

流行病學與生物統計計算 Homework 7

學號：b07401048 系級：醫學五 姓名：賴柏瑞

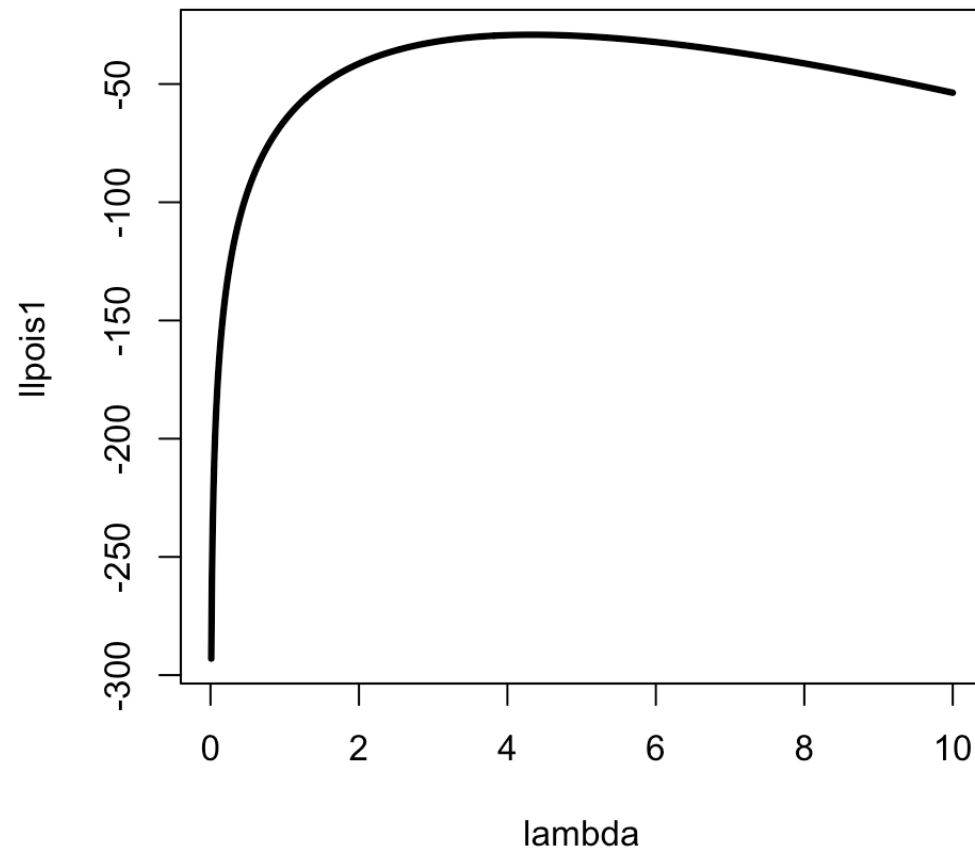
Homework7

#EX 18_1

```
# HW7
# Ex 18_1
# plot log-likelihood of for mean of a Poisson dis.
llpois <- function(data, param) {
  ans <- 0
  param <- lambda
  for (i in 1 : length(data)) {
    ans <- ans + log(((exp((-1) * lambda) * (lambda ^ data[i])) /
factorial(data[i]))) #nolint
  }
  return(ans)
}

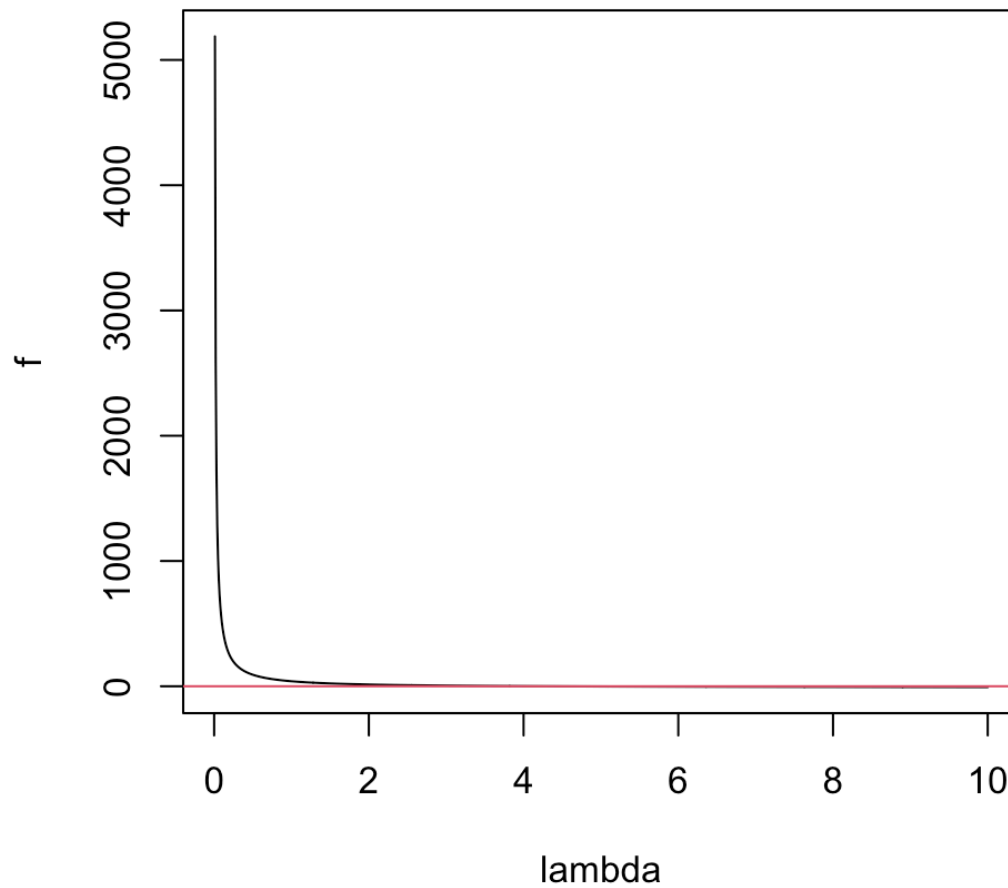
x1 <- c(5, 5, 6, 0, 1, 2, 4, 4, 3, 5, 7, 10)
lambda <- seq(0, 10, by = 0.01)
llpois1 <- llpois(data = x1, lambda)

png(filename = "hwk7.1.png", width = 1000, height = 1000, res = 200)
plot(lambda, llpois1, col = 1, type = "l", lwd = 3)
dev.off()
```



```
# maximum likelihood estimate of lambda by Newton-Raphson
# finding suitable x0
x <- c(5, 5, 6, 0, 1, 2, 4, 4, 3, 5, 7, 10)
f <- (-length(x)) + (sum(x) / lambda)
lambda <- seq(0, 10, by = 0.01)

png(filename = "hwk7.2.png", width = 1000, height = 1000, res = 200)
plot(lambda, f, col = 1, type = "l")
abline(h = 0, col = 2)
dev.off()
```



```

# constructing ftn

ftn <- function(lambda) {
  x <- c(5, 5, 6, 0, 1, 2, 4, 4, 3, 5, 7, 10)
  f <- (-length(x)) + (sum(x) / lambda)
  df <- -(lambda ^ (-2)) * sum(x)
  return(c(f, df))
}

# Newton-Raphson method

root <- function(ftn, x0, tol, max_iter) {
  x <- x0
  y <- ftn(x)
  iter <- 0
  while ((abs(y[1]) > tol) && (iter < max_iter)) {
    x <- x - y[1] / y[2]
    y <- ftn(x)
    iter <- iter + 1
    cat("at iteration", iter, "value of x is", x, "\n")
  }

  if (abs(y[1]) > tol) {
    cat("algorithm failed to converge\n")
    return(NULL)
  } else {
    cat("algorithm converges to \n")
    return(x)
  }
}

