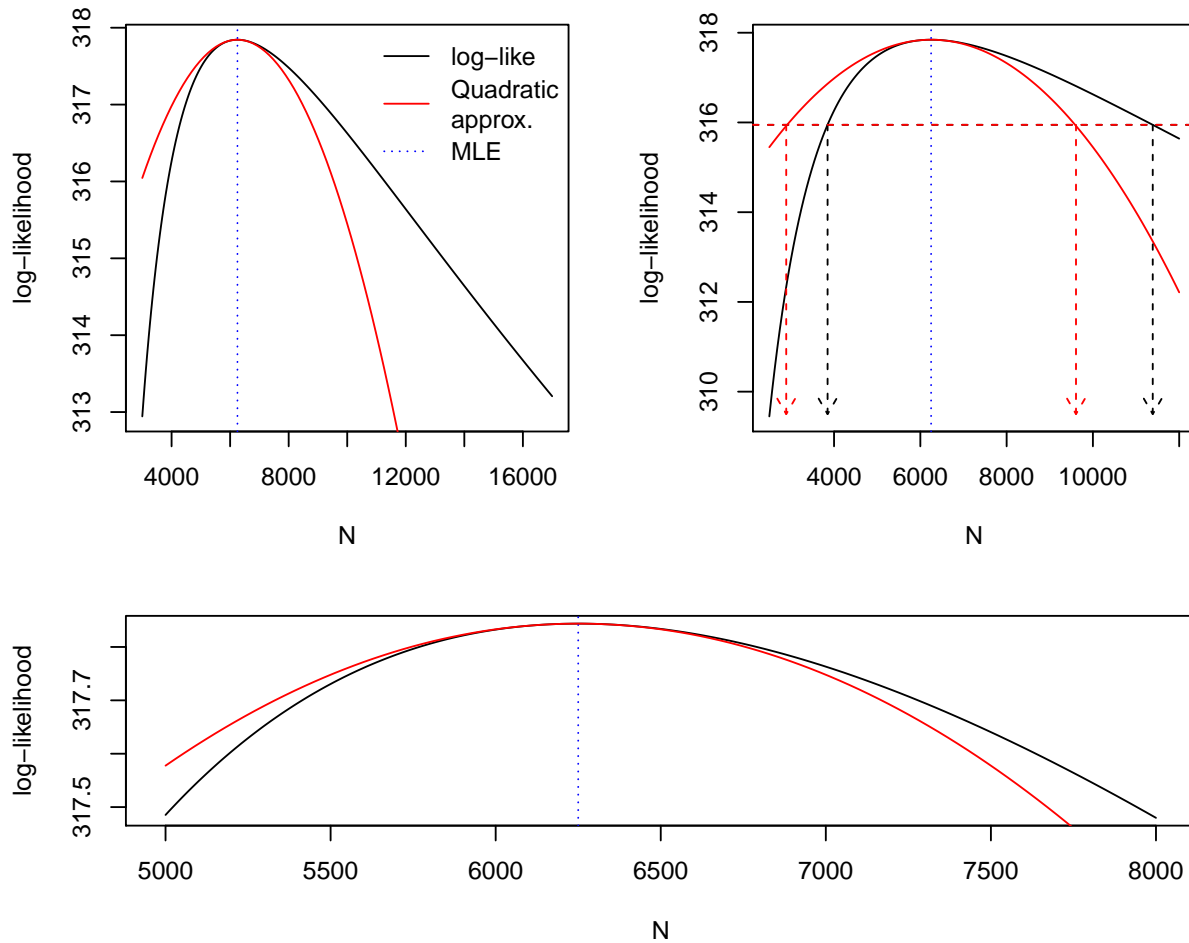


Figure 6: log-likelihood function and MLE of N in Hypergeometric(N , $K = 300$, $n = 250$) based on $k = 12$. In the topleft, a quadratic approximation in red. In the topright, two intervals for N - one based in the likelihood (in black) and one based in the quadratic approximation (in red). In the bottom we provide a better look in the quadratic approximation.

The quadratic approximation and the intervals were obtained in the same way that in the exercises before, with the only difference that here the hessian was obtained numerically, just for simplicity.

Based in a cut in the likelihood, we obtain (3850, 11387) as a 95% interval for the total number of fans in the game. With the wald interval (quadratic approximation) we obtain (2892, 9608) as a 95% interval. *A considerable difference.*

- c) **Repeat and compare the results if there were 500 shirts and 20 with shirts out of the 250.**

The procedure here is exactly the same.

We have

$$\begin{aligned}\Pr[X = k] &= \frac{\binom{K}{k} \binom{N-K}{n-k}}{\binom{N}{n}}, & \Pr[X = 20] &= \frac{\binom{500}{20} \binom{N-500}{250-20}}{\binom{N}{250}} \\ & & &= \frac{500! \, 250!}{480! \, 230! \, 20!} \frac{(N-500)! \, (N-250)!}{(N-730)! \, N!} \\ & & &= \text{constant} \times \frac{(N-500)! \, (N-250)!}{(N-730)! \, N!}.\end{aligned}$$

With likelihood

$$\begin{aligned}L(N) &= \Pr[X = 20] \\ &= \text{constant} \frac{(N-500)! \, (N-250)!}{(N-730)! \, N!} \\ l(N) &= \log L(N) = \log \text{constant} + \log \frac{(N-500)! \, (N-250)!}{(N-730)! \, N!} \\ &\approx \log \frac{(N-500)! \, (N-250)!}{(N-730)! \, N!}.\end{aligned}$$

In Figure 7 we provide the likelihood graphs and intervals for N .

```
# <r code> -----
# likelihood -----
# always starting from N = 731
lkl.hypergeo <- function(N) {
  N.init <- 731
  size <- N - N.init
  n1 <- n2 <- n3 <- n4 <- numeric(size)
  N <- N.init
  for (i in 1:size) {
    n1[i] = log(N - 500)
```

```

        n2[i] = log(N - 250)
        n3[i] = log(N - 730)
        n4[i] = log(N)
        N = N + 1
    }
    lkl <- sum(n1) + sum(n2) - sum(n3) - sum(n4)
    return(lkl)
}

# plotting -----
par(mar = c(4, 4, 2, 2) + .1) # cosmetics

layout(matrix(c(1, 2, 3, 3), nrow = 2, byrow = TRUE),
        heights = c(1.5, 1)) # more cosmetics
## likelihood -----
n.grid <- seq(3000, 17000, by = 20)

plot(n.grid, compute.lkl(n.grid), "l",
     xlab = "N", ylab = "log-likelihood")
abline(v = 6250, lty = 3, col = 4)
## quadratic approximation -----
hess <- numDeriv::hessian(lkl.hypergeo, x = 6250)

curve(quadprox.hypergeo(x), col = 2, add = TRUE)
legend(10500, 382.5, c("log-like", "Quadratic\napprox.", "MLE"),
     col = c(1, 2, 4), lty = c(1, 1, 3), bty = "n")
# intervals for N -----
# first, we plot again the likelihood and the quadratic approx.
n.grid <- seq(2750, 11000, by = 20)

plot(n.grid, compute.lkl(n.grid), "l",
     xlab = "N", ylab = "log-likelihood")
abline(v = 6250, lty = 3, col = 4)

curve(quadprox.hypergeo(N = x), col = 2, add = TRUE)
## probability-based interval -----
# cutoff's corresponding to a 95% confidence interval for N
cut <- log(.15) + lkl.hypergeo(6250)
abline(h = cut, lty = 2)

ic.95.prob <- rootSolve::uniroot.all(ic.lkl.hypergeo, range(n.grid))

arrows(x0 = ic.95.prob, y0 = rep(cut, 2),
      x1 = ic.95.prob, y1 = rep(370.25, 2), lty = 2, length = .1)
## wald confidence interval -----
cut <- log(.15) + quadprox.hypergeo(N = 6250)
abline(h = cut, lty = 2, col = 2)

```

```

se.n.est <- sqrt(as.vector(-1 / hess))
wald.95 <- 6250 + qnorm(c(.025, .975)) * se.n.est

arrows(x0 = wald.95, y0 = rep(cut, 2),
       x1 = wald.95, y1 = rep(370.25, 2), lty = 2, length = .1, col = 2)
# a better look in the approximation around the MLE -----
n.grid <- seq(5000, 7500, by = 10)

plot(n.grid, compute.lkl(n.grid), "l",
     xlab = "N", ylab = "log-likelihood")
abline(v = 6250, lty = 3, col = 4)
curve(quadprox.hypergeo(N = x), col = 2, add = TRUE)
# </r code> -----

