# HW3_yc4384_Cynthia

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2024-02-29

## Problem 1

**(a) Fit a prospective model to the data to study the relation between alcohol consumption, age, and disease (model age as a continuous variable taking values 25, 35, 45, 55, 65, and 75). Interpret the result.**

Using logistics regression model to fit data from prospective study:

$$log(\frac{\pi}{1-\pi}) = \beta_0 + \beta_1 X_{alc} + \beta_2 X_{age}$$

```
# load data
age = seq(from = 25, to = 75, by = 10) |>
  rep(2)
case = c(1, 4, 25, 42, 19, 5, 0, 5, 21, 34, 36, 8)
control = c(9, 26, 29, 27, 18, 0, 106, 164, 138, 139, 88, 31)
alc = c(rep(1,6), rep(0, 6))
resp = cbind(case, control)

# Model fitting using logit link
glm_logit=glm(resp ~ alc + age, family=binomial(link='logit'))
summary(glm_logit)
```

```
##
## Call:
## glm(formula = resp ~ alc + age, family = binomial(link = "logit"))
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -5.023449   0.418224 -12.011   <2e-16 ***
## alc          1.780000   0.187086   9.514   <2e-16 ***
## age          0.061579   0.007291   8.446   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 211.608  on 11  degrees of freedom
## Residual deviance:  31.932  on  9  degrees of freedom
## AIC: 78.259
##
## Number of Fisher Scoring iterations: 4
```

Hence, the logistics regression model is:

$$log(\frac{\pi}{1-\pi}) = -5.02 + 1.78X_{alc} + 0.06 * X_{age}$$

Interpretation:

- The model suggests a significant relationship between esophageal cancer, daily alcohol consumption adjusted and age.
- $\beta_1$: the log odds ratio of having the disease among heavy drinkers is 1.78 times the odds odds ratio of non-heavy drinkers, keeping age fixed.
- $exp(\beta_1)$: odds ratio for the association between disease and alcohol consumption, holding age constant.
- $\beta_2$: the log odds ratio of having the disease will increase by 0.06 for every unit increment in age, keeping alcohol consumption fixed.
- $exp(\beta_2)$: the odds ratio for the association between disease and age, holding alcohol consumption constant.
- This model appears to fit the data well, as indicated by the significant coefficients and the reduction in deviance from the null model to the fitted model.

(b)

```
age = c(1:6) |>
  factor()
ind = dummy.code(age)
grp1 = rep(ind[,1],2)
grp2 = rep(ind[,2],2)
grp3 = rep(ind[,3],2)
grp4 = rep(ind[,4],2)
grp5 = rep(ind[,5],2)
grp6 = rep(ind[,6],2)

M_0 = glm(resp ~ grp1 + grp2 + grp3 + grp4 + grp5 + grp6, family = binomial(link = 'logit'))
summary(M_0)
```

```
##
## Call:
## glm(formula = resp ~ grp1 + grp2 + grp3 + grp4 + grp5 + grp6,
##     family = binomial(link = "logit"))
##
## Coefficients: (1 not defined because of singularities)
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.86904    0.33043  -2.630 0.008537 **
## grp1        -3.87589    1.05728  -3.666 0.000246 ***
## grp2        -2.18076    0.47493  -4.592 4.39e-06 ***
## grp3        -0.42031    0.37001  -1.136 0.255977
## grp4         0.08778    0.35828   0.245 0.806445
## grp5         0.21293    0.36986   0.576 0.564812
## grp6              NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 211.608  on 11  degrees of freedom
## Residual deviance:  90.563  on  6  degrees of freedom
## AIC: 142.89
##
## Number of Fisher Scoring iterations: 6
```

```r
dev_m0 = residuals(M_0, type = "deviance")^2 |> sum()

M_1 = glm(resp ~ alc + grp1 + grp2 + grp3 + grp4 + grp5 + grp6, family = binomial(link = 'logit'))
summary(M_1)
```

```
##
## Call:
## glm(formula = resp ~ alc + grp1 + grp2 + grp3 + grp4 + grp5 +
##     grp6, family = binomial(link = "logit"))
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.092158   0.344216  -3.173 0.001509 **
## alc          1.669890   0.189602   8.807  < 2e-16 ***
## grp1        -3.962190   1.065035  -3.720 0.000199 ***
## grp2        -2.419896   0.491328  -4.925 8.43e-07 ***
## grp3        -0.763428   0.389837  -1.958 0.050192 .
## grp4        -0.248700   0.376735  -0.660 0.509161
## grp5         0.004692   0.387043   0.012 0.990328
## grp6               NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 211.608  on 11  degrees of freedom
## Residual deviance:  11.041  on  5  degrees of freedom
## AIC: 65.369
##
## Number of Fisher Scoring iterations: 5
```

```r
# Define the data
Model <- c("$M_0$", "$M_1$")
Linear_predictor <- c("$\\alpha_j$", "$\\alpha_j + \\beta X$")
Deviance <- c(90.56, 11.04)
df <- c(6, 5)

# Create a data frame
outp <- data.frame(Model, Linear_predictor, Deviance, df, stringsAsFactors = FALSE)

# Set column names
colnames(outp) <- c("Model", "Linear Predictor", "Deviance", "df")

# Print the data frame using knitr::kable() with format = "latex" and escape = FALSE

knitr::kable(outp, format = "latex", escape = FALSE, align = "c", booktabs = TRUE)
```

