

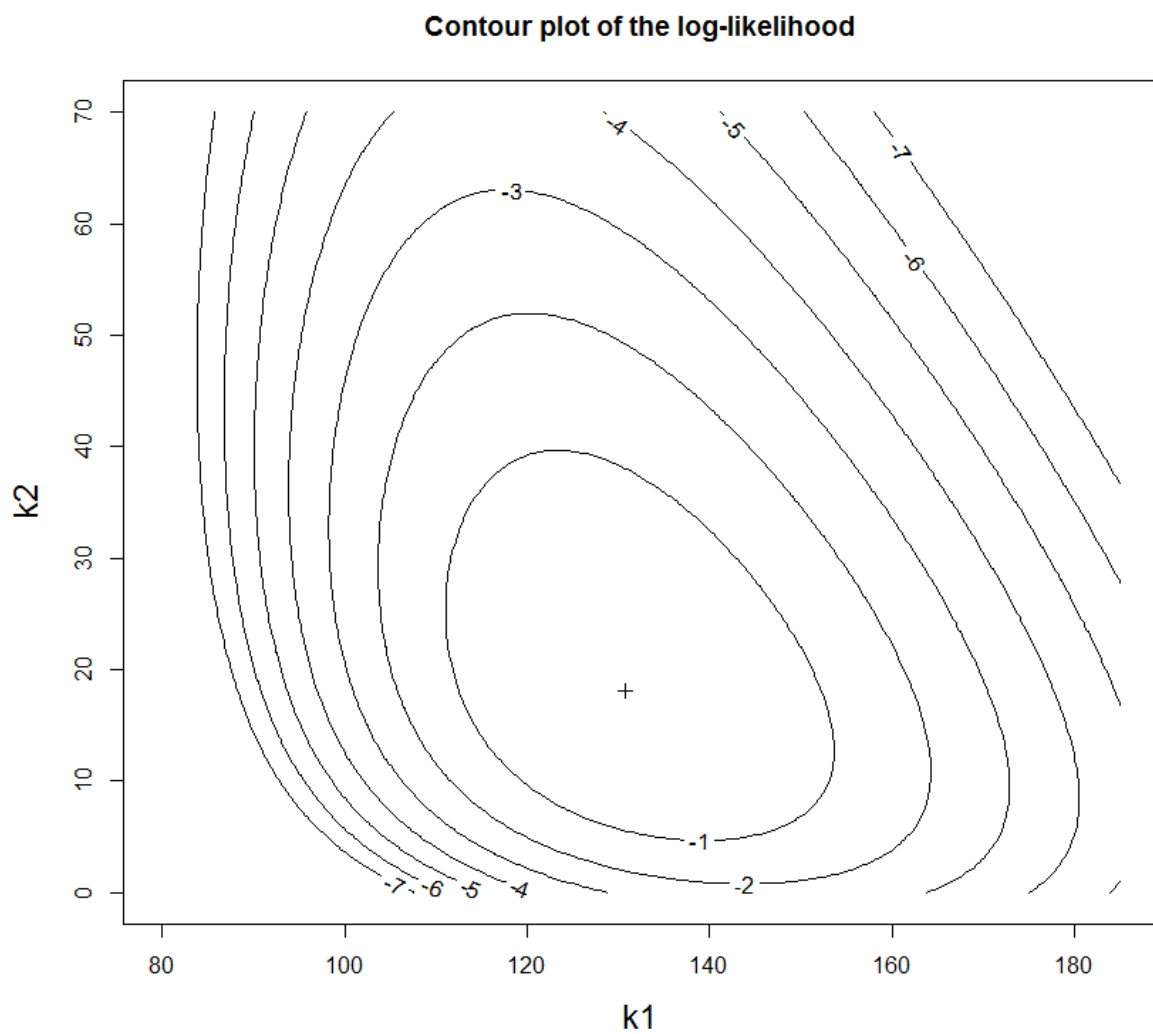
Practical 4 (25 Feb 2021)

i. Yesterday's Question 3, part iii. We observed $y = 35$ heads from $n = 50$ independent tosses. The likelihood function for p , the probability of getting a head, is $L(p) = \binom{n}{y} p^y (1 - p)^{n-y}$. Use R to plot the log-likelihood function and find the 95% confidence interval.

ii. Find the 95% C.I. for p by assuming normality.