```

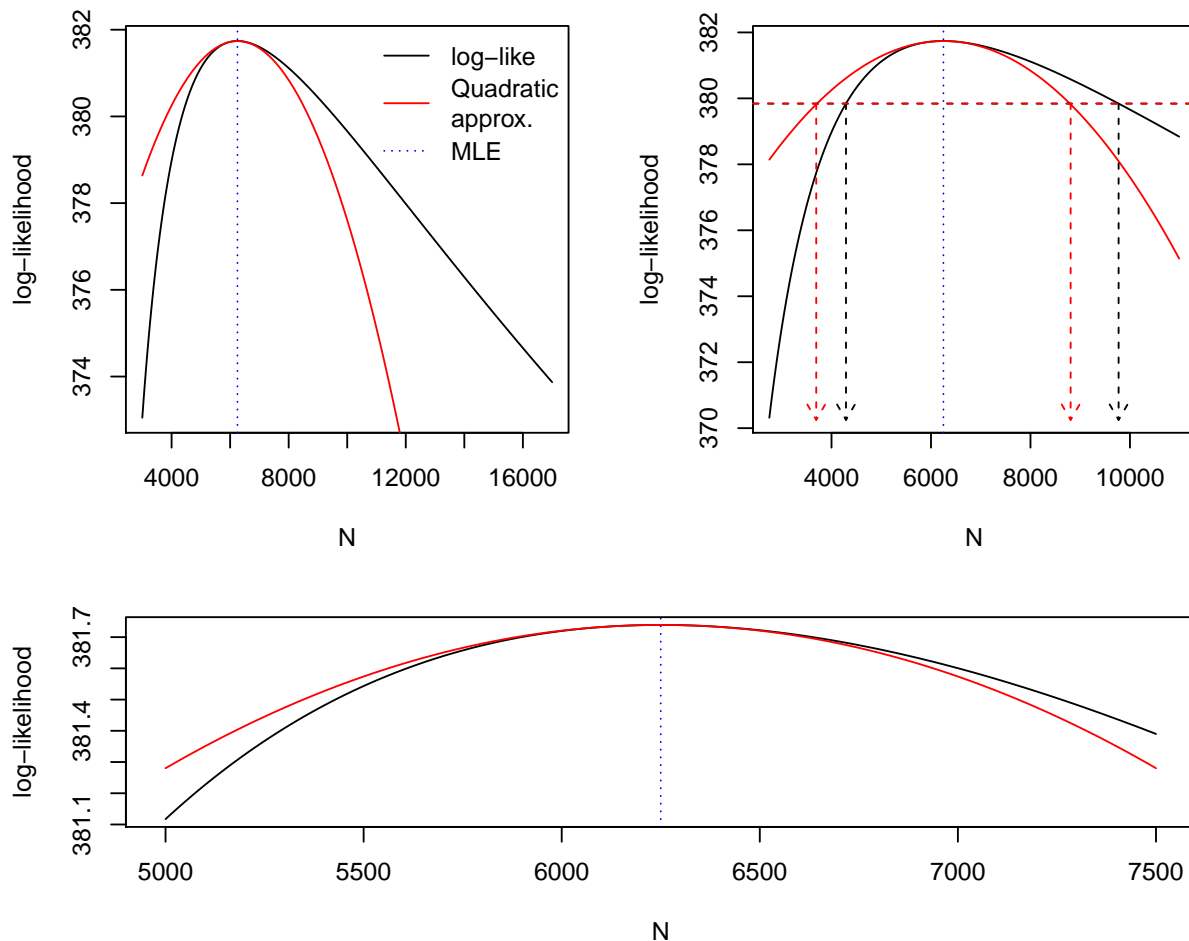


Figure 7: log-likelihood function and MLE of N in Hypergeometric(N , $K = 500$, $n = 250$) based on $k = 20$. In the topleft, a quadratic approximation in red. In the topright, two intervals for N - one based in the likelihood (in black) and one based in the quadratic approximation (in red). In the bottom we provide a better look in the quadratic approximation.

The MLE is exactly the same that the one in the previous scenario, since

$$\hat{N} = \lfloor Kn/k \rfloor = \lfloor 300 \times 250 / 12 \rfloor = \lfloor 500 \times 250 / 20 \rfloor = 6250.$$

- Based in a cut in the likelihood, we obtain (4291, 9772) as a 95% interval for the total number of fans in the game.
- With the wald interval (quadratic approximation) we obtain (3693, 8807) as a 95% interval for the total number of fans.

A considerable difference.

Comparing with the previous scenario the intervals changed considerably, even with MLE retain the same.

The likelihood shape is the same that before, just with a vertical increase. Before the maximum log-likelihood estimate was around 318, now is around 382.

4 Gaussian distribution with interval data

The following independent observations were taken from one r.v. $X \sim N(\mu, \sigma^2)$.

- [1] 56.4 54.2 65.3 49.2 50.1 56.9 58.9 62.5 70.0 61.0
- another 5 observations are known to be less than 50.
- it is known that 3 other observations are greater than 65.

(a) **Write the likelihood function.**

The likelihood can be expressed as

$$\begin{aligned} L(\theta) &= \left(\prod_{i=1}^{10} f(x_i) \right) \times (F(50))^5 \times (1 - F(65))^3 \\ &= \left(\prod_{i=1}^{10} \phi \left(\frac{y_i - \mu}{\sigma} \right) \right) \times \left(\Phi \left(\frac{50 - \mu}{\sigma} \right) \right)^5 \times \left(1 - \Phi \left(\frac{65 - \mu}{\sigma} \right) \right)^3 \\ l(\theta) &= \sum_{i=1}^{10} \log \phi \left(\frac{y_i - \mu}{\sigma} \right) + 5 \log \Phi \left(\frac{50 - \mu}{\sigma} \right) + 3 \log \left(1 - \Phi \left(\frac{65 - \mu}{\sigma} \right) \right). \end{aligned}$$

```

# <r code> -----
# likelihood -----
## if logsigma = TRUE, we do the parametrization using log(sigma)
lkl.norm <- function(par, xs, less.than, more.than, logsigma = FALSE) {
  if (logsigma) par[2] <- exp(par[2])
  l1 <- sum(dnorm(xs, mean = par[1], sd = par[2], log = TRUE))
  l2 <- 5 * log(pnorm(less.than, mean = par[1], sd = par[2]))
  l3 <- 3 * log(1 - pnorm(more.than, mean = par[1], sd = par[2]))
  lkl <- l1 + l2 + l3
  # we return the negative of the log-likelihood,
  # since the optim routine performs a minimization
  return(-lkl)
}
# </r code> -----

```

(b) Obtain estimates of maximum likelihood.

```

# <r code> -----
# providing an initial guess based uniquely in the ten points sample
init.guess <- c(mean(data), sd(data))
# parameters estimation
(par.est <- optim(init.guess, lkl.norm, logsigma = FALSE,
                  xs = data, less.than = 65, more.than = 50)$par)
# </r code> -----

[1] 58.10630  5.66888

```

$$\hat{\mu} = 58.106, \quad \hat{\sigma} = 5.669.$$

FYI: In the ten points sample we have $\bar{x} = 58.45$ and $s^2 = 6.527$.

(c) Obtain profiles of likelihood.

First, we do the graph of the likelihood surface in the deviance scale, since this scale is much more convenient. This requires the value of the likelihood evaluated in the parameter estimates.

The deviance here is basically

$$D(\theta) = -2(l(\theta) - l(\hat{\theta})),$$

with θ being the vector of parameters μ and σ .

In Figure 8 we have the likelihood surfaces for two parametrizations: σ and $\log \sigma$.

```

# <r code> -----
# deviance -----
dev.norm <- function(theta, est, ...) {
  # remember: here we have the negative of the log-likelihoods,
  # so the sign the different
  return(2 * (lkl.norm(theta, ...) - lkl.norm(est, ...)))
}
dev.norm.surf <- Vectorize(function(x, y, ...) dev.norm(c(x, y), ...))

par(mfrow = c(1, 2), mar = c(4, 4, 2, 2) + .1) # cosmetics
## parametrization: sigma -----
mu.grid <- seq(52, 63.75, length.out = 100)
sigma.grid <- seq(3.25, 12.5, length.out = 100)

outer.grid <- outer(mu.grid, sigma.grid, FUN = dev.norm.surf,
  est = par.est, xs = data,
  less.than = 65, more.than = 50)

contour.levels <- c(.99, .95, .9, .7, .5, .3, .1, .05)

contour(mu.grid, sigma.grid, outer.grid,
  levels = qchisq(contour.levels, df = 2),
  labels = contour.levels,
  xlab = expression(mu), ylab = expression(sigma))

# converting par.est to a matricial object
points(t(par.est), col = 2, pch = 19, cex = .75)
## parametrization: log sigma -----
mu.grid <- seq(52, 63.75, length.out = 100)
sigma.grid <- seq(1.225, 2.5, length.out = 100)

par.est <- optim(init.guess, lkl.norm, logsigma = TRUE,
  xs = data, less.than = 65, more.than = 50)$par

outer.grid <- outer(mu.grid, sigma.grid, FUN = dev.norm.surf,
  est = par.est, xs = data,
  logsigma = TRUE, less.than = 65, more.than = 50)

contour.levels <- c(.99, .95, .9, .7, .5, .3, .1, .05)

contour(mu.grid, sigma.grid, outer.grid,
  levels = qchisq(contour.levels, df = 2),
  labels = contour.levels,
  xlab = expression(mu), ylab = expression(log(sigma)))

points(t(par.est), col = 2, pch = 19, cex = .75)
# </r code> -----

