Homework 3

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1

```
# data prep
df_ec = data.frame(
  age = c(25, 25, 35, 35, 45, 45, 55, 55, 65, 65, 75, 75),
  alcohol = c(rep(c("less", "more"), length.out = 12)),
  case = c(0, 1, 5, 4, 21, 25, 24, 42, 36, 19, 8, 5),
  control = c(106, 9, 164, 26, 138, 29, 139, 27, 88, 18, 31, 0)
)

resp = cbind(df_ec$case, df_ec$control)
```

We coded daily alcohol consumption 0-79g as “less”, and 80+g as “more”.

a

```
# fit a prospective logit model
logit.prosp = glm(resp ~ df_ec$alcohol + df_ec$age, family = binomial(link = 'logit'))

summary(logit.prosp)
```

```
##
## Call:
## glm(formula = resp ~ df_ec$alcohol + df_ec$age, family = binomial(link = "logit"))
##
## Coefficients:
##                    Estimate Std. Error z value Pr(>|z|)
## (Intercept)       -5.142771   0.432049 -11.903   <2e-16 ***
## df_ec$alcoholmore  1.887764   0.190502   9.909   <2e-16 ***
## df_ec$age          0.061805   0.007485   8.258   <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: 214.750  on 11  degrees of freedom
## Residual deviance:  29.988  on  9  degrees of freedom
## AIC: 76.03
```

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

```
exp(coef(logit.prosp)) # odds ratio estimates
```

```
##       (Intercept) df_ec$alcoholmore         df_ec$age
##       0.005841482       6.604582479       1.063755249
```

In this model, we treat disease status (case vs control) as response and exposures (daily alcohol consumption and age) as predictors.

$logit(\pi_i) = \beta_0 + \beta_1 x_1 + \beta_2 x_2$
x_1 : the indicator of heavier daily alcohol consumption (80+g)
x_2 : the indicator of age (as a continuous variable)

- The odds ratio of having esophageal cancer is 6.605 in heavier daily alcohol consumer (80+g) compared to lighter consumer (0-79g) holding other covariates constant
- As age increases by one year, the odds ratio of having esophageal cancer increases by 1.064 holding other covariates constant

b

Ψ_j : the odds ratio relating alcohol consumption and disease in the j^{th} age group ($j = 1, ..., 6$)
Compare the following two models:
$M_0 : \Psi_j = 1$ for all j
$M_1 : \Psi_j = \Psi$ (where Ψ is an unknown constant)

```
# Model 0 has age (as categorical variable) as a covariate
m0 = glm(resp ~ factor(df_ec$age), family = binomial(link = 'logit'))

summary(m0)
```

```
##
## Call:
## glm(formula = resp ~ factor(df_ec$age), family = binomial(link = "logit"))
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -4.745      1.004  -4.725 2.31e-06 ***
## factor(df_ec$age)35    1.695      1.061   1.598 0.110006
## factor(df_ec$age)45    3.456      1.018   3.394 0.000688 ***
## factor(df_ec$age)55    3.823      1.015   3.767 0.000165 ***
## factor(df_ec$age)65    4.089      1.018   4.017 5.90e-05 ***
## factor(df_ec$age)75    3.876      1.057   3.666 0.000246 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 214.75  on 11  degrees of freedom
## Residual deviance: 101.67  on  6  degrees of freedom
```

```
## AIC: 153.71
##
## Number of Fisher Scoring iterations: 6
```

```
# Model 1 has alcohol and age (as categorical variable) as covariates
m1 = glm(resp ~ df_ec$alcohol + factor(df_ec$age), family = binomial(link = 'logit'))

summary(m1)
```

```
##
## Call:
## glm(formula = resp ~ df_ec$alcohol + factor(df_ec$age), family = binomial(link = "logit"))
##
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -5.0937     1.0105  -5.041 4.64e-07 ***
## df_ec$alcoholmore     1.7876     0.1931   9.259  < 2e-16 ***
## factor(df_ec$age)35   1.5300     1.0670   1.434 0.151586
## factor(df_ec$age)45   3.1882     1.0241   3.113 0.001851 **
## factor(df_ec$age)55   3.5160     1.0207   3.445 0.000572 ***
## factor(df_ec$age)65   3.9749     1.0242   3.881 0.000104 ***
## factor(df_ec$age)75   3.9857     1.0666   3.737 0.000186 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 214.750  on 11  degrees of freedom
## Residual deviance:  12.963  on  5  degrees of freedom
## AIC: 67.005
##
## Number of Fisher Scoring iterations: 5
```

