Tutorial 9 Solutions

STAT 3013/4027/8027

- 1. SI Example 4.8. Simply write out the steps as outlined in the example. This is the classic t-test. **the solution is in the textbook.**
- 2. Consider a Poission regression model using the canonical link function (how do we determine the canonical link function?):

$$Y_1, \dots, Y_n \overset{\text{indep.}}{\sim} \operatorname{Poisson}(\lambda_i)$$

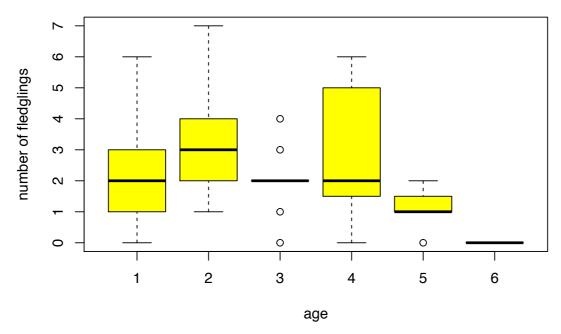
 $\log(\lambda_i) = \beta_0 + \beta_1 x_i + \beta_2 x_i^2$
for $i = 1, \dots, n$.

- Using optim() and the data on the website to find the MLEs: $\hat{\beta}_0, \hat{\beta}_1, \hat{\beta}_2$, as well as their estimated asymptotic variances.
- Additionally, using the bootstrap procedure discussed in class, provide the estimated biases and variances for the parameters.
- Data: A sample from a population of 52 female song sparrows was studied over the course of a summer and their reproductive activities were recorded. In particular, the age and number of new offspring were recorded for each sparrow (Arcese et al, 1992). Let Y = fledged (number of offspring), and X = age (age of mother).

Ans. Let's first examine the data:

```
D <- read.table("Data", header=TRUE)</pre>
summary(D)
##
       fledged
                         age
    Min. :0.000
                   Min. :1.000
##
##
    1st Qu.:1.000
                    1st Qu.:2.000
    Median :2.000
                    Median :3.000
    Mean :2.404
                    Mean :3.077
    3rd Qu.:3.000
                    3rd Qu.:4.000
         :7.000
                    Max. :6.000
   Max.
n \leftarrow nrow(D)
y < -D[,1]
x <- D[,2]
```

boxplot(y ~ x, col="yellow", xlab="age", ylab="number of fledglings")



It appears that there is some curvature, so using a quadratic term seems reasonable in order to allow for some flexibility.

• The likelihood for the model is:

$$L(\beta_0, \beta_1, \beta_2, | \mathbf{y}) = \prod_{i=1}^n \left(\frac{e^{-\lambda_i} \lambda_i^{-y_i}}{y_i!} \right)$$
$$log(\lambda_i) = \beta_0 + \beta_1 x_i + \beta_2 x_i^2$$

• We will use optim() to get the MLEs:

[1] 0.2762872 0.6821119 -0.1345834

• To get the estimated standard errors, recall that asymptotically:

 $\hat{\boldsymbol{\theta}} \sim \text{multivaritate normal}_3(\boldsymbol{\theta}, I(\boldsymbol{\theta})^{-1})$

$$\hat{\theta} = \{\hat{\beta}_0, \hat{\beta}_1, \hat{\beta}_2\}$$

 $I(\theta)$ is a 3 × 3 Fisher information matrix. To get an estimate we note [-Hessian matrix] $\to I(\hat{\theta})$.

```
var.beta.hat <- diag(solve(-out$hessian))
var.beta.hat</pre>
```

[1] 0.195488995 0.114536655 0.003345583

```
se.beta.hat <- sqrt(var.beta.hat)
se.beta.hat</pre>
```