```

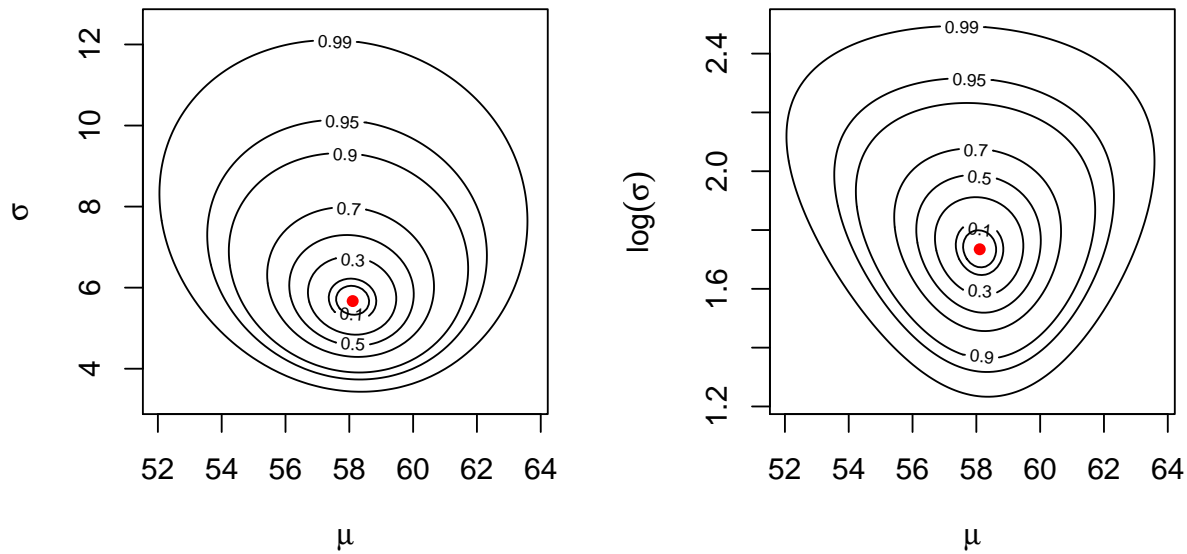


Figure 8: Deviances of (μ, σ) and $(\mu, \log \sigma)$ for a Gaussian sample made of interval data.

From Figure 8 two things are important to mention. First, with interval data, the surface doesn't exhibit orthogonally between the parameters. Second, in the log parametrization of sigma we have better behavior in the surface.

Now, we obtain the likelihood profiles for each parameter. The profiles are presented in Figure 9.

To obtain the likelihood profile for μ , let's say, we need to create a grid of values of μ and for each value of this grid find the value, let's say, $\hat{\sigma}_\mu$ that maximizes the profile likelihood. We do this below for μ and σ , the results can be seen in Figure 9.

```
# <r code> -----
# profiles -----
## likelihood -----
## optimizing one parameter per time.
## to use the optimize routine (single parameter optimization)
## we need to split the par argument in two
lkl.norm.profiles <- function(mu, sigma, xs, less.than, more.than) {
  l1 <- sum(dnorm(xs, mean = mu, sd = sigma, log = TRUE))
  l2 <- 5 * log(pnorm(less.than, mean = mu, sd = sigma))
  l3 <- 3 * log(1 - pnorm(more.than, mean = mu, sd = sigma))
  lkl <- l1 + l2 + l3
  return(lkl)}
par(mfrow = c(1, 2), mar = c(4, 4, 2, 2) + .1) # cosmetics
## mu -----
mu.grid <- seq(45, 69.25, length.out = 100)
# with the optimize routine we obtain two numbers:
# the optimal sigma for the given value of mu.grid,
```



```

# and the respective log-likelihood value
mu.perf <- matrix(0, nrow = length(mu.grid), ncol = 2)
for (i in 1:length(mu.grid)) {
  mu.perf[i, ] <- unlist(
    optimize(lkl.norm.profiles, lower = 0, upper = 50,
             mu = mu.grid[i],
             xs = data, less.than = 65, more.than = 50,
             maximum = TRUE))}
plot(mu.grid, mu.perf[, 2], type = "l",
     xlab = expression(mu), ylab = expression(l(mu[sigma])))
abline(v = par.est[1], col = 2)
## sigma -----
sigma.grid <- seq(3.25, 13.75, length.out = 100)
sigma.perf <- matrix(0, nrow = length(sigma.grid), ncol = 2)

for (i in 1:length(sigma.grid)) {
  sigma.perf[i, ] <- unlist(
    optimize(lkl.norm.profiles, lower = 0, upper = 100,
             sigma = sigma.grid[i],
             xs = data, less.than = 65, more.than = 50,
             maximum = TRUE))}
plot(sigma.grid, sigma.perf[, 2], type = "l",
     xlab = expression(sigma), ylab = expression(l(sigma[mu])))
# we apply the exponential, since we did log sigma optimization by last
abline(v = exp(par.est[2]), col = 2)
# </r code> -----

```

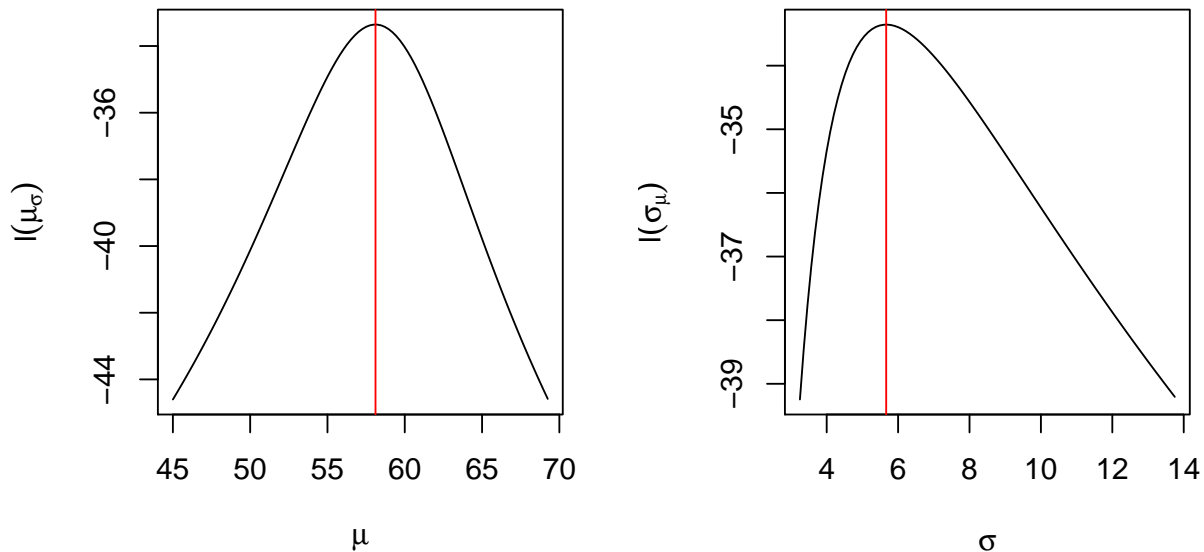


Figure 9: log-likelihood profiles for μ and σ for a Gaussian sample made of interval data. In red, the respective MLE's.

(d) Obtain the standard error estimates.

With the `optim` routine we obtain the hessian.

```
# <r code> -----  
# initial guess  
init.guess <- c(mean(data), sd(data))  
  
# parameters estimation, now also computing the hessian  
(hess <- optim(init.guess, lkl.norm,  
              xs = data,  
              less.than = 65, more.than = 50,  
              hessian = TRUE)$hessian)  
# </r code> -----
```

```
          [,1]      [,2]  
[1,] 0.38190632 0.04403561  
[2,] 0.04403561 0.80092515
```

And we know that the hessian, $H(\theta)$, is the negative of the observed information, $I_O(\theta)$, and that asymptotically the variance of $\hat{\theta}$ is $I_O(\theta)^{-1}$. Thus,

```
# <r code> -----  
# standard error  
(se <- diag(sqrt(1 / hess)))  
# </r code> -----
```

```
[1] 1.618160 1.117388
```

The standard errors, `se`, are

$$\text{se}(\hat{\mu}) = 1.618, \quad \text{se}(\hat{\sigma}) = 1.117.$$

5 Gaussian regression

Consider the following data table (adapted/modified from Montgomery & Runger, 1994) to which we wish to fit a simple linear regression model by relating the response variable Y (purity in %) to an explanatory variable X (hydrocarbon level).

