### R15 - Interactions in Logistic and Poisson Regression

HCI/PSYCH 522 Iowa State University

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#### Interactions

#### Independent variables

- Categorical-continuous
- Categorical-categorical
- Continuous-continuous (not discussed)

#### Generalized linear models

- Poisson regression
- Logistic regression

#### Poisson regression

Poisson regression with two (continuous) independent variables:

Data model

$$Y_i \stackrel{ind}{\sim} Po(\lambda_i)$$

Main effects model

$$\log(\lambda_i) = \beta_0 + \beta_1 X_{i,1} + \beta_2 X_{i,2}$$

Interaction model

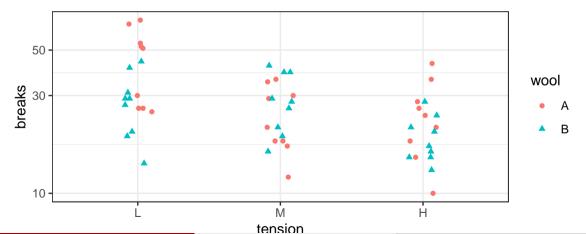
$$\log(\lambda_i) = \beta_0 + \beta_1 X_{i,1} + \beta_2 X_{i,2} + \beta_3 X_{i,1} X_{i,2}$$

The interaction occurs on the log scale.

### Warpbreaks - Descriptive Statistics

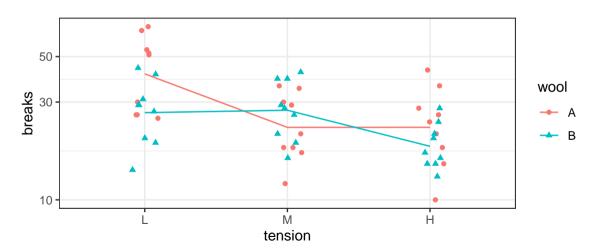
```
head(warpbreaks)
    breaks wool tension
## 1
        54 A
        25 A
        70 A
## 5
## 6
summary(warpbreaks)
       breaks
                   Loom
                         tension
   Min. :10.00
                  A:27
                         L:18
    1st Qu.:18.25
                  B:27
                         M:18
   Median :26.00
                         H:18
    Mean :28.15
    3rd Qu.:34.00
   Max. :70.00
```

### Warpbreaks - Graphical Statistics



# Warpbreaks - Graphical Statistics

```
g + stat_summary(fun = mean, geom = "line")
```



### Warpbreaks - Poisson Regression Models

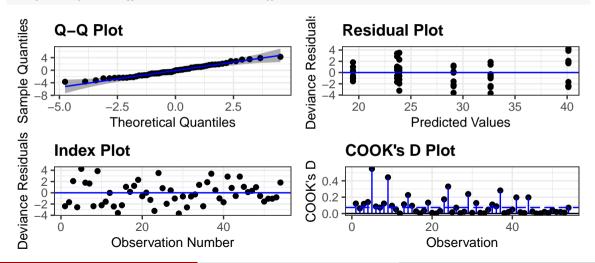
```
mM <- glm(breaks "wool * tension, data = warpbreaks, family = poisson) # Main effects model
mI <- glm(breaks "wool * tension, data = warpbreaks, family = poisson) # Interaction model

drop1(mI, test="Chi")

## Single term deletions
##
## Model:
## breaks "wool * tension
## Df Deviance AIC LRT Pr(>Chi)
## <-one> 182.31 468.97
## wool:tension 2 210.39 493.06 28.087 7.962e-07 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#### Warpbreaks - Diagnostics

resid\_panel(mM, plots = c("qq", "resid", "index", "cookd"), qqbands = TRUE)

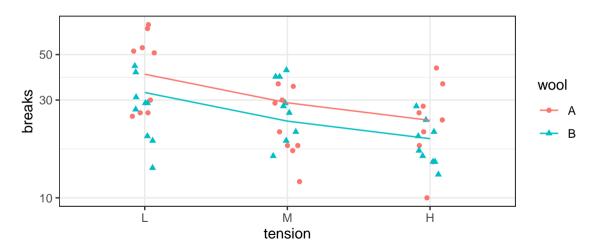


