P8131_hw5_xy2395

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Problem 1

```
crab_df =
  read.table("./hw5/HW5-crab.txt", header = TRUE) %>%
  as.tibble()
```

(1-a)

Model 1 : Sa ~ W

```
fit1 = glm(Sa ~ W, family = poisson, data = crab_df)

# Calculate Pearson statistic
G = sum(residuals(fit1, type = 'deviance')^2); G
```

```
## [1] 567.8786
```

```
1 - pchisq(G, df = fit1$df.residual) # df = 171
```

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

The p-value is lower than 0.05, indicating the deviance from the full model is too large, so the fit is not good.

```
fit1 %>%
  broom::tidy() %>%
  mutate(exp_estimate = exp(estimate)) %>%
  select(term, estimate, exp_estimate, p.value) %>%
  knitr::kable()
```

term	estimate	exp_estimate	p.value
(Intercept)	-3.3047572	0.0367081	0
W	0.1640451	1.1782674	0

Interpretation: The estimated coefficient of W (carapace width) is 0.164. exp(0.164) = 1.18. This means the number of satellites is estimated to increase 1.18 folds with one-unit increase in carapace width.

(1-b)

Model 2: Sa ~ W + Wt

```
fit2 = glm(Sa ~ W + Wt, family = poisson, data = crab_df)

fit2 %>%
  broom::tidy() %>%
  mutate(exp_estimate = exp(estimate)) %>%
  select(term, estimate, exp_estimate, p.value) %>%
  knitr::kable()
```

term	estimate	exp_estimate	p.value
(Intercept)	-1.2916790	0.274809	0.1509076
W	0.0458980	1.046968	0.3264035
Wt	0.4474357	1.564296	0.0047949

```
# Deviance analysis
test.stat = fit1$deviance - fit2$deviance; test.stat
```

```
## [1] 7.993392
```

```
df = fit1$df.residual - fit2$df.residual
1 - pchisq(test.stat, df = df) # df = 1
```

```
## [1] 0.004694838
```

Deviance analysis was conducted to compare the two models. The p-value is smaller than 0.05, so we reject the null hypothesis and conclude that the larger model (M2) is superior to the smaller model (M1).

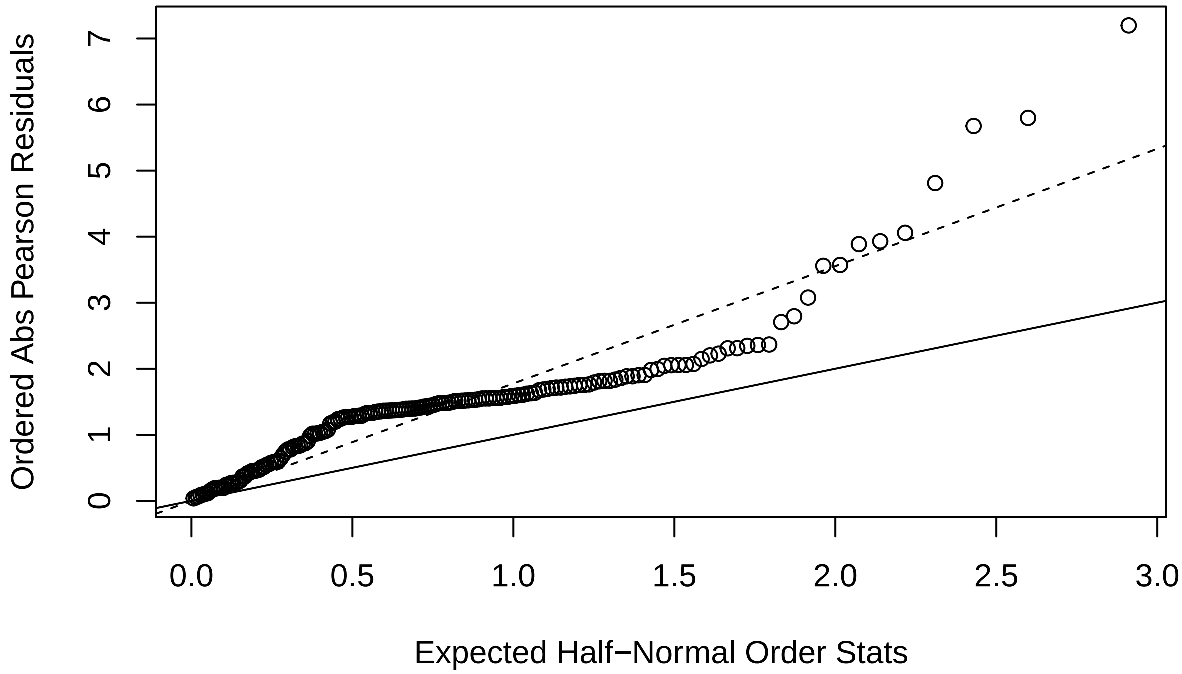
(1-c)

Check Over Dispersion.

```
resid = residuals(fit2, type = 'pearson')
phi = sum(resid^2) / fit2$df.residual
phi
```

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

```
n = fit2$df.null + 1
plot(qnorm((n + 1:n + 0.5)/(2*n + 1.125)), sort(abs(resid)),
     xlab = 'Expected Half-Normal Order Stats',
     ylab = 'Ordered Abs Pearson Residuals')
abline(a = 0, b = 1)
abline(a = 0, b = sqrt(phi), lty = 2)
```



```
summary(fit2, dispersion = phi)$coef %>%
  broom::tidy() %>%
  mutate(exp_estimate = exp(Estimate)) %>%
  select(.rownames, Estimate, exp_estimate) %>%
  knitr::kable()
```

.rownames	Estimate	exp_estimate
(Intercept)	-1.2916790	0.274809
W	0.0458980	1.046968
Wt	0.4474357	1.564296

As shown in the plot, there is over-dispersion in Model 2.