Question 2

You are given a contour plot of a log-likelihood surface. Can you find the approximate 95% confidence interval for parameters k_1 and k_2 respectively by looking at the log-likelihood function? Also, can you circle the joint 95% confidence region for k_1 and k_2 ?



Question 3 Profile likelihood with flowering.txt

Yesterday we fitted a four-parameter logistic regression model to relate the `State` of a plant to the number of `Flowers` it had produced and its `Root` size. This model also includes the interaction between the two explanatory variables. This exercise demonstrates how we can infer confidence intervals or joint confidence regions for a subset of parameters via profiling. For instance, we would like to find the 95% C.I. for b , the coefficient of `Flowers`.

I hope you have already maximised `logistic.log.likelihood.int` and stored the outputs as `M2`. `M2$par` are the ML estimates for the four parameters, and `M2$value` is the maximised log-likelihood value.

The ML estimate for b is $\hat{b} = -0.07889$. If we move parameter b away from \hat{b} , the log-likelihood value should drop. The next sensible question to ask will be “what is the log-likelihood value when $b = -0.05$? what about at $b = -0.03$?” and so on. A naïve (incorrect) approach is to set $b = -0.03$ and keep all other estimates unchanged and then evaluate the log-likelihood at this point.

```
# THE WRONG APPROACH. SET b=-0.03, AND KEEP OTHERS AT THEIR MLE
logistic.log.likelihood.int(parm=c(M2$par[1], -0.03, M2$par[3],
M2$par[4]), dat=flowering)
```

This is because there is no guarantee that at $b = -0.03$ the log-likelihood is also maximised at $(\hat{a}, \hat{c}, \hat{d})$. The correct procedure is to fix $b = -0.03$, and then re-maximise the log-likelihood with respect to the remaining three parameters. The maximised log-likelihood value under this restricted parameter space is the profile log-likelihood value for b at $b = -0.03$. We can translate this procedure into R code:

```
# PROFILE LOG-LIKELIHOOD FOR b. OBVIOUSLY IT IS A FUNCTION OF b
profile.log.likelihood<-function(b)
{
  f<-function(parm_acd)
  {logistic.log.likelihood.int(c(parm_acd[1], b,
    parm_acd[2], parm_acd[3]), dat=flowering)}

  temp<-optim(c(0, 0, 0), f, control=list(fnscale=-1))
  return(temp$value)
}
```

The argument `parm_acd` for the inner function `f` is a vector with length three, referring to the remaining three parameters `a`, `c`, and `d`. `f` is maximised with respect to these three parameters.

```
# PROFILE LOG-LIKELIHOOD VALUE FOR b AT b=-0.03
profile.log.likelihood(b=-0.03)
```

Now we can evaluate the profile log-likelihood for b in the neighbourhood of \hat{b} . Note that each point on the profile log-likelihood involves a maximisation, which can be computationally intensive. The code below may take a while to run.

```
# PLOT THE PROFILE LOG-LIKELIHOOD FOR A RANGE OF b, USUALLY AROUND
ITS MLE

b<-seq(-0.19, -0.004, 0.002)

profile.log.likelihood.value<-rep(NA, length(b))

for (i in 1:length(b))
{profile.log.likelihood.value[i]<-profile.log.likelihood(b[i])}

# PLOT THE PROFILE LOG-LIKELIHOOD

plot(b, profile.log.likelihood.value, type='l')

# DRAW A HORIZONTAL LINE WHICH IS 1.92 UNITS BELOW THE MAXIMUM

abline(h=M2$value-1.92, col='red', lty=2)
```

As we are studying a single parameter, the 95% C.I. for b is the region where the profile log-likelihood descends by no more than 1.92 units (indicated by the red dotted line) from the maximum. The same principle can be applied to the profiling of two (or more) parameters. For example, if we are profiling a and b , then at each given (a_0, b_0) , a partial maximisation is performed on the remaining two parameters. And the joint 95% confidence region for a and b will be the region where the profile log-likelihood decreases by no more than $0.5 * \chi^2_{0.95, df=2} = 2.99$ units from the maximum.

[Optional task #1] Find the 95% C.I. for b by assuming normality.

[Optional task #2] Perform the same analysis with `glm()`.