```
summary (mM)
##
## Call:
## glm(formula = breaks ~ wool + tension, family = poisson, data = warpbreaks)
##
## Deviance Residuals:
      Min
                10 Median
                                 30
                                         Max
## -3.6871 -1.6503 -0.4269 1.1902
                                    4.2616
##
## Coefficients:
              Estimate Std. Error z value Pr(>|z|)
## (Intercept) 3.69196
                         0.04541 81.302 < 2e-16 ***
## woolB
              -0.20599
                         0.05157 -3.994 6.49e-05 ***
## tensionM -0.32132
                         0.06027 -5.332 9.73e-08 ***
## tensionH
            -0.51849
                          0.06396 -8.107 5.21e-16 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for poisson family taken to be 1)
##
      Null deviance: 297.37 on 53 degrees of freedom
## Residual deviance: 210.39 on 50 degrees of freedom
## AIC: 493.06
##
## Number of Fisher Scoring iterations: 4
```

```
em <- emmeans(mM, pairwise ~ wool)
cm <- confint(em. type = "unlink"): cm
## $emmeans
   wool rate SE df asymp.LCL asymp.UCL
        30.3 1.061 Inf
                           28.3
                                     32.5
        24.7 0.955 Inf
                           22.9
                                     26.6
##
## Results are averaged over the levels of: tension
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
## $contrasts
   contrast ratio SE df asymp.LCL asymp.UCL
   A / B
          1.23 0.0634 Inf 1.11 1.36
## Results are averaged over the levels of: tension
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
```

```
et <- emmeans(mM, pairwise ~ tension)
ct <- confint(et. type = "unlink"): ct
## $emmeans
   tension rate SE df asymp.LCL asymp.UCL
           36.2 1.42 Inf
                              33.5
                                       39.1
           26.2 1.21 Inf
                              24.0
                                        28.7
           21.6 1.09 Inf
                          19.5
                                       23.8
##
## Results are averaged over the levels of: wool
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
## $contrasts
   contrast ratio
                      SE df asymp.LCL asymp.UCL
   L / M
            1.38 0.0831 Inf
                                 1.20
                                           1.59
   I. / H
           1.68 0.1074 Inf
                                 1.45
                                           1.95
   M / H
           1.22 0.0832 Inf
                              1.04
                                           1.43
## Results are averaged over the levels of: wool
## Confidence level used: 0.95
## Conf-level adjustment: tukey method for comparing a family of 3 estimates
## Intervals are back-transformed from the log scale
```

```
g + geom_line(mapping=aes(y=predict(mM, warpbreaks, type = "response")))
```



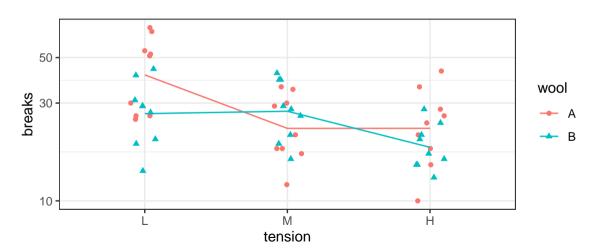
```
summary(mI)
##
## Call:
## glm(formula = breaks ~ wool * tension, family = poisson, data = warpbreaks)
## Deviance Residuals:
      Min
                10 Median
                                         Max
  -3.3383 -1.4844 -0.1291 1.1725 3.5153
## Coefficients:
                 Estimate Std. Error z value Pr(>|z|)
## (Intercept) 3.79674
                            0.04994 76.030 < 2e-16 ***
## woolB
                -0.45663
                            0.08019 -5.694 1.24e-08 ***
## tensionM
              -0.61868
                            0.08440 -7.330 2.30e-13 ***
            -0.59580
                            0.08378 -7.112 1.15e-12 ***
## tensionH
## woolR:tensionM 0 63818
                            0.12215
                                     5 224 1 75e-07 ***
## woolB:tensionH 0.18836
                            0.12990
                                     1.450
                                               0.147
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
      Null deviance: 297.37 on 53 degrees of freedom
## Residual deviance: 182.31 on 48 degrees of freedom
## AIC: 468.97
## Number of Fisher Scoring iterations: 4
```