| Model | Linear Predictor | Deviance | df |
|:---:|:---:|:---:|:---:|
| $M_0$ | $\alpha_j$ | 90.56 | 6 |
| $M_1$ | $\alpha_j + \beta X$ | 11.04 | 5 |

Hypothesis Testing:

$$H_0 : \beta_{alc} = 0 \ H_1 : \beta_{alc} \neq 0$$
$$stat = 79.52 \sim \chi_1^2$$
$$p - value < 0.0001$$

Hence, we reject the null hypothesis and we have sufficient evidence to conlcude that there's an significant association between disease and alcohol consumption.

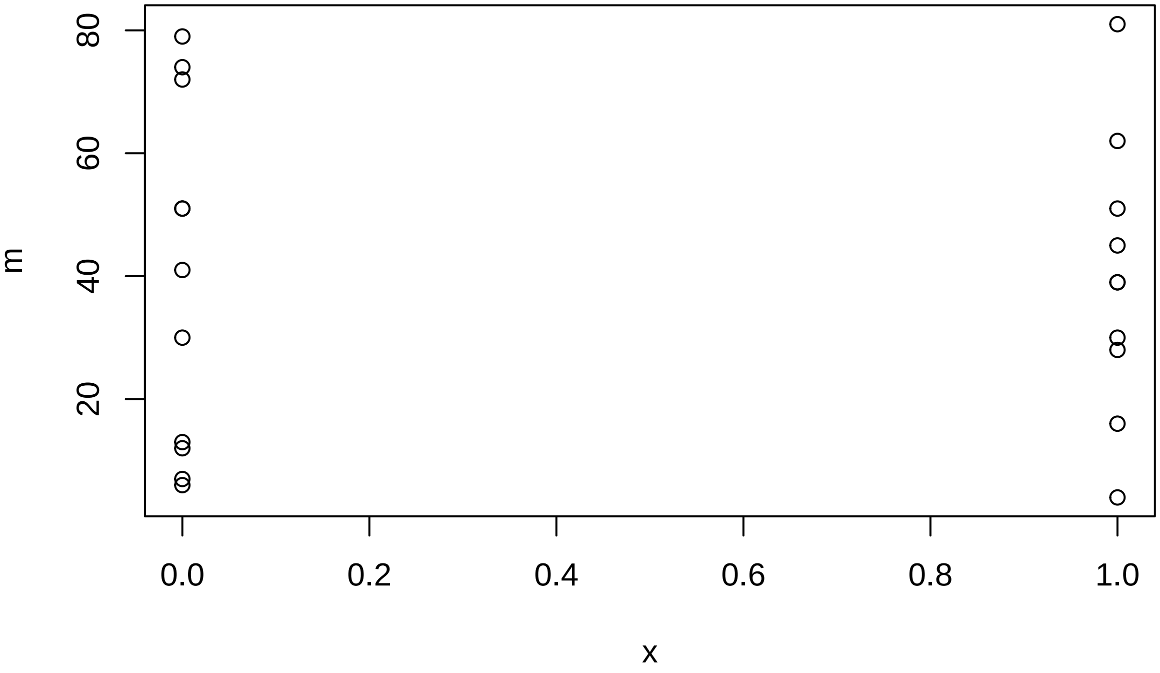
## Problem 2

### (a) Fit a logistic regression model to study the relation between germination rates and different types of seed and root extract. Interpret the result.

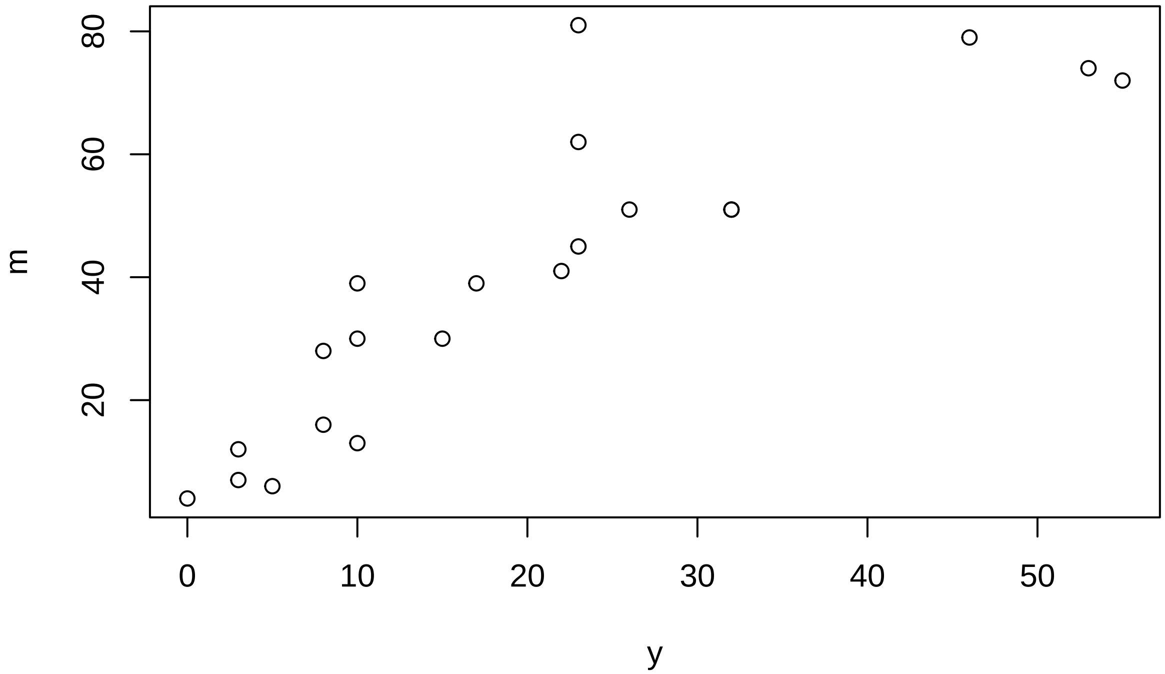
Let $Y_i$ denote the number of seeds germinates among $m_i$ seeds with the $ith$ covariate pattern. The logistic regression model:

