Homework 5

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```
# data prep
df_crab = read.table("/Users/yukijoyama/Library/CloudStorage/GoogleDrive-jikeyu1995@gmail.com/My Drive/
df_para = read.table("/Users/yukijoyama/Library/CloudStorage/GoogleDrive-jikeyu1995@gmail.com/My Drive/
```

1

(a)

I will fit a Poisson model (M1) with log link with carapace width (W) as the single predictor.

```
# M1: Poisson model with log link
m1_fit <- glm(Sa ~ W, family = poisson(link = "log"), data = df_crab)
summary(m1_fit)
```

```
##
## Call:
## glm(formula = Sa ~ W, family = poisson(link = "log"), data = df_crab)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.30476    0.54224  -6.095  1.1e-09 ***
## W            0.16405    0.01997   8.216  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 632.79  on 172  degrees of freedom
## Residual deviance: 567.88  on 171  degrees of freedom
## AIC: 927.18
##
## Number of Fisher Scoring iterations: 6
```

```
exp(m1_fit$coefficients)
```

```
## (Intercept)           W
##  0.03670812  1.17826744
```

The expected number of satellites (Sa) given carapace width (W) = 0 is 0.037. With every unit increase in W, the expected number of Sa has multiplicative effect of 1.178 on $\mu = E(Y)$.

```
# Goodness of fit
G = sum(residuals(m1_fit, type = "pearson") ^ 2)
G
```

```
## [1] 544.157
```

```
1 - pchisq(G, m1_fit$df.residual)
```

```
## [1] 0
```

Thus, we reject the null, which indicates that the model does not have a good fit.

(b)

Now, I will fit a Poisson model (M2) with log link with carapace width (W) and weight (Wt) as predictors.

```
# M2: W and Wt as predictors
m2_fit <- glm(Sa ~ W + Wt, family = poisson(link = "log"), data = df_crab)
summary(m2_fit)
```

```
##
## Call:
## glm(formula = Sa ~ W + Wt, family = poisson(link = "log"), data = df_crab)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.29168    0.89929  -1.436  0.15091
## W            0.04590    0.04677   0.981  0.32640
## Wt           0.44744    0.15864   2.820  0.00479 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 632.79  on 172  degrees of freedom
## Residual deviance: 559.89  on 170  degrees of freedom
## AIC: 921.18
##
## Number of Fisher Scoring iterations: 6
```

```
exp(m2_fit$coefficients)
```

```
## (Intercept)           W          Wt
##    0.274809    1.046968    1.564296
```

The expected number of Sa given W = 0 and Wt = 0 is 0.275. All else being equal, with every unit increase in W, the expected number of Sa has multiplicative effect of 1.047 on $\mu = E(Y)$. Similarly, holding other

variables constant, with every unit increase in Wt, the expected number of Sa has multiplicative effect of 1.564 on $\mu = E(Y)$.

M1 is nested within M2, so I will perform ANOVA to compare the two models.

```
# compare with M1
anova(m1_fit, m2_fit)
```

```
## Analysis of Deviance Table
##
## Model 1: Sa ~ W
## Model 2: Sa ~ W + Wt
##   Resid. Df Resid. Dev Df Deviance
## 1       171     567.88
## 2       170     559.89  1   7.9934
```

The residual deviance appears to be reduced in M2 compared to M1, indicating that M2 has a better fit by adding Wt as a predictor. We need to note that the coefficient in W in M2 is not statistically significant unlike M1.

(c)

```
# over-dispersion in M2
# calculate dispersion parameter
G.stat = sum(residuals(m2_fit, type = 'pearson', data = df_crab) ^ 2) # pearson chisq
G.stat
```