```
em <- emmeans(mI, pairwise ~ wool | tension)
cm <- confint(em, type = "unlink"); cm$emmeans</pre>
## tension = L:
   wool rate SE df asymp.LCL asymp.UCL
        44.6 2.22 Inf
                          40.4
                                 49.1
        28.2 1.77 Inf
                           25.0
                                    31.9
## tension = M:
   wool rate SE df asymp.LCL asymp.UCL
        24.0 1.63 Inf
                           21.0
                                    27.4
        28.8 1.79 Inf
                           25.5
                                    32.5
## tension = H:
   wool rate SE df asymp.LCL asymp.UCL
        24.6 1.65 Inf
                           21.5
                                     28.0
        18.8 1.44 Inf
                      16.1
                                    21.8
## Confidence level used: 0.95
## Intervals are back-transformed from the log scale
```

cm\$contrasts

```
et <- emmeans(mI, pairwise ~ tension | wool)
ct <- confint(et, type = "unlink"): ct$contrasts
## wool = A:
                      SE df asymp.LCL asymp.UCL
   contrast ratio
   L / M
           1.856 0.1567 Inf
                                 1.523
                                           2.26
   I. / H
           1.814 0.1520 Inf
                              1.491
                                           2.21
   M / H
            0.977 0.0935 Inf
                                 0.781
                                           1.22
##
## wool = B:
   contrast ratio
                      SE df asymp.LCL asymp.UCL
   L / M
            0.981 0.0866 Inf
                                 0.797
                                           1.21
   L / H
           1.503 0.1492 Inf
                              1.191
                                           1.90
   M / H
           1.533 0.1515 Inf
                              1.216
                                           1.93
## Confidence level used: 0.95
## Conf-level adjustment: tukev method for comparing a family of 3 estimates
## Intervals are back-transformed from the log scale
```

```
g + stat_summary(fun = mean, geom = "line")
```



#### Logistic regression

Logistic regression with two (continuous) independent varibles.

Data model

$$Y_g \stackrel{ind}{\sim} Bin(n_g, \theta_g)$$

Main effects model

$$\log\left(\frac{\theta_g}{1-\theta_g}\right) = \beta_0 + \beta_1 X_{g,1} + \beta_2 X_{g,2}$$

Interaction model

$$\log\left(\frac{\theta_g}{1 - \theta_g}\right) = \beta_0 + \beta_1 X_{g,1} + \beta_2 X_{g,2} + \beta_3 X_{g,1} X_{g,2}$$

The interaction occurs on the log-odds scale.

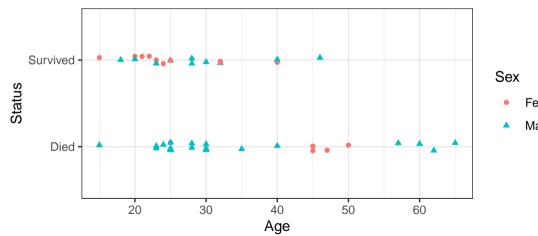
# Donner Party - Descriptive Statistics

```
Age
           Sex
                Status
     23
          Male
                  Died
    40 Female Survived
          Male Survived
         Male
                  Died
## 5
         Male
                  Died
## 6 40
         Male
                  Died
summary(case2001)
                     Sex
                                  Status
        Age
   Min. :15.0 Female:15
                             Died
                                     :25
   1st Qu.:24.0
                 Male :30
                             Survived:20
   Median:28.0
   Mean :31.8
   3rd Qu.:40.0
   Max. :65.0
```

head(case2001)

# Donner Party - Graphical Statistics

```
g <- ggplot(case2001, aes(x = Age, y = Status, color = Sex, shape = Sex)) +
  geom_jitter(width=0, height = 0.05)
```



- Female
- Male

# Donner Party - Logistic Regression Models

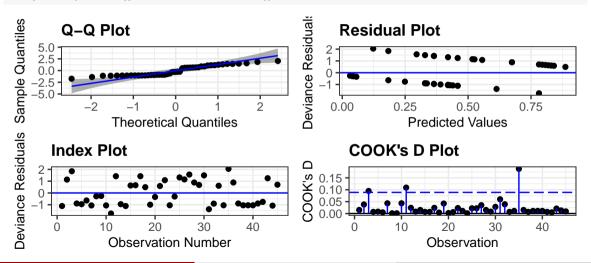
```
mM <- glm(Status == "Survived" ~ Sex + Age, data = case2001, family = binomial) # Main effects model
mI <- glm(Status == "Survived" ~ Sex * Age, data = case2001, family = binomial) # Interaction model

drop1(mI, test="Chi")