$$log(\frac{\pi}{1-\pi}) = \beta_0 + \beta_1 X_{seed} + \beta_2 X_{root};$$

```r
# input data
x=c(rep(1,10),rep(0,11)) # roots category
z=c(rep(1,5), rep(0,6), rep(1,5), rep(0,5)) # seeds category
y=c(10,23,23,26,17,8,10,8,23,0,5,53,55,32,46,10,3,22,15,32,3) # survive=1
m=c(39,62,81,51,39,16,30,28,45,4,6,74,72,51,79,13,12,41,30,51,7)
data=data.frame(x,y,m)
plot(x,m)
```



```r
plot(y,m)
```



```
summary(m-y) ## m >= y
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    1.00    9.00   19.00   19.38   22.00   58.00
```

```
# fit binomial (logistic) without dispersion
none.disp=glm(cbind(y,m-y)~x+z, family=binomial(link='logit'))
summary(none.disp)
```

```
##
## Call:
## glm(formula = cbind(y, m - y) ~ x + z, family = binomial(link = "logit"))
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.3884     0.1410   2.755  0.00588 **
## x            -1.0668     0.1442  -7.396  1.4e-13 ***
## z             0.2391     0.1538   1.555  0.12004
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 98.719  on 20  degrees of freedom
## Residual deviance: 40.328  on 18  degrees of freedom
## AIC: 122.92
##
## Number of Fisher Scoring iterations: 4
```

```
G.stat=sum(residuals(none.disp,type='pearson')^2) # pearson chisq
G.stat
```

```
## [1] 38.8492
```

The binomial logistic without dispersion was fitted with the following results:

$$log(\frac{\pi}{1-\pi}) = 0.3884 - 1.0668 * X_{root} + 0.2391 * X_{seed}$$

Interpretation:

$$\hat{b_0} = 0.3884,\ standard\ error(b_0) = 0.1410;$$

- The log odds ratio of a O.aegyptiaca 73 seed grown in cucumber extract for germinating is 0.38.

$$\hat{b_1} = 0.2391,\ standard\ error(b_1) = 0.1538;$$

- The estimated log odds ratio for comparing O.aegyptiaca 75 seeds and O.aegyptiaca 73 seeds, holding root extract fixed is 0.2391.

$$\hat{b_2} = -1.0668,\ standard\ error(b_2) = 0.1442;$$

- The estimated odds ratio for comparing bean and cucumber extract amongst O.aegyptiaca 73 seeds, holding seed species fixed is -1.0668.

$$Pearson - \chi^2 statistic : X^2 = \sum X_i^2 = 41.226\ and\ Deviance\ D = \sum d_i^2 = 40.328.$$

```
# goodness of fit
pval=1-pchisq(none.disp$deviance,21-3)
pval # bad fit, reject the fitting
```

```
## [1] 0.001882762
```

- Comparing $X^2$ and $D$ with $\chi^2(18)$, we concluded that the model appears to fit bad.

**(b) Is there over dispersion? If so, what is the estimate of dispersion parameter? Update your model and reinterpret the result.**

Estimating the dispersion parameter by following two methods:

First,

$$\hat{\phi} = G_0/(n-p),$$

where

$$G_0 = \sum_{i=1}^{n} \frac{(y_i - m_i\hat{\pi}_i)^2}{m_i\hat{\pi}_i(1-\hat{\pi}_i)\phi} \sim \chi^2(n-p)$$

is the generalized Pearson $\chi^2$ from the original model fitting without over-dispersion.