```
## [1] 536.5963
```

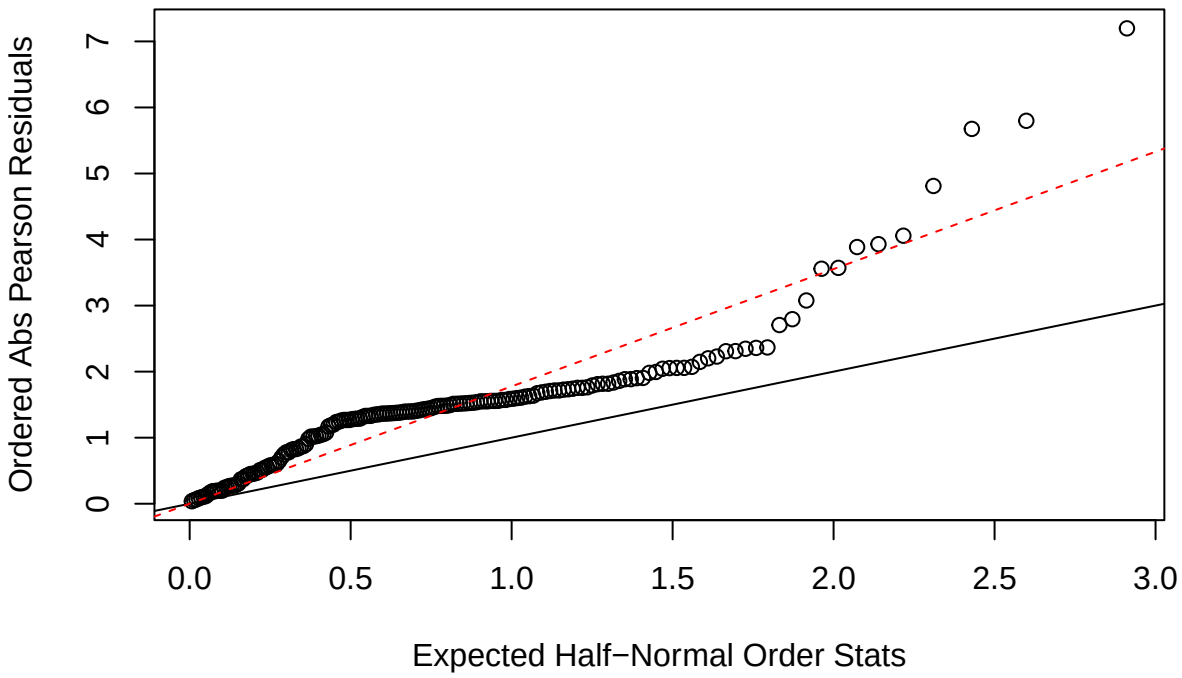
```
phi = G.stat / m2_fit$df.residual
phi
```

```
## [1] 3.156449
```

```
tilde.phi = m2_fit$deviance / m2_fit$df.residual
tilde.phi
```

```
## [1] 3.293442
```

```
# test over-dispersion (half normal plot)
res = residuals(m2_fit, type = 'pearson')
plot(qnorm((173 + 1: 173 + 0.5)/(2 * 173 + 1.125)), sort(abs(res)), xlab = 'Expected Half-Normal Order S
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 of the data exceeds the μ assumed by the model.
Hence, we can say that there is over-dispersion in the original model.
The estimate of dispersion parameter: $\hat{\phi} = 3.16$

```
# adjust for over-dispersion
summary(m2_fit, dispersion = phi)
```

```
##
## Call:
## glm(formula = Sa ~ W + Wt, family = poisson(link = "log"), data = df_crab)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.29168    1.59771  -0.808    0.419
## W            0.04590    0.08309   0.552    0.581
## Wt           0.44744    0.28184   1.588    0.112
##
## (Dispersion parameter for poisson family taken to be 3.156449)
##
##     Null deviance: 632.79  on 172  degrees of freedom
## Residual deviance: 559.89  on 170  degrees of freedom
## AIC: 921.18
##
## Number of Fisher Scoring iterations: 6
```

After adjusting for over-dispersion, The coefficient values remain the same. However, the standard errors of each variable differ from the unadjusted model. Now, all coefficients are not statistically significant.

2

a

I will fit a Poisson model with log link with area, year, and leangth of the fish as predictors. Area and Year are treated as categorical variables.

```
# Poisson model with log link
poi_fit <- glm(Intensity ~ factor(Area) + factor(Year) + Length, family = poisson(link = "log"), data =
summary(poi_fit)
```

```
##
## Call:
## glm(formula = Intensity ~ factor(Area) + factor(Year) + Length,
##     family = poisson(link = "log"), data = df_para)
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)        2.6431709  0.0542838  48.692  < 2e-16 ***
## factor(Area)2     -0.2119557  0.0491691  -4.311 1.63e-05 ***
## factor(Area)3     -0.1168602  0.0428296  -2.728  0.00636 **
## factor(Area)4      1.4049366  0.0356625  39.395  < 2e-16 ***
## factor(Year)2000   0.6702801  0.0279823  23.954  < 2e-16 ***
## factor(Year)2001  -0.2181393  0.0287535  -7.587 3.29e-14 ***
## Length            -0.0284228  0.0008809 -32.265  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 25797  on 1190  degrees of freedom
## Residual deviance: 19153  on 1184  degrees of freedom
##   (63 observations deleted due to missingness)
## AIC: 21089
##
## Number of Fisher Scoring iterations: 7
```

```
exp(poi_fit$coefficients)
```

```
##      (Intercept)    factor(Area)2    factor(Area)3    factor(Area)4
##       14.0577088        0.8090006        0.8897096        4.0752685
## factor(Year)2000 factor(Year)2001           Length
##        1.9547848        0.8040134        0.9719773
```