## Single term deletions
##
## Model:
## Status == "Survived" ~ Sex * Age
## Df Deviance AIC LRT Pr(>Chi)
## <none> 47.346 55.346
## Sex:Age 1 51.256 57.256 3.9099 0.048 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#### Donner Party - Diagnostics

resid\_panel(mM, plots = c("qq", "resid", "index", "cookd"), qqbands = TRUE)



```
summary (mM)
##
## Call:
## glm(formula = Status == "Survived" ~ Sex + Age, family = binomial,
      data = case2001)
## Deviance Residuals:
      Min
              10 Median
                                        Max
  -1.7445 -1.0441 -0.3029 0.8877 2.0472
## Coefficients:
             Estimate Std. Error z value Pr(>|z|)
## (Intercept) 3.23041
                                  2.329
                         1.38686
                                         0.0198 *
## SexMale -1.59729
                         0.75547 -2.114 0.0345 *
## Age
       -0.07820
                         0.03728 -2.097 0.0359 *
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
      Null deviance: 61.827 on 44 degrees of freedom
## Residual deviance: 51.256 on 42 degrees of freedom
## AIC: 57.256
##
## Number of Fisher Scoring iterations: 4
```

```
em <- emmeans(mM, pairwise ~ Sex | Age, at = list(Age = c(15,28,65)))
cm <- confint(em, type = "unlink"): cm$emmeans
## Age = 15:
## Sex
          response SE df asymp.LCL asymp.UCL
   Female 0.8867 0.0918 Inf 0.56620
                                           0.979
   Male
            0.6130 0.1484 Inf 0.31742
                                           0.844
##
## Age = 28:
   Sex
          response
                      SE df asymp.LCL asymp.UCL
            0.7390 0.1217 Inf 0.45129
                                           0.907
   Female
   Male
            0.3643 0.0949 Inf 0.20429
                                           0.561
##
## Age = 65:
   Sex
          response
                       SE df asymp.LCL asymp.UCL
   Female
            0.1355 0.1539 Inf
                             0.01181
                                           0.673
   Male
            0.0308 0.0433 Inf 0.00185
                                           0.353
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
```

cm\$contrasts

```
## Age = 15:
## contrast odds.ratio SE df asymp.LCL asymp.UCL
## Female / Male 4.94 3.73 Inf 1.12 21.7

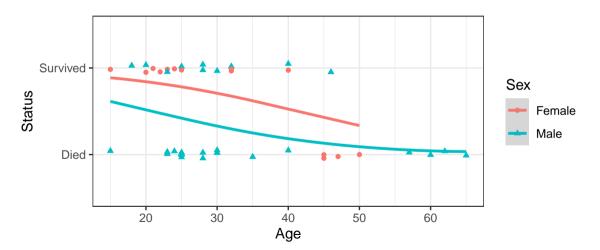
## ## Age = 28:
## contrast odds.ratio SE df asymp.LCL asymp.UCL
## Female / Male 4.94 3.73 Inf 1.12 21.7

## ## Age = 65:
## contrast odds.ratio SE df asymp.LCL asymp.UCL
## Female / Male 4.94 3.73 Inf 1.12 21.7

## ## Confidence level used: 0.95
## Intervals are back-transformed from the log odds ratio scale
```

```
et <- emtrends(mM, pairwise ~ Sex, var = "Age")
ct <- confint(et): ct
## $emtrends
   Sex
          Age.trend SE df asymp.LCL asymp.UCL
   Female -0.0782 0.0373 Inf -0.151 -0.00513
   Male
         -0.0782 0.0373 Inf -0.151 -0.00513
##
## Results are given on the == (not the response) scale.
## Confidence level used: 0.95
## $contrasts
   contrast estimate SE df asymp.LCL asymp.UCL
   Female - Male
                       0 0 Tnf
## Note: contrasts are still on the == scale