Second,

$$\hat{\phi} = \frac{D_0}{n-p}$$

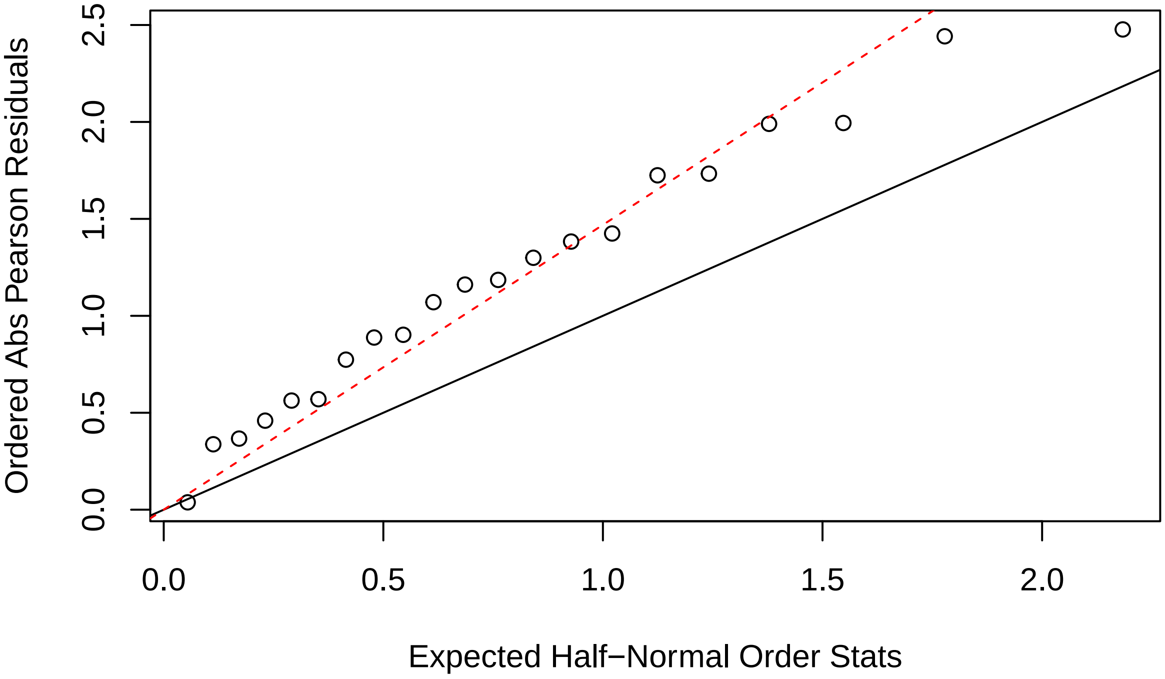
```
# calc dispersion para in 2 methods
# the first method
phi=G.stat/(21-3)
phi
```

```
## [1] 2.158289
```

```
# the second method
tilde.phi=none.disp$deviance/none.disp$df.residual
tilde.phi # similar to the one estimated from pearson chisq
```

```
## [1] 2.240455
```

```
# test over-dispersion (half normal plot)
res=residuals(none.disp,type='pearson')
plot(qnorm((21+1:21+0.5)/(2*21+1.125)),sort(abs(res)),xlab='Expected Half-Normal Order Stats',ylab='Orde
abline(a=0,b=1)
abline(a=0,b=sqrt(phi),lty=2, col = 'red')
```



- Therefore, there exists over-dispersion in our model and the estimate of dispersion parameter: $\hat{\phi} = 2.1697$.
- Half-normal plot using residuals from this model shows evidence of over-dispersion.
- Next, we updated regression model.

```
# fit model with constant over-dispersion
summary(none.disp,dispersion=phi)
```

```
##
## Call:
## glm(formula = cbind(y, m - y) ~ x + z, family = binomial(link = "logit"))
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.3884     0.2071   1.875   0.0608 .
## x            -1.0668     0.2119  -5.034 4.79e-07 ***
## z             0.2391     0.2259   1.058   0.2900
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 2.158289)
##
##     Null deviance: 98.719  on 20  degrees of freedom
## Residual deviance: 40.328  on 18  degrees of freedom
## AIC: 122.92
##
```

```
## Number of Fisher Scoring iterations: 4
```

The binomial logistic with dispersion was fitted with the following results:

$$b_0 = 0.3884,\ standard\ error(b_1) = 0.2071;$$

$$b_1 = -1.0668,\ standard\ error(b_1) = 0.2119;$$

$$b_2 = 0.2391,\ standard\ error(b_2) = 0.2259;$$

$$Pearson - \chi^2 statistic : X^2 = \sum X_i^2 = 41.226\ and\ Deviance\ D = \sum d_i^2 = 40.328.$$

### (c) What is a plausible cause of the over dispersion?

Since different groups may have different germination rate which follow the same distribution, the response variables should follows a beta-binomial distribution rather than binomial distribution.