

Lec21_2

2

```
library(dplyr)
```

```
##  
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':  
##  
## filter, lag
```

```
## The following objects are masked from 'package:base':  
##  
## intersect, setdiff, setequal, union
```

```
library(mcpprofile)
```

```
## Loading required package: ggplot2
```

a.

```
bird <- read.csv("bird.csv")  
bird$Degradation <- factor(bird$Degradation, levels = levels(bird$Degradation[c(3, 1, 2)]))  
bfit <- glm(Count ~ ., family = poisson(link = "log"), data = bird)  
summary(bfit)$deviance # Residual deviance
```

```
## [1] 78.11879
```

```
summary(bfit)$df[2] # Residual degrees of freedom
```

```
## [1] 12
```

b.

```
bfit2 <- glm(Count ~ .*., family = poisson(link = "log"), data = bird) # Saturated model  
anova(bfit, bfit2, test = "LR")
```

```
## Analysis of Deviance Table  
##  
## Model 1: Count ~ Guild + Degradation  
## Model 2: Count ~ (Guild + Degradation) * (Guild + Degradation)  
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)  
## 1         12      78.119  
## 2          0       0.000 12   78.119 9.417e-12 ***  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

LR test:

H0: all parameters of interaction terms are 0, Ha: at least one parameter of interaction terms are not 0

P-value = 9.417e-12

Reject H0 and conclude that 'Guild' and 'Degradation' are associated.

c.

```
# look at coefficients to see the position of each  
coef(bfit2)
```



```

# Similar to the last part
# By doing algebra on the log scale, ratio of mean ratios can be represented by coefficients
# Make coefficient matrix
krr <- matrix(c(0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, -1, 0, 0, 0, 0, 0, 0,
               0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, -1, 0, 0, 0, 0, 0, 0,
               0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, -1, 0, 0, 0, 0, 0, 0,
               0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, -1, 0, 0, 0, 0, 0, 0,
               0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, -1, 0, 0, 0, 0, 0, 0,
               0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, -1, 0, 0, 0, 0, 0, 0), nrow = 6, byrow = TRUE)
rr.est <- mcprofile(bfit2, krr)
table.rr <- exp(confint(rr.est))

table.rr$estimate %>% unlist() -> d
table.rr$confint %>% unlist() -> dd
op.rr <- data.frame(Ratio = d, lower = dd[1:6], upper = dd[7:12])
op.rr <- `rownames<-`(op.rr, c("Wood vs Fruit", "Wood vs Ground", "Wood vs Leaf", "Wood vs Nectar", "Wood vs
Seeds", "Wood vs Air"))
op.rr

```

##	Ratio	lower	upper
## Wood vs Fruit	0.03200000	0.002922659	0.1585807
## Wood vs Ground	0.18400000	0.017814509	0.8049141
## Wood vs Leaf	0.07594203	0.007523628	0.3112642
## Wood vs Nectar	0.07600000	0.007575377	0.3063901
## Wood vs Seeds	0.10857143	0.009298463	0.6572132
## Wood vs Air	0.24000000	0.021455071	1.3246449

ii.

All estimated odds ratios are smaller than 1, which says comparing to all others Wood-Arth guild group experiences higher abundance reduction in high vs low degradation. However Wood vs Air ratio has CI with upper limit bigger than 1, so in Wood guild the reduction effect can potentially be smaller than or same as in Air guild.