X	0.99	1.02	1.15	1.29	1.46	1.36	0.87	1.23	1.55	1.40
Y	99.01	89.05	91.43	93.74	96.73	94.45	87.59	91.77	99.42	93.65
X	1.19	1.15	0.98	1.01	1.11	1.20	1.26	1.32	1.43	0.95
Y	93.54	92.52	90.56	89.54	89.85	90.39	93.25	93.41	94.98	87.33

(a) Find the likelihood function.

```
# <r code> -----
data <- data.frame(
  x = c(.99, 1.02, 1.15, 1.29, 1.46, 1.36, .87, 1.23, 1.55, 1.4,
        1.19, 1.15, .98, 1.01, 1.11, 1.2, 1.26, 1.32, 1.43, .95),
  y = c(99.01, 89.05, 91.43, 93.74, 96.73, 94.45, 87.59, 91.77, 99.42,
        93.65, 93.54, 92.52, 90.56, 89.54, 89.85, 90.39, 93.25, 93.41,
        94.98, 87.33)
)
par(mar = c(4, 4, 2, 2) + .1)
plot(y ~ x, data,
      xlab = "hydrocarbon level", ylab = expression("purity"~("%")))
# </r code> -----
```

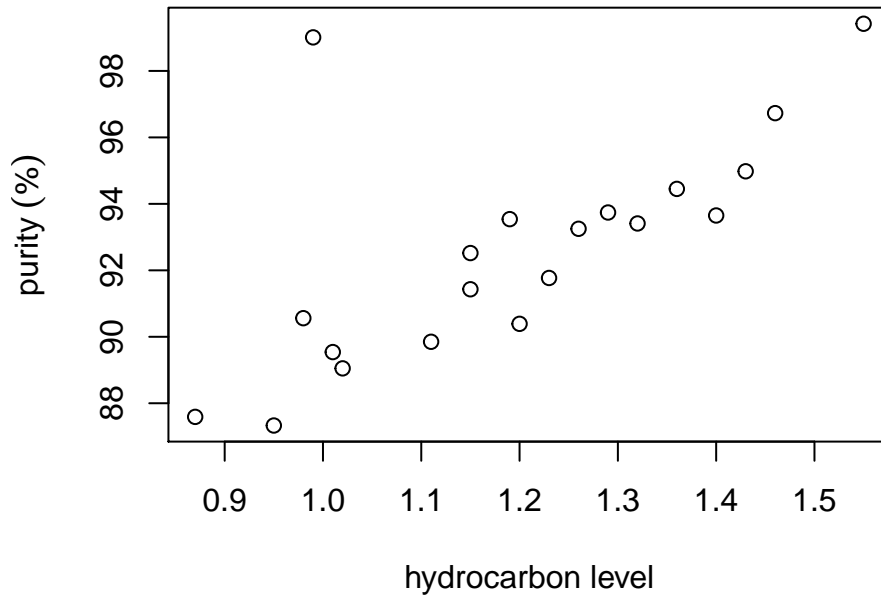


Figure 10: Dispersion between hydrocarbon level \times purity (%).

Assuming a Normal distribution for $Y|X$, we have the following log-likelihood, in matrix form

$$\begin{aligned}
 l(\theta; Y) &= -\frac{n}{2} \log 2\pi - n \log \sigma - \frac{1}{2\sigma^2} \|Y - X\beta\|^2 \\
 &= \text{constant} - n \log \sigma - \frac{1}{2\sigma^2} \|Y - X\beta\|^2,
 \end{aligned}$$

where $\theta = [\beta_0 \ \beta_1 \ \sigma]^\top$, $\beta = [\beta_0 \ \beta_1]^\top$, and $\mu_i = \beta_0 + \beta_1 x_i$.

(b) Find the estimates of maximum likelihood.

```
# <r code> -----
# likelihood -----
lkl.model.norm <- function(b0, b1, sigma, y, x, logsigma = FALSE) {
  ## if logsigma = TRUE, we do the parametrization using log(sigma)
  if (lowsigma) sigma <- exp(sigma)
  mu <- b0 + b1 * x
  lkl <- sum(dnorm(y, mean = mu, sd = sigma, log = TRUE))
  # we return the negative of the log-likelihood,
  # since the optim routine performs a minimization
  return(-lkl)
}
library(bbmle)
par.est <- mle2(lkl.model.norm,
               start = list(b0 = min(data$y),
                           b1 = 1.5,
                           sigma = sd(data$y)),
               data = list(y = data$y, x = data$x), method = "BFGS")
par.est@coef
# </r code> -----
```

	b0	b1	sigma
	77.988429	12.225489	2.343799

Just checking...

```
# <r code> -----
lm(y ~ x, data)$coef # beta_0 and beta_1
```

(Intercept)	x
77.98996	12.22453

```
# sigma^2
```

```
par.est@coef[[3]]**2
```

```
[1] 5.493392
```

```
(summary(lm(y ~ x, data))$sigma**2) * (nrow(data) - 2) / nrow(data)
```

```
[1] 5.493386
```

```
# </r code> -----
```

Checked, ✓.

(c) Obtain the joint likelihood for the parameters β_0 and β_1 :

i. considering σ fixed with value equal to its estimate.

```
# <r code> -----
# deviance -----
dev.model.norm <- function(beta, theta.est, ...) {
  b0 <- beta[1]
  b1 <- beta[2]
  b0.est <- theta.est[[1]]
  b1.est <- theta.est[[2]]
  sigma.est <- theta.est[[3]]
  lkl.grid <- lkl.model.norm(b0, b1, sigma.est, ...)
  lkl.est <- lkl.model.norm(b0.est, b1.est, sigma.est, ...)
  lkl.diff <- lkl.grid - lkl.est
  # remember: here we have the negative of the log-likelihoods,
  # so the sign the different
  return(2 * lkl.diff)
}

# deviance, vectorized version -----
dev.model.norm.surf <- Vectorize(
  function(a, b, ...) dev.model.norm(c(a, b), ...)
)

# deviance contour, plotting -----
b0.grid <- seq(67.5, 88.5, length.out = 100)
b1.grid <- seq(3.5, 21, length.out = 100)

outer.grid <- outer(b0.grid, b1.grid,
  FUN = dev.model.norm.surf,
  theta.est = par.est@coef,
  y = data$y, x = data$x)

contour.levels <- c(.99, .95, .9, .7, .5, .3, .1, .05)

par(mar = c(4, 4, 2, 2) + .1) # cosmetics

contour(b0.grid, b1.grid,
  outer.grid,
  levels = qchisq(contour.levels, df = 2),
  labels = contour.levels,
  xlab = expression(beta[0]),
  ylab = expression(beta[1]))

# converting par.est@coef to a matricial object
points(t(par.est@coef[1:2]), col = 2, pch = 19, cex = .75)
# </r code> -----
```

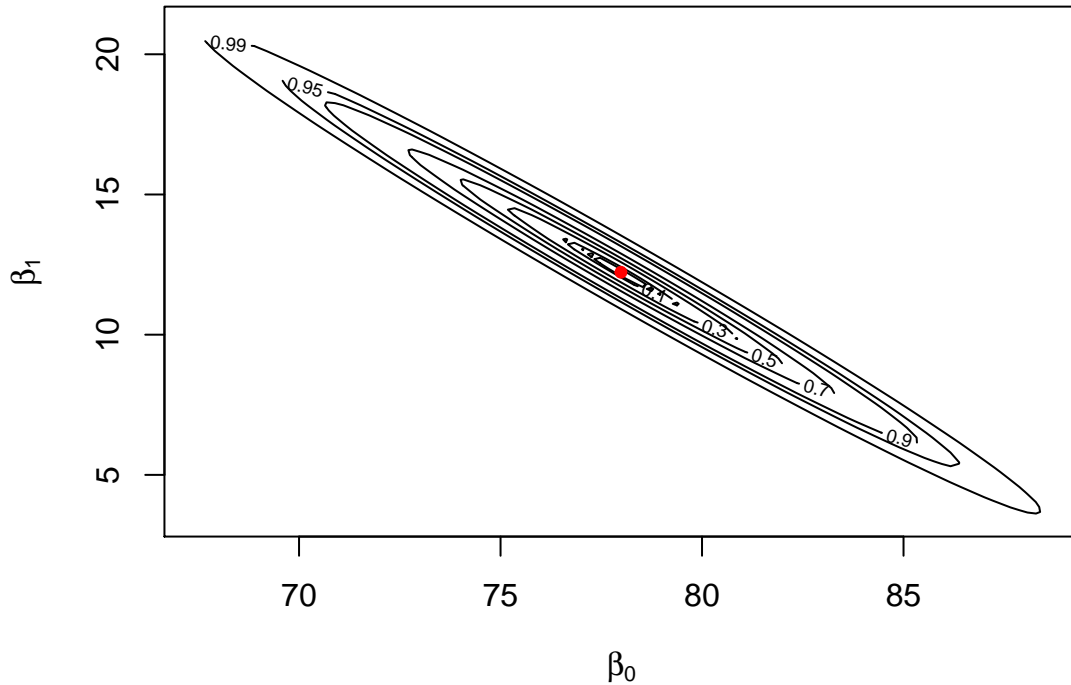


Figure 11: Deviance of (β_0, β_1) with σ fixed in it's estimative, for a Gaussian regression.

