Exercise for Lecture 7 and 8

Rei Monden

Exercise 7-1

The outputs of the code below:

```
LI          <- c(8, 8, 10, 10, rep(c(12, 14, 16), each = 3),
                 18, 20, 20, 20, 22, 22, 24, 26, 28, 32, 34, rep(38, 3))
y           <- c(rep(0, 13), 1, 1, 1, 0, 1, 0, 0, 1, 1, 0, 1, 1, 1, 0)
cancer.fit <- glm(y ~ LI, family = binomial)
summary(cancer.fit)
```

```
##
## Call:
## glm(formula = y ~ LI, family = binomial)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.77714    1.37862  -2.740  0.00615 **
## LI           0.14486    0.05934   2.441  0.01464 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 34.372  on 26  degrees of freedom
## Residual deviance: 26.073  on 25  degrees of freedom
## AIC: 30.073
##
## Number of Fisher Scoring iterations: 4
```

```
confint(cancer.fit)
```

```
## Waiting for profiling to be done...
```

```
##                   2.5 %      97.5 %
## (Intercept) -6.9951909 -1.4098443
## LI           0.0425232  0.2846668
```

From the above results, we can answer to the questions as follows:

a. The prediction equation gives $\hat{\pi} = e^{-3.7771+0.1449(26)}/\left[1 + e^{-3.7771+0.1449(26)}\right] = 0.5$ (rounded to 1 decimal place).

b. This is given by the exponential of the regression slope of LI: $\exp(0.14486) = 1.16$ (rounded to 2 decimal places).

c. The estimated log odds of remission increase $\hat{\beta} = 0.14$ per 1% increase of "labeled" cells (rounded to 2 decimal places).

d. At $LI = 18$, $\hat{\pi} = e^{-3.7771+0.1449(18)}/\left[1 + e^{-3.7771+0.1449(18)}\right] = 0.237$. The rate of change is therefore equal to $\hat{\beta}\hat{\pi}(1 - \hat{\pi}) = 0.1449(0.237)(1 - 0.237) = 0.026$.

Exercise 7-2

a. $z_W = (0.14486/0.05934) = 2.441$, based on the $N(0,1)$ sampling distribution. The p-value is equal to $p = 2 \times P(N(0,1) > 2.441) = .015$.
Equivalently, $z_W^2 = (0.14486/0.05934)^2 = 5.959$, based on the $\chi^2(1)$ sampling distribution. The p-value is equal to $p = P(\chi(1)^2 > 5.959) = .015$.
Therefore, with 5% significance level, we reject the null-hypothesis that $\beta_{LI} = 0$.

b. The R code is `exp( confint.default(cancer.fit) )`. The output shows that the required CI is (1.03, 1.30). We conclude that the odds of remission at $LI = (x + 1)$ are estimated to fall between 1.03 and 1.30 times the odds of remission at $LI = x$.

c. The R code is `drop1(cancer.fit, test = "LRT")`. The output shows the following result: $\chi^2(1) = 8.30$, $p = .004$.
Therefore, with 5% significance level, we reject the null-hypothesis that $\beta_{LI} = 0$.

d. The R code is `exp( confint(cancer.fit) )`. The output shows that the required CI is (1.04, 1.33). We conclude that the odds of remission at $LI = (x + 1)$ are estimated to fall between 1.04 and 1.33 times the odds of remission at $LI = x$.