$\Psi_j = 1$ means that the coefficient of alcohol (log odds) equals to zero in Model 0.
Model 0 is nested within Model 1, so I will perform ANOVA for the deviance analysis.

```
# deviance analysis for nested models
anova(m0, m1)
```

```
## Analysis of Deviance Table
##
## Model 1: resp ~ factor(df_ec$age)
## Model 2: resp ~ df_ec$alcohol + factor(df_ec$age)
##   Resid. Df Resid. Dev Df Deviance
## 1         6    101.671
## 2         5     12.963  1   88.708
```

The residual deviance appears to be reduced in Model 1 compared to Model 0, indicating that Model 1 has a better fit by adding alcohol as the response variable.

2

```r
# data prep
df_ger <- data.frame(
  seeds = c(rep(c("oa_75", "oa_73"), times = c(11, 10))),
  root = c(rep(c("bean", "cucumber"), times = c(5, 6)), rep(c("bean", "cucumber"), times = c(5, 5))),
  y = c(10, 23, 23, 26, 17, 5, 53, 55, 32, 46, 10, 8, 10, 8, 23, 0, 3, 22, 15, 32, 3),
  m = c(39, 62, 81, 51, 39, 6, 74, 72, 51, 79, 13, 16, 30, 28, 45, 4, 12, 41, 30, 51, 7)
)

# response variable
resp = cbind(df_ger$y, df_ger$m - df_ger$y)
```

a

```r
# fit a logistic regression model
logit.ger = glm(resp ~ df_ger$seeds + df_ger$root, family = binomial(link = 'logit'))

summary(logit.ger)
```

```
##
## Call:
## glm(formula = resp ~ df_ger$seeds + df_ger$root, family = binomial(link = "logit"))
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)          -0.7005     0.1507  -4.648 3.36e-06 ***
## df_ger$seedsoa_75     0.2705     0.1547   1.748   0.0804 .
## df_ger$rootcucumber   1.0647     0.1442   7.383 1.55e-13 ***
## ---
## 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: 39.686  on 18  degrees of freedom
## AIC: 122.28
##
## Number of Fisher Scoring iterations: 4
```

```r
exp(coef(logit.ger)) # odds ratio estimates
```

```
##         (Intercept)   df_ger$seedsoa_75 df_ger$rootcucumber
##           0.4963454           1.3105554           2.9001133
```

In this model, we treat germination status (germinated vs not germinated) as a response variable and exposures (types of seed and root extract) as predictors.

$logit(\pi_i) = \beta_0 + \beta_1 x_1 + \beta_2 x_2$
x_1 : the type of seeds
x_2 : the type of root extract media

- The odds ratio of having germination is 1.311 in *O. aegyptiaca 75* compared to *O. aegyptiaca 73* holding other covariates constant. However, given p-value > 0.05 of this coefficient, no statistically significant association is implied between the type of seeds and the germination status

- The odds ratio of having germination is 2.9 in cucumber compared to bean root extract holding other covariates constant

b

```
# goodness of fit
hltest(logit.ger)
```

```
##
##    The Hosmer-Lemeshow goodness-of-fit test
##
##  Group Size Observed  Expected
##      1  123       49  40.79973
##      2  272       99 107.20027
##      3  141       75  83.20027
##      4  295      201 192.79973
##
##          Statistic =  6.47991
## degrees of freedom =  2
##            p-value =  0.039166
```

The Hosmer-Lemeshow goodness-of-fit test indicates that the model in (a) has a lack of fit.

```
# calculate dispersion parameter
G.stat = sum(residuals(logit.ger, type = 'pearson') ^ 2) # pearson chisq
G.stat
```

```
## [1] 38.31062
```