ii. obtaining the profile likelihood (joint - 2D) with respect to σ .

```
# <r code> -----
# profile -----
sigma.grid <- seq(1.7, 3.5, length.out = 100)
# with the optim routine we obtain three numbers: the estimates
# of beta_0, beta_1, and the corresponding log-likelihood
beta.perf <- matrix(0, nrow = length(sigma.grid), ncol = 3)
for (i in 1:length(sigma.grid)) {
  beta.perf[i, ] <- unlist(
    mle2(lkl.model.norm,
        start = list(b0 = min(data$y), b1 = 1.5),
        data = list(
          y = data$y, x = data$x, sigma = sigma.grid[i]),
        method = "BFGS"
      )@details[1:2]
  )
}
par(mar = c(4, 4, 2, 2) + .1) # cosmetics
plot(sigma.grid, -1 * beta.perf[, 3], type = "l",
     xlab = expression(sigma), ylab = "log-likelihood")
abline(v = par.est@coef[[3]], lty = 2)
# </r code> -----
```

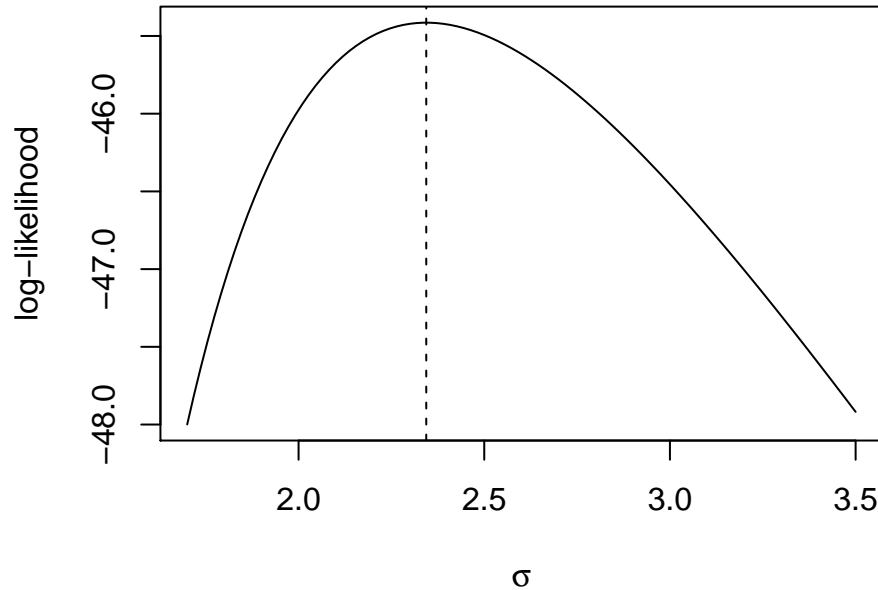


Figure 12: log-likelihood profile for σ , for a Gaussian regression. In dashed, the respective MLE.

And how the β 's fluctuates across the grid of σ ?

```
# <r code> -----
summary(beta.perf[ , 1]) # beta_0

  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
77.98  77.99   77.99   77.99  78.00   78.01

summary(beta.perf[ , 2]) # beta_1

  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
12.21  12.22   12.22   12.22  12.22   12.23

# </r code> -----
```

Very few, as expected. Since the estimation of β doesn't depend on σ .

(d) Obtain the profile likelihood for the parameters β_0 and β_1 individually.

```
# <r code> -----
par(mfrow = c(1, 2), mar = c(4, 4, 2, 2) + .1) # cosmetics
# beta_0 profile -----
b0.grid <- seq(67.5, 88.5, length.out = 100)
# with the optim routine we obtain two numbers:
# the estimate of beta_1 and the log-likelihood
b0.perf <- matrix(0, nrow = length(b0.grid), ncol = 2)
```

```

for (i in 1:length(b0.grid)) {
  b0.perf[i, ] <- unlist(
    mle2(lkl.model.norm, start = list(b1 = 1.5),
      data = list(
        y = data$y, x = data$x,
        b0 = b0.grid[i], sigma = par.est@coef[[3]]),
      method = "BFGS")@details[1:2]))}
plot(b0.grid, -1 * b0.perf[, 2], type = "l",
  xlab = expression(beta[0]), ylab = "log-likelihood")
abline(v = par.est@coef[[1]], lty = 2)
# beta_1 profile -----
b1.grid <- seq(3.5, 21, length.out = 100)
# with the optim routine we obtain two numbers:
# the estimate of beta_0 and the log-likelihood
b1.perf <- matrix(0, nrow = length(b1.grid), ncol = 2)
for (i in 1:length(b1.grid)) {
  b1.perf[i, ] <- unlist(
    mle2(lkl.model.norm, start = list(b0 = min(data$y)),
      data = list(
        y = data$y, x = data$x,
        b1 = b1.grid[i], sigma = par.est@coef[[3]]),
      method = "BFGS")@details[1:2]))}
plot(b1.grid, -1 * b1.perf[, 2], type = "l",
  xlab = expression(beta[1]), ylab = "log-likelihood")
abline(v = par.est@coef[[2]], lty = 2)
# </r code> -----

```

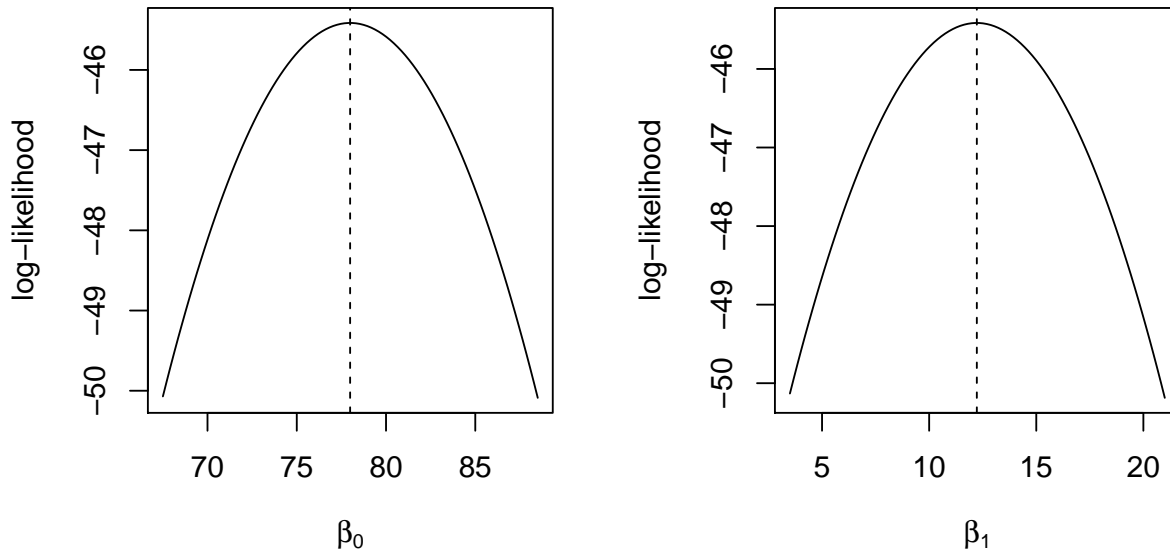


Figure 13: log-likelihood profiles for β_0 and β_1 for a Gaussian regression. In dashed, MLE's.

6 Poisson regression

Consider a sample of a r.v. Y where it is assumed that $Y_i \sim P(\lambda_i)$ where the parameter λ_i is described by a function of an explanatory variable $\log(\lambda_i) = \beta_0 + \beta_1 x_i$ with values known from x_i .

Simulated data with $(\beta_0 = 2, \beta_1 = 0.5)$ are shown below.

Y	10	15	11	37	70	19	12	12	13	88
X	1.7	1.5	0.5	2.8	4.4	1.8	0.4	0.7	1.3	5.1

```
# <r code> -----
data <- data.frame(y = c(10, 15, 11, 37, 70, 19, 12, 12, 13, 88),
                  x = c(1.7, 1.5, .5, 2.8, 4.4, 1.8, .4, .7, 1.3, 5.1))
par(mar = c(4, 4, 2, 2) + .1) ; plot(y ~ x, data)
# </r code> -----
```

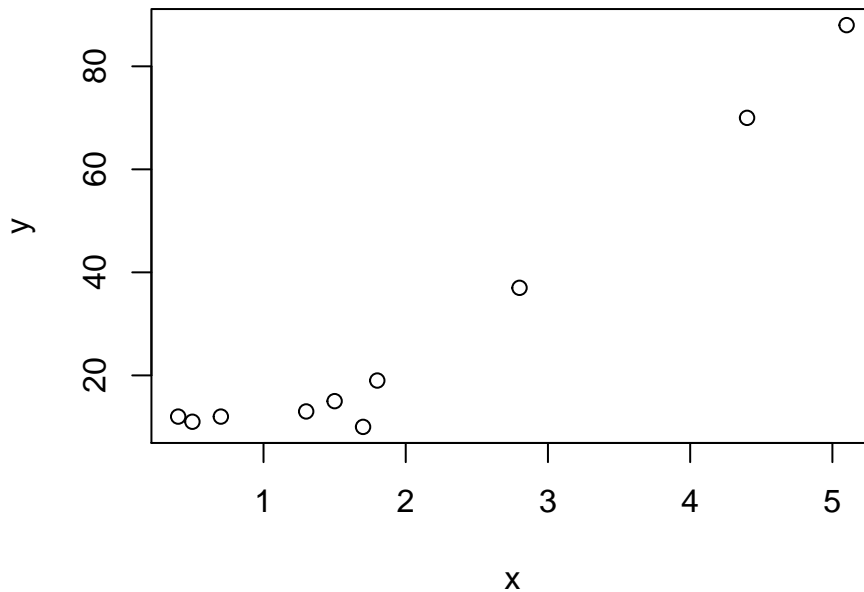


Figure 14: Dispersion between the variables Y and X.