root(ftn, x0 = 3, tol = 1e-09, max_iter = 100)

```

```

> root(ftn, x0 = 3, tol = 1e-09, max_iter = 100)
at iteration 1 value of x is 3.923077
at iteration 2 value of x is 4.294492
at iteration 3 value of x is 4.332985
at iteration 4 value of x is 4.333333
at iteration 5 value of x is 4.333333
algorithm converges to
[1] 4.333333

```

EX S5_1

```
# EX S5_1 BMI3 ~ SEX + AGE + Treatment

setwd("/Users/raymond/Desktop/R/course/data/")
data <- read.csv("/Users/raymond/Desktop/R/course/data/BMIrepeated.csv")
dim(data)
head(data)
mode(data$SEX) # data$SEX is character, so i have to convert it to numeric

# convert sex to numeric, setting "M" be 1, "F" be 0
datama <- as.data.frame(data)
for (i in 1 : length(data$SEX)) {
  if (datama[i, 2] == "M") {
    datama[i, 2] <- 1
  } else {
    datama[i, 2] <- 0
  }
}
head(datama)
(sex <- as.numeric(datama[, 2]))

# design matrix
x <- cbind(rep(1, length(data$BMI3)), sex, data$AGE, data$Treatment)
head(x)

# regression coefficients
beta <- solve(t(x) %*% x) %*% t(x) %*% matrix(data$BMI3, ncol = 1)

> (beta <- solve(t(x) %*% x) %*% t(x) %*% matrix(data$BMI3, ncol = 1))
      [,1]
16.1010705
sex  0.8314382
     0.2516927
    -3.4052445

# residual
residual <- data$BMI3 - x %*% beta
```

```
# sigma square
```

```
sigmasqr <- sum(residual ^ 2) / length(data$BMI3)
```

```
> # sigma square
```

```
> (sigmasqr <- sum(residual ^ 2) / length(data$BMI3))
```

```
[1] 49.82738
```

```
# log likelihood
```

```
(lldata <- (-length(data$BMI3) / 2) * (log(2 * pi) + log(sigmasqr) + 1))
```

```
> # log likelihood
```

```
> (lldata <- (-length(data$BMI3) / 2) * (log(2 * pi) + log(sigmasqr) + 1))
```

```
[1] -337.3221
```