The expected number of parasites given Area = 1, Year = 1999, and Length = 0 is 14.058. All else being equal, the expected number of parasites has multiplicative effect of 0.809 on $\mu = E(Y)$ when Area = 2; 0.89 when Area = 3; 4.075 when Area = 4. Similarly, holding other variables constant, the expected number of parasites has multiplicative effect of 1.955 on $\mu = E(Y)$ when Year = 2000; 0.804 when Year = 2001. Finally, with every unit increase in Length, the expected number of parasites has multiplicative effect of 0.972 on $\mu = E(Y)$ with other predictors unchanged.

b

```
# Goodness of fit
G = sum(residuals(poi_fit, type = "pearson") ^ 2)
G
```

```
## [1] 42164.97
```

```
1 - pchisq(G, poi_fit$df.residual)
```

```
## [1] 0
```

Given the chi-squared goodness of fit statistic and its p-value, we reject the null and conclude that the model does not have a good fit.

c

```
# check zero-inflation
check_zeroinflation(poi_fit)
```

```
## # Check for zero-inflation
##
##    Observed zeros: 651
##   Predicted zeros: 84
##             Ratio: 0.13
```

I will refit the model using the same predictors accounting for the zero-inflation issue.

```
# fit zero-inflated poisson model
zip_fit <- zeroinfl(Intensity ~ factor(Area) + factor(Year) + Length, data = df_para) # child and campe
summary(zip_fit)
```

```
##
## Call:
## zeroinfl(formula = Intensity ~ factor(Area) + factor(Year) + Length,
##     data = df_para)
##
## Pearson residuals:
##     Min      1Q  Median      3Q     Max
## -2.1278 -0.8265 -0.5829 -0.1821 25.4837
##
## Count model coefficients (poisson with log link):
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)        3.8431714  0.0583793  65.831  < 2e-16 ***
## factor(Area)2      0.2687835  0.0500467   5.371 7.85e-08 ***
## factor(Area)3      0.1463173  0.0439485   3.329 0.000871 ***
## factor(Area)4      0.9448068  0.0368342  25.650  < 2e-16 ***
## factor(Year)2000   0.3919831  0.0282952  13.853  < 2e-16 ***
```

```
## factor(Year)2001 -0.0448455  0.0296057  -1.515 0.129833
## Length           -0.0368067  0.0009747 -37.762  < 2e-16 ***
##
## Zero-inflation model coefficients (binomial with logit link):
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)       0.552585   0.275762   2.004  0.04509 *
## factor(Area)2     0.718676   0.189552   3.791  0.00015 ***
## factor(Area)3     0.657708   0.167402   3.929 8.53e-05 ***
## factor(Area)4    -1.022868   0.188201  -5.435 5.48e-08 ***
## factor(Year)2000 -0.752119   0.172965  -4.348 1.37e-05 ***
## factor(Year)2001  0.456535   0.143962   3.171  0.00152 **
## Length           -0.009889   0.004629  -2.136  0.03266 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of iterations in BFGS optimization: 22
## Log-likelihood: -6950 on 14 Df
```

```
exp(coef(zip_fit))
```

```
##      count_(Intercept)    count_factor(Area)2    count_factor(Area)3
##              46.6732618              1.3083718              1.1575634
##    count_factor(Area)4 count_factor(Year)2000 count_factor(Year)2001
##              2.5723163              1.4799127              0.9561452
##           count_Length       zero_(Intercept)     zero_factor(Area)2
##              0.9638624              1.7377394              2.0517145
##     zero_factor(Area)3     zero_factor(Area)4  zero_factor(Year)2000
##              1.9303630              0.3595621              0.4713669
##  zero_factor(Year)2001            zero_Length
##              1.5785947              0.9901598
```

All of the predictors in both the count and zero-inflation model are statistically significant except Year = 2001 in count model.

The zero-inflation model tells us that the baseline odds of being fish that are not susceptible to parasites (Intensity = 0) is 1.738. Area 2, 3 (versus Area 1), and Year 2001 (versus 1999) increase the odds of being fish that are susceptible to parasites (Intensity $\neq$ 0) by 2.052, 1.93, 1.579 accordingly.
The odds is decreased by one unit increase in Length by 0.99, Area 4 by 0.36, and Year 2000 by 0.471.

The count model indicates that the baseline number of parasite is 46.673 among fish with more than one parasites. Area 2, 3, 4 (versus Area 1), and 2000 (versus 1999) increase the number of parasites by 1.308, 1.158, 2.572, 1.48 times accordingly. Year 2001 and one unit increase in Length decrease Intensity by 0.956 and 0.964 times (Year 2001 is insignificant).