- (a) Obtain the graph of the likelihood function indicating the position of the true values of the parameters.

The log-likelihood is given by

$$l(\lambda) = -n\lambda + \log \lambda \sum_{i=1}^n y_i - \sum_{i=1}^n \log y_i! , \quad \lambda_i = \exp\{\beta_0 + \beta_1 x_i\}.$$

```

# <r code> -----
# likelihood -----
lkl.model.poi <- function(b0, b1, data) {
  n <- nrow(data)
  lambda <- exp(b0 + b1 * data$x)
  lkl <- sum(dpois(data$y, lambda = lambda, log = TRUE))
  # we return the negative of the log-likelihood,
  # since the optim routine performs a minimization
  return(-lkl)
}

# deviance -----
dev.model.poi <- function(beta, beta.est, ...) {
  b0 <- beta[1]
  b1 <- beta[2]
  b0.est <- beta.est[1]
  b1.est <- beta.est[2]
  lkl.grid <- lkl.model.poi(b0, b1, ...)
  lkl.est <- lkl.model.poi(b0.est, b1.est, ...)
  lkl.diff <- lkl.grid - lkl.est
  # remember: here we have the negative of the log-likelihoods,
  # so the sign the different
  return(2 * lkl.diff)
}

# deviance, vectorized version -----
dev.model.poi.surf <- Vectorize(
  function(a, b, ...) dev.model.poi(c(a, b), ...)
)

# deviance contour, plotting -----
b0.grid <- seq(1.625, 2.475, length.out = 100)
b1.grid <- seq(.375, .6, length.out = 100)

outer.grid <- outer(b0.grid, b1.grid,
  FUN = dev.model.poi.surf,
  beta.est = c(2, .5), data = data)

contour.levels <- c(.99, .95, .9, .7, .5, .3, .1, .05)

par(mar = c(4, 4, 2, 2) + .1) # cosmetics

contour(b0.grid, b1.grid, outer.grid,
  levels = qchisq(contour.levels, df = 2),
  labels = contour.levels,
  xlab = expression(beta[0]), ylab = expression(beta[1]))

# true parameter values
points(c(2, .5), col = 2, pch = 19, cex = .75)
# </r code> -----

```

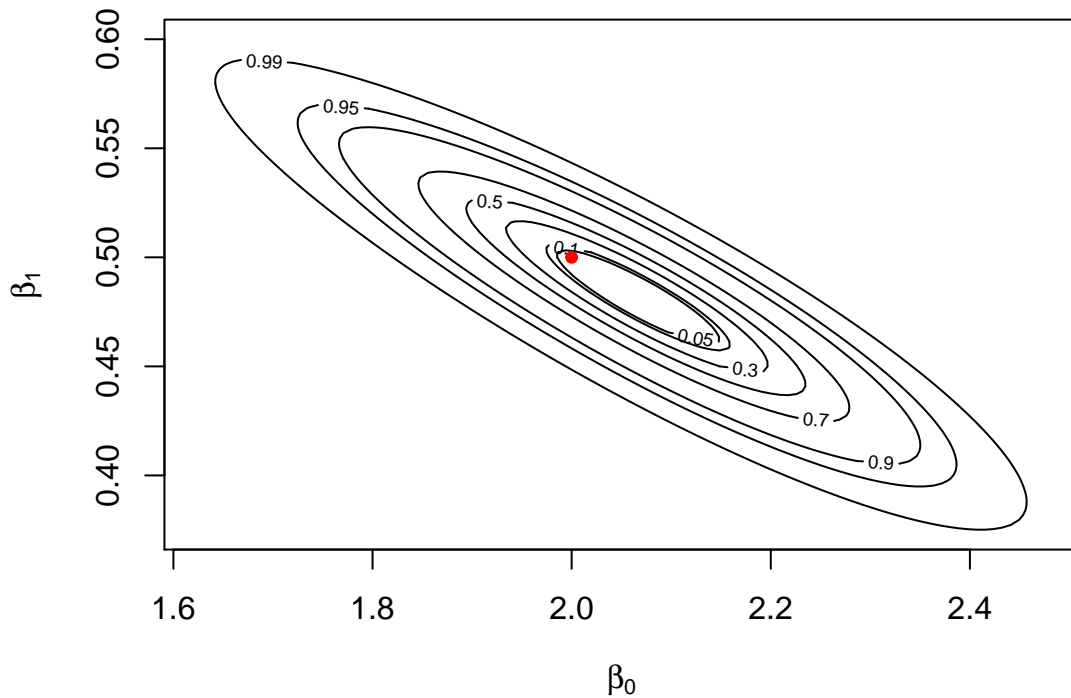


Figure 15: Deviance of (β_0, β_1) for a Poisson regression based on `data`.

(b) Obtain the likelihood profiles of the parameters.

```
# <r code> -----
par(mfrow = c(1, 2), mar = c(4, 4, 2, 2) + .1) # cosmetics
# beta_0 profile -----
b0.grid <- seq(1.25, 2.75, length.out = 100)
# profiled likelihood of beta_0
pl.b0 <- function(grid) {
  n <- length(grid)
  p.lkl <- numeric(n)
  for (i in 1:n) {
    p.lkl[i] <- mle2(lkl.model.poi,
                     start = list(b1 = .5),
                     data = list(data = data, b0 = grid[i]),
                     method = "BFGS"
                    )@details[[2]]
  }
  return(-p.lkl)
}
p.b0 <- pl.b0(b0.grid)

plot(b0.grid, p.b0, type = "l",
     xlab = expression(beta[0]), ylab = "log-likelihood")
```

```

abline(v = 2, lty = 2)
# beta_1 profile -----
b1.grid <- seq(.3, .675, length.out = 100)
# profiled likelihood of beta_1
pl.b1 <- function(grid) {
  n <- length(grid)
  p.lkl <- numeric(n)
  for (i in 1:n) {
    # for some points of the grid can happen that the hessian
    # not be invertible, with tryCatch we can skip these points
    tryCatch({
      p.lkl[i] <- mle2(lkl.model.poi,
        start = list(b0 = min(data$y)),
        data = list(data = data, b1 = grid[i]),
        method = "BFGS")@details[[2]]
    },
    warning = function(w) w
  )}
  return(-p.lkl)
}
p.b1 <- pl.b1(b1.grid)

ind <- complete.cases(p.b1) # indicator for only the not NA cells
plot(b1.grid[ind], p.b1[ind], type = "l",
  xlab = expression(beta[1]), ylab = "log-likelihood")
abline(v = .5, lty = 2)
# </r code> -----

```

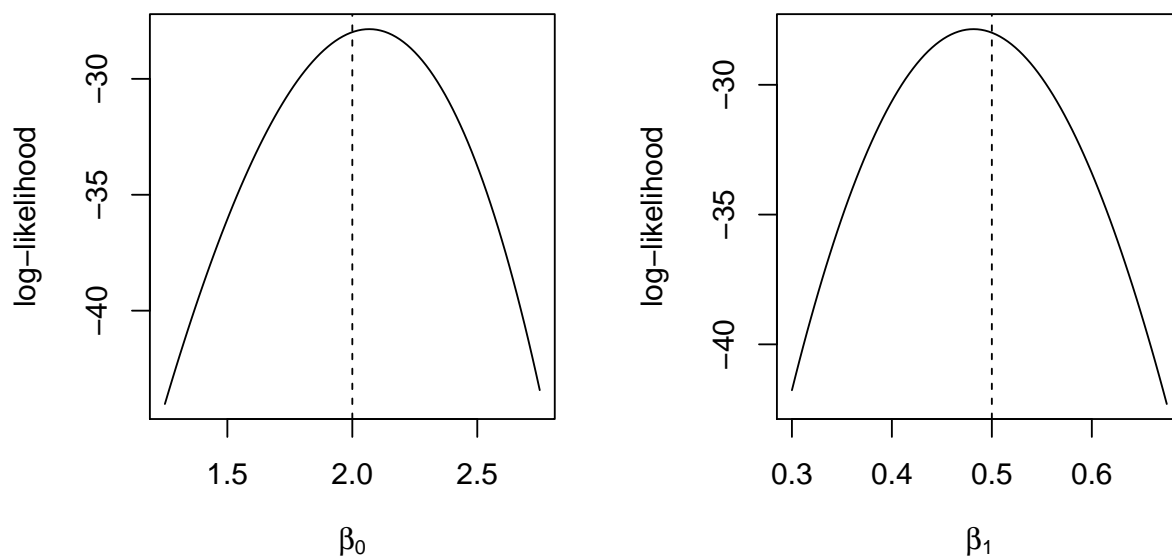


Figure 16: log-likelihood profiles for β_0 and β_1 for a Poisson regression. In dashed, the MLE's.