Interpretation: The number of satellites is estimated to increase to 1.05 folds with one-unit increase in female crab's carapace width. The number of satellites is estimated to increase 1.56 folds with one-unit increase in female crab's weight.

Problem 2

```
parasite_df =
  read.table("./hw5/HW5-parasite.txt", header = TRUE) %>%
  as.tibble() %>%
  select(Sample, Intensity, Year, Length, Area) %>%
  janitor::clean_names() %>%
  mutate(year = as.factor(year),
         area = as.factor(area))
head(parasite_df)
levels(parasite_df$year)
levels(parasite_df$area)
```

```
## # A tibble: 6 x 5
##   sample intensity year  length area 
##    <int>     <int> <fct>  <int> <fct>
## 1      1         0 1999      26 2    
## 2      2         0 1999      26 2    
## 3      3         0 1999      27 2    
## 4      4         0 1999      26 2    
## 5      5         0 1999      17 2    
## 6      6         0 1999      20 2
```

```
## [1] "1999" "2000" "2001"
```

```
## [1] "1" "2" "3" "4"
```

(2-a)

```r
fit_fish1 = glm(intensity ~ area + year + length, family = poisson, data = parasite_df)
fit_fish1 %>% 
  broom::tidy() %>% 
  mutate(exp_estimate = exp(estimate)) %>% 
  knitr::kable(digits = 3)
```

term	estimate	std.error	statistic	p.value	exp_estimate
(Intercept)	2.643	0.054	48.692	0.000	14.058
area2	-0.212	0.049	-4.311	0.000	0.809
area3	-0.117	0.043	-2.728	0.006	0.890
area4	1.405	0.036	39.395	0.000	4.075
year2000	0.670	0.028	23.954	0.000	1.955
year2001	-0.218	0.029	-7.587	0.000	0.804
length	-0.028	0.001	-32.265	0.000	0.972

Interpretation

Adjusting for other variables, the number of parasites in Area 2 is estimated to be 0.809 times the number in Area 1. The number of parasites in Area 3 is estimated to be 0.890 times the number in Area 1. The number of parasites in Area 4 is estimated to be 4.075 times the number in Area 1.

Adjusting for other variables, the number of parasites in year 2000 is 1.955 times the number in 1999. The number of parasites in year 2001 is 0.804 times the number in 1999.

The number of parasites changes 0.972 fold with one-unit increase in length of the fish, holding other variables constant.

(2-b)

```r
G = sum(residuals(fit_fish1, type = 'pearson')^2)
1 - pchisq(G, df = fit_fish1$df.residual)
```

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

The p-value is smaller than 0.05 and we conclude that the fit is not good.

(2-c)

```r
fit_zip = zeroinfl(intensity ~ area + year + length | area + year + length, data = parasite_df)
```

Zero-inflation model coefficients

```r
summary(fit_zip)$coefficients$zero %>%
  broom::tidy() %>%
  mutate(exp_estimate = exp(Estimate)) %>%
  select(.rownames, Estimate, exp_estimate) %>%
  knitr::kable(digits = 3)
```

.rownames	Estimate	exp_estimate
(Intercept)	0.553	1.738
area2	0.719	2.052
area3	0.658	1.930
area4	-1.023	0.360
year2000	-0.752	0.471
year2001	0.457	1.579
length	-0.010	0.990

Interpretation

The areas 2 - 4 have different odds of parasite-susceptible fish than Area 1. Area 2 has 2.052 times the odds of susceptible fish than Area 1. Area 3 has 1.93 times the odds of susceptible fish than Area 1. Area 4 has 0.36 times the odds of susceptible fish than Area 1.

The odds of parasite-susceptible fish in 2000 and 2001 differ from that in 1999. The odds of susceptible fish in 2000 is 0.471 times the odds in 1999. The odds of susceptible fish in 2001 is 1.579 times the odds in 1999.

The odds of parasite-susceptiblity changes 0.99 fold with one-unit increase in length of fish. (i.e. The longer the fish, the less susceptible to parasites.

Count model coefficients

```r
summary(fit_zip)$coefficients$count %>%
  broom::tidy() %>%
  mutate(exp_estimate = exp(Estimate)) %>%
  select(.rownames, Estimate, exp_estimate) %>%
  knitr::kable(digits = 3)
```

.rownames	Estimate	exp_estimate
(Intercept)	3.843	46.673
area2	0.269	1.308
area3	0.146	1.158
area4	0.945	2.572
year2000	0.392	1.480
year2001	-0.045	0.956
length	-0.037	0.964

Interpretation

Adjusting for other variables, the number of parasites in Area 2 is estimated to be 1.308 times the number in Area 1. The number of parasites in Area 3 is estimated to be 1.158 times the number in Area 1. The number of parasites in Area 4 is estimated to be 2.572 times the number in Area 1.

Adjusting for other variables, the number of parasites in year 2000 is 1.480 times the number in 1999. The number of parasites in year 2001 is 0.956 times the number in 1999.

The number of parasites changes 0.964 fold with one-unit increase in length of the fish, holding other variables constant.