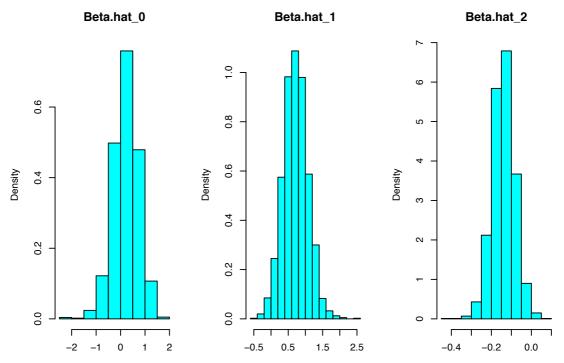
- ## [1] 0.44214137 0.33843264 0.05784102
 - Of course R already has a nice function to do all of this. But now you know how to code up non-standard likelihoods and estimate the parameters:

```
## We can do the same thing using the glm() function mod <- glm(y ~ x + I(x^2), family="poisson") summary(mod)
```

```
##
## Call:
## glm(formula = y \sim x + I(x^2), family = "poisson")
##
## Deviance Residuals:
##
      Min
                1Q
                     Median
                                  ЗQ
                                          Max
## -2.4650 -0.6355 -0.2298
                                       2.0429
                              0.4937
##
## Coefficients:
##
              Estimate Std. Error z value Pr(>|z|)
## (Intercept) 0.27662
                         0.44219
                                  0.626
                                            0.5316
## x
               0.68174
                          0.33850
                                    2.014
                                            0.0440 *
## I(x^2)
              -0.13451
                          0.05786 -2.325
                                            0.0201 *
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
       Null deviance: 76.081 on 51 degrees of freedom
##
## Residual deviance: 67.837 on 49 degrees of freedom
## AIC: 198.78
##
## Number of Fisher Scoring iterations: 5
```

- Now let's consider using the bootstrap (WE will talk about the bootstrap later in the course.):
 - 1. Randomly sample the data with replacement.
 - 2. Estimate the parameters through optim() or glm() function. Note: this fitting procedure is a statistic.
 - 3. Store the estimated parameters.
 - 4. Repeat steps 1-3 2,000 times.

```
set.seed(1001)
S <- 2000
Out <- matrix(0, S, 3)
n \leftarrow nrow(D)
for(s in 1:S){
  Sam <- sample(1:n, n, replace=TRUE)</pre>
  D.b <- D[Sam,]</pre>
  y <- D.b$fledged
  x <- D.b$age
  mod \leftarrow glm(y \sim x + I(x^2), family="poisson")
  Out[s, ] <- mod$coef</pre>
}
  y <- D$fledged
  x <- D$age
 bias.boot <- apply(Out, 2, mean) - glm(y - x + I(x^2), family="poisson")$coef
bias.boot
## (Intercept)
                                    I(x^2)
                            X
## -0.059474960 0.032231969 -0.004655707
v.boot <- apply(Out, 2, var)</pre>
 sd.boot <- sqrt(v.boot)</pre>
sd.boot
## [1] 0.51035201 0.35713958 0.05631127
  par(mfrow=c(1,3))
  hist(Out[,1], main="Beta.hat_0", col="cyan", xlab="", prob=TRUE)
  hist(Out[,2], main="Beta.hat_1", col="cyan", xlab="", prob=TRUE)
hist(Out[,3], main="Beta.hat_2", col="cyan", xlab="", prob=TRUE)
```



- Note that the 'sd.boot' values are somewhat similar to the values under the assumption of asymptotic normality. We can see from the plot that the histograms for $\hat{\beta}_0$ and $\hat{\beta}_1$ are just a bit skewed, but can be considered approximately normal.
- $3. \ \, SI\ \, 4.19,\ \, 5.1.$

$$= \left(\frac{\varepsilon_{1}}{\varepsilon_{1}} - n\right)^{2} \frac{s_{0}}{n} \stackrel{\sim}{\sim} \chi^{2}$$

$$b.) \text{ Lat } d + cs + :$$

$$\hat{G} = \overline{\chi} \qquad \Rightarrow T_{\hat{G}} = \frac{n}{\overline{\chi}}$$

$$W = \left(\hat{G} - \theta_{0}\right)^{T} T_{\hat{G}} \left(\hat{G} - \theta_{0}\right)$$

$$= \left(\overline{\chi} - \theta_{0}\right)^{2} \frac{n}{\overline{\chi}} \sim \chi^{2}_{1}$$