(c) Get estimates.

```
# <r code> -----
(par.est <- mle2(lkl.model.poi,
               start = list(b0 = min(data$y), b1 = 0),
               data = list(data = data),
               method = "BFGS"))
# </r code> -----
```

Call:

```
mle2(minuslogl = lkl.model.poi, start = list(b0 = min(data$y),
      b1 = 0), method = "BFGS", data = list(data = data))
```

Coefficients:

```
      b0      b1
2.0675572 0.4816563
```

Log-likelihood: -27.86

(d) Get intervals (use different methods).

```
# <r code> -----
par(mfrow = c(2, 1), mar = c(4, 4, 2, 2) + .1) # cosmetics
library(rootSolve) # function uniroot
# beta_0 -----
## first, plotting the profile with point estimates -----
plot(b0.grid, p.b0, type = "l",
     xlab = expression(beta[0]), ylab = "log-likelihood")
abline(v = 2, lty = 2)
abline(v = par.est@coef[1], lty = 2, col = 2)
## intervals -----
### probability-based interval -----
# cutoff's corresponding to a 95\% confidence interval for beta
# minus, since lkl.model.poi return -lkl
cut <- log(.15) - lkl.model.poi(par.est@coef[1], par.est@coef[2], data)
abline(h = cut, col = 2)
# finding the cutoff values
ic.b0.poi <- function(grid, ...) {
  lkl.perf <- unlist(
    mle2(lkl.model.poi,
         start = list(b1 = 0),
         data = list(data = data, b0 = grid), method = "BFGS"
    )@details[2])
  -1 * lkl.perf - cut
}
# for some "mysterious" reason the uniroot.all
```

```

# doesn't work here, but uniroot works perfectly
ic.95.prob.b0 <- c(uniroot(ic.b0.poi, c(1, par.est@coef[1]))$root,
                  uniroot(ic.b0.poi, c(par.est@coef[1], 3))$root)

arrows(x0 = ic.95.prob.b0, y0 = rep(cut, 2),
       x1 = ic.95.prob.b0, y1 = rep(-43.5, 2),
       lty = 2, length = .1, col = 2)
### wald confidence interval -----
# quadratic approximation
library(numDeriv) # hessian function
quad.b0.poi <- function(grid) {
  b0.hat <- par.est@coef[1] ; b1.hat <- par.est@coef[2]
  pl.hat <- pl.b0(b0.hat)
  hess <- hessian(pl.b0, x = b0.hat)
  # app2: quadratic (2) approximation (app)
  app2 <- numeric(length(grid))
  for (i in 1:length(grid)) {
    app2[i] <- pl.hat + .5 * hess * (grid[i] - b0.hat)**2
  }
  return(app2)
}
app2.b0.poi <- quad.b0.poi(b0.grid)

lines(b0.grid, app2.b0.poi, col = 4)

cut <- log(.15) + quad.b0.poi(par.est@coef[1])
abline(h = cut, col = 4)
# now, finding the cutoff values
ic.b0.quad.poi <- function(grid, ...) {
  quad.b0.poi(grid) - cut
}
wald.95.b0 <- uniroot.all(ic.b0.quad.poi, range(b0.grid))

arrows(x0 = wald.95.b0, y0 = rep(cut, 2),
       x1 = wald.95.b0, y1 = rep(-43.5, 2),
       lty = 2, length = .1, col = 4)
### from the mle2 output we get the standard error of each parameter -----
se.b0 <- summary(par.est)@coef[1, 2]
mle2.95.b0 <- par.est@coef[1] + qnorm(c(.025, .975)) * se.b0

arrows(x0 = mle2.95.b0, y0 = rep(cut, 2),
       x1 = mle2.95.b0, y1 = rep(-43.5, 2),
       lty = 2, length = .1, col = 3)
# beta_1 -----
## first, plotting the profile with point estimates -----
plot(b1.grid, p.b1, type = "l",
     xlab = expression(beta[1]), ylab = "log-likelihood")

```

```

abline(v = .5, lty = 2)
abline(v = par.est@coef[2], lty = 2, col = 2)
## intervals -----
### probability-based interval -----
abline(h = cut, col = 2) # remember, the cutoff is the same
# finding the cutoff values
ic.b1.poi <- function(grid, ...) {
  lkl.perf <- unlist(
    mle2(lkl.model.poi,
        start = list(b0 = min(data$y)),
        data = list(data = data, b1 = grid), method = "BFGS"
    )@details[2])
  -1 * lkl.perf - cut
}
# for some "mysterious" reason the uniroot.all
# doesn't work here, but uniroot works perfectly
ic.95.prob.b1 <- c(uniroot(ic.b1.poi, c(.2, par.est@coef[2]))$root,
  uniroot(ic.b1.poi, c(par.est@coef[2], .8))$root)

arrows(x0 = ic.95.prob.b1, y0 = rep(cut, 2),
  x1 = ic.95.prob.b1, y1 = rep(-42, 2),
  lty = 2, length = .1, col = 2)
### wald confidence interval -----
# quadratic approximation
quad.b1.poi <- function(grid) {
  b0.hat <- par.est@coef[1] ; b1.hat <- par.est@coef[2]
  pl.hat <- pl.b1(b1.hat)
  hess <- hessian(pl.b1, x = b1.hat)
  # app2: quadratic (2) approximation (app)
  app2 <- numeric(length(grid))
  for (i in 1:length(grid)) {
    app2[i] <- pl.hat + .5 * hess * (grid[i] - b1.hat)**2
  }
  return(app2)
}
app2.b1.poi <- quad.b1.poi(b1.grid)

lines(b1.grid, app2.b1.poi, col = 4)

cut <- log(.15) + quad.b1.poi(par.est@coef[2])
abline(h = cut, col = 4)
# now, finding the cutoff values
ic.b1.quad.poi <- function(grid, ...) {
  quad.b1.poi(grid) - cut
}
wald.95.b1 <- uniroot.all(ic.b1.quad.poi, range(b1.grid))

```

```

arrows(x0 = wald.95.b1, y0 = rep(cut, 2),
       x1 = wald.95.b1, y1 = rep(-42, 2),
       lty = 2, length = .1, col = 4)
### from the mle2 output we get the standard error of each parameter -----
se.b1 <- summary(par.est)@coef[2, 2]
mle2.95.b1 <- par.est@coef[2] + qnorm(c(.025, .975)) * se.b1

arrows(x0 = mle2.95.b1, y0 = rep(cut, 2),
       x1 = mle2.95.b1, y1 = rep(-42, 2),
       lty = 2, length = .1, col = 3)
# </r code> -----

