Lab Assignment 1

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Likelihood methods for the Poisson distribution

- Put your name in the author section and fill in the date section above.
- Write R code in the R chunks provided to answer the questions posed.
- Execute each chunk of code to ensure that your code works properly.
- If you cannot compile all of your code without errors before the end of the lab, comment out the chunks that are not working.
- Save the Rmd file in your personal directory (refer to Lab 0 instructions if needed)
- knit to pdf (or Word/HTML, but then print those to pdf)
- Upload the pdf file to the Lab Assignment 1 Activity in Brightspace.

1. First generate 1 observation from the Poisson(lambda=5) distribution and print the value.

```
set.seed(12345)   #use this seed!

pdat <- rpois(1, lambda = 5)
pdat
```

```
## [1] 6
```

2. Compute the Log-likelihood for a vector sequence of lambda values from 2 to 7 in steps of .05 .

(Hint: See help for the R function called *dpois*.)

```
lambda <- seq(2,7,by=1)

ploglike <- dpois(pdat, lambda, log = TRUE)
ploglike
```

```
## [1] -4.420368 -2.987577 -2.261485 -1.922624 -1.828694 -1.903790
```

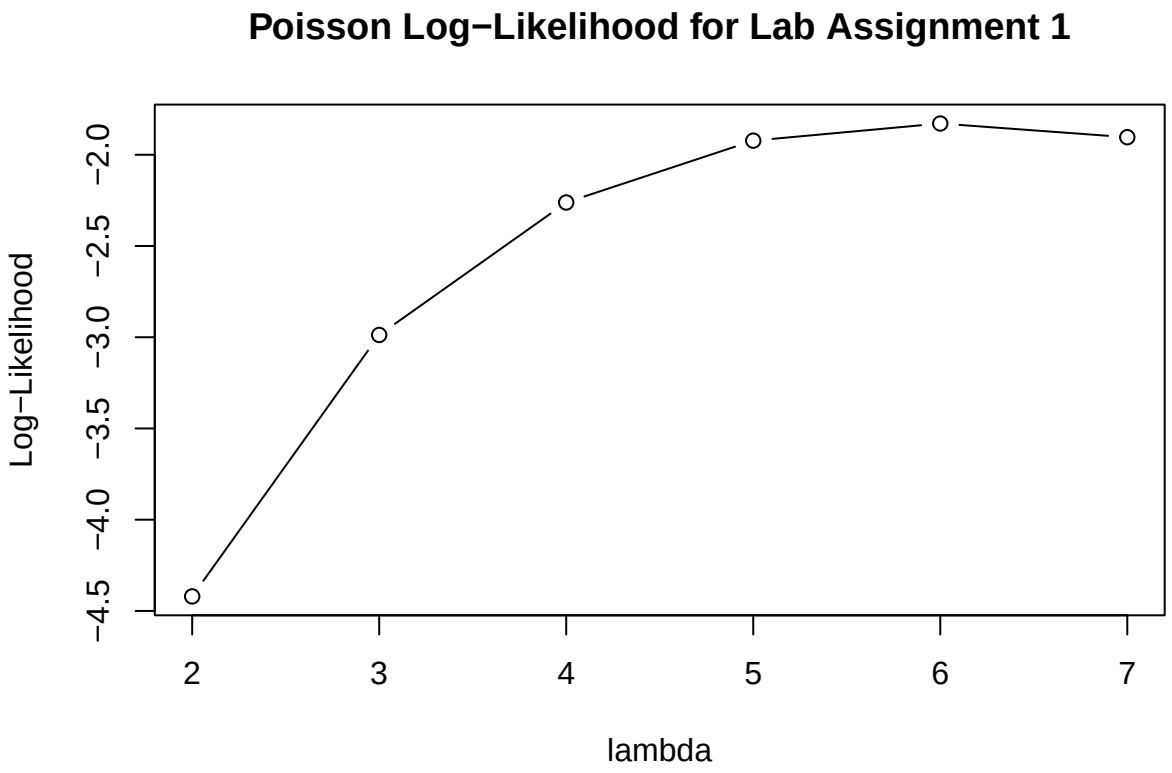
3. Plot the Log-Likelihood function values from your answer in 2 versus lambda. Axes must be labelled and the plot must have a title.

```
head(cbind(lambda, ploglike))
```

```
##      lambda  ploglike
## [1,]      2 -4.420368
## [2,]      3 -2.987577
## [3,]      4 -2.261485
```

```
## [4,]      5 -1.922624
## [5,]      6 -1.828694
## [6,]      7 -1.903790
```

```
plot(ploglike ~ lambda, ylab='Log-Likelihood', xlab='lambda', type='b', main='Poisson Log-Likelihood fo
```



4. Generate n=10 observations from the same distribution and compute the sample mean of the 10 observations.

(Hint: See help for the R function called *mean*.)

```
set.seed(12345) #use this seed!
n <- 10
pdat3 <- rpois(n, lambda = 5)
pdat3
```

```
##  [1]  6  8  6  8  5  3  4  5  6 11
```

```
sample_mean = mean(pdat3)
sample_mean
```

```
## [1] 6.2
```

5. Plot the log-likelihood function given the n=10 observations. Axes must be labelled and the plot must have a title.

```
lambda <- seq(2,7,by=1)

ploglike3 <- 0
for (i in 1:n){
  ploglike3 <- ploglike3 + dpois(pdat3[i], lambda, log=TRUE)
```

```
}

head(cbind(lambda, ploglike3))
```

```
##      lambda ploglike3
## [1,]      2 -50.01894
## [2,]      3 -34.88010
## [3,]      4 -27.04381
## [4,]      5 -23.20891
## [5,]      6 -21.90498
## [6,]      7 -22.34763
```

```
plot(ploglike3 ~ lambda, ylab='Log-Likelihood', xlab='lambda', type='b', main='Poisson Log-Likelihood fo
```