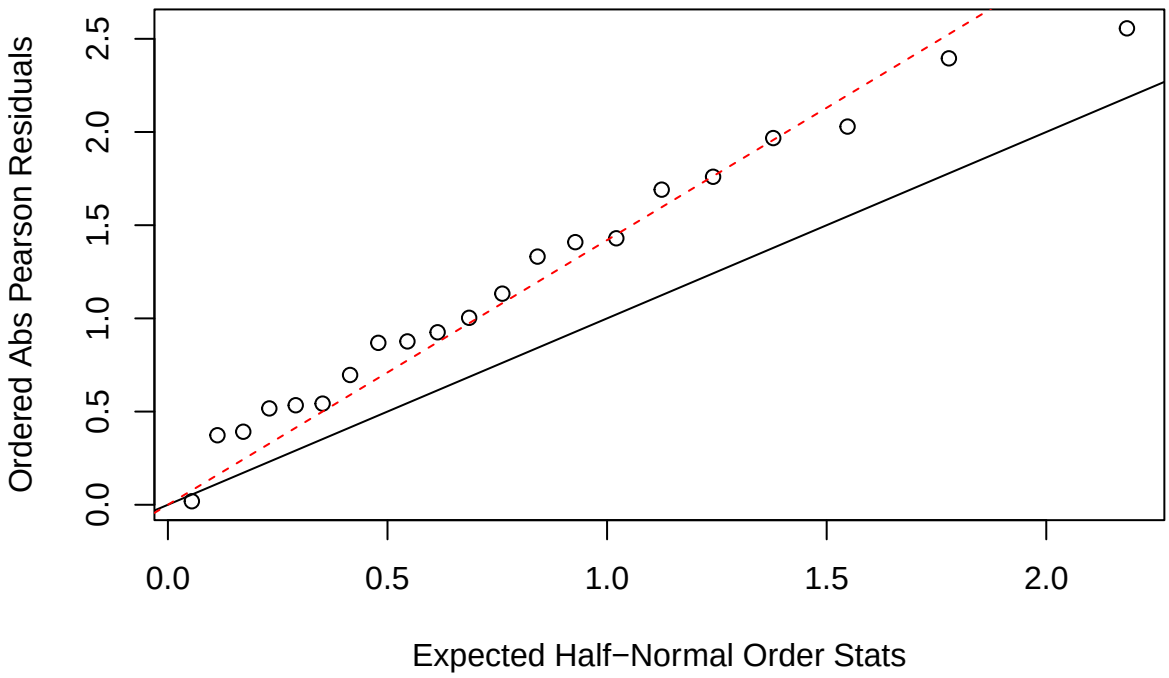
```
phi = G.stat / (21 - 2)
phi
```

```
## [1] 2.016348
```

```
tilde.phi = logit.ger$deviance / logit.ger$df.residual
tilde.phi
```

```
## [1] 2.204772
```

```
# test over-dispersion (half normal plot)
res = residuals(logit.ger, type='pearson')
plot(qnorm((21 + 1: 21 + 0.5)/(2 * 21 + 1.125)), sort(abs(res)), xlab = 'Expected Half-Normal Order Sta
abline(a = 0, b = 1)
abline(a = 0, b = sqrt(phi), lty = 2, col = 'red')
```



There is a linear deviation from the reference line in the half normal plot, suggesting that the response variance Y_i exceeds the variance assumed by the model.
Hence, we can say that there is over-dispersion in the original model.
The estimate of dispersion parameter: $\hat{\phi} = 2.02$

```
summary(logit.ger, dispersion = phi)
```

```
##
## Call:
## glm(formula = resp ~ df_ger$seeds + df_ger$root, family = binomial(link = "logit"))
##
## Coefficients:
##                      Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -0.7005     0.2140  -3.273  0.00106 **
## df_ger$seedsoa_75      0.2705     0.2197   1.231  0.21828
## df_ger$rootcucumber    1.0647     0.2048   5.199    2e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 2.016348)
##
##     Null deviance: 98.719  on 20  degrees of freedom
## Residual deviance: 39.686  on 18  degrees of freedom
## AIC: 122.28
##
## Number of Fisher Scoring iterations: 4
```

After adjusting for over-dispersion, the coefficient for the type of seeds still has p-value larger than 0.05. This implies that no statistically significant association is detected between the type of seeds and response variable in the updated model.

c

One of plausible cause of the over-dispersion in this experiment is the potential heterogeneity of the data within each group. We do not know how old each seed was, what the room temperature and humidity were during the observation period, or how much water each seed received. Many underlying factors may affect seed germination and our data classification/model cannot account for them.