```

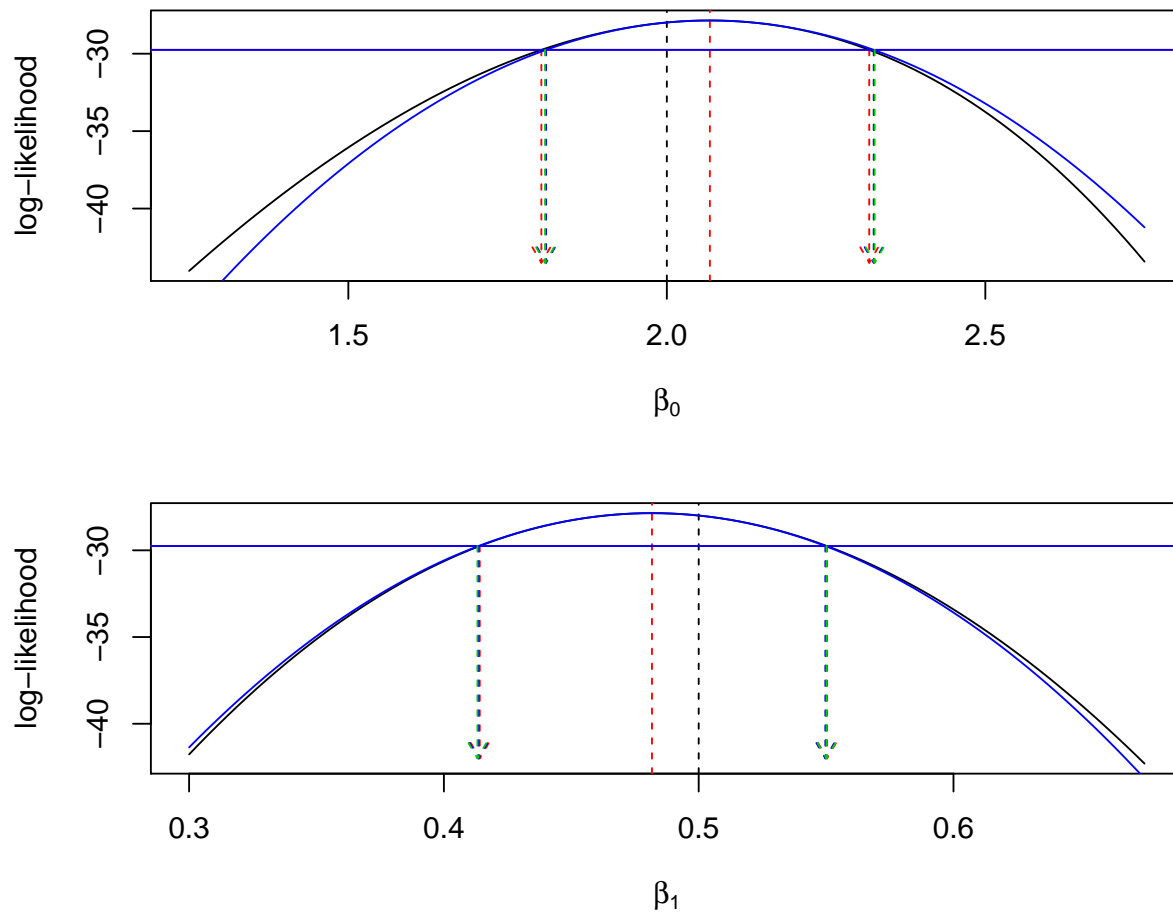


Figure 17: log-likelihood profiles, in black, for β_0 and β_1 for a Poisson regression with some intervals. In black dashed, the original parameter value. In red dashed, the MLE. The blue curve is a quadratic approximation for the log-likelihood profile, with the blue arrows corresponding to its 95% interval. The red arrows correspond to the 95% interval based in a cut in the likelihood. The green arrows correspond to the 95% interval based in the `mle2` output.

By the amount of code provided in this question, we can see that isn't so straightforward to obtain intervals and quadratic approximations of profiled likelihoods of parameters.

A very nice and interesting thing that we can see in Figure 17 is how all the three obtained intervals match. A brief, but enough, description is already given in the Figure caption, and for more details, we have the code above.

- (e) **Compare the previous results with those provided by the `glm()` function and discuss the findings.**

```
# <r code> -----
# fitting the model via glm() -----
model.glm <- glm(y ~ x, data, family = poisson)
# parameter estimates -----
model.glm$coef

(Intercept)          x
    2.0675451    0.4816599

# at three decimal cases, the estimates are equal
round(model.glm$coef, 3) == round(par.est$coef, 3)

(Intercept)          x
          TRUE          TRUE

# maximum log-likelihood -----
logLik(model.glm)

'log Lik.' -27.85527 (df=2)

# at eight decimal cases, the max. log-likes are equal
round(logLik(model.glm), 8) == round(par.est$details[[2]] * (-1), 8)

[1] TRUE

# standard errors -----
summary(model.glm)$coef[, 2]

(Intercept)          x
    0.13201821    0.03494989

## at six decimal cases, the standard errors are equal
round(
  summary(model.glm)$coef[, 2], 6) == round(
  summary(par.est)$coef[, 2], 6)

(Intercept)          x
          TRUE          TRUE

# </r code> -----
```

As a general reference guide for questions 2 to 6,
I read and used (in portuguese): www.leg.ufpr.br/mcie

```
@conference{mcie,
  author      = {Wagner Hugo Bonat and Paulo Justiniano Ribeiro Jr and
                  Elias Teixeira Krainski and Walmes Marques Zeviani},
  title       = {Computational Methods in Statistical Inference},
  year        = {2012},
  publisher    = {20th National Symposium on Probability and Statistics (SINAPE)},
  address     = {João Pessoa - PB - Brazil},
}
```

7 Poisson regression (*focus on the profile likelihood*)

In the previous exercise, we computed the profile likelihood for each parameter of a simple Poisson regression with just one covariate, i.e., an intercept, β_0 , and an angular coefficient, β_1 .

Together with the profile and an interval based in a cut in this profile likelihood (let's say, a probability-based interval), we did a quadratic approximation in this profile likelihood. In the "real" world, with "real" problems, this isn't a very smart thing to do, but here, just as an exercise, I believe that is extremely valid.

Using the same functions created before, we first show, in Figure 18, the profiles likelihood together with its respective quadratic approximations, providing in this way a better contextualization to what we'll do next.

```
# <r code> -----
par(mfrow = c(2, 1), mar = c(4, 4, 2, 2) + .1) # cosmetics
# beta_0 -----
## first, plotting the profiles with point estimate -----
plot(b0.grid, p.b0, type = "l",
      xlab = expression(beta[0]), ylab = "log-likelihood")
abline(v = par.est@coef[1], lty = 2)
## now, the quadratic approximations of the profiles -----
lines(b0.grid, app2.b0.poi, col = 2)
# beta_1 -----
plot(b1.grid, p.b1, type = "l",
      xlab = expression(beta[1]), ylab = "log-likelihood")
abline(v = par.est@coef[2], lty = 2)

lines(b1.grid, app2.b1.poi, col = 2)
# </r code> -----
```

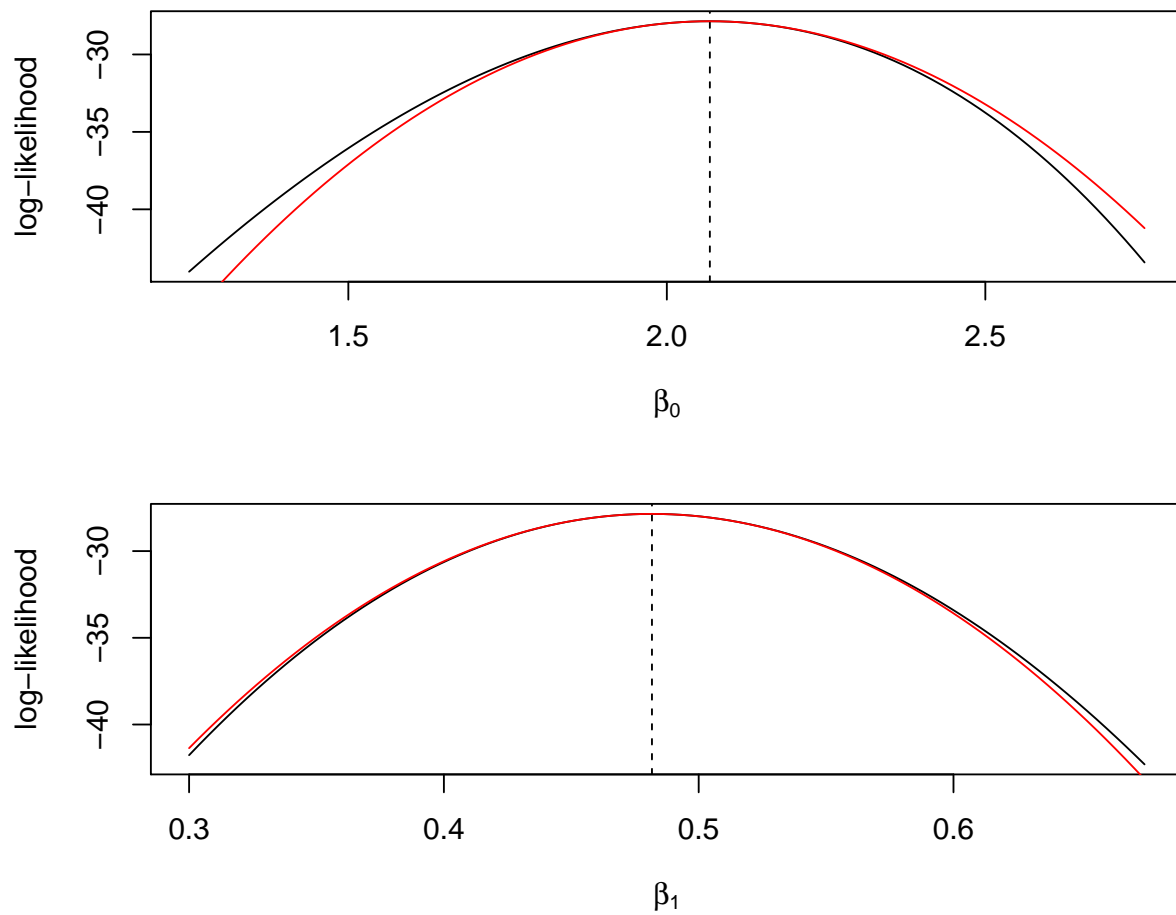


Figure 18: log-likelihood profiles, in black, for β_0 and β_1 for a Poisson regression. In black dashed, the MLE. In red, the quadratic approximations of the profiles.

last modification on ...

[1] "2019-07-04 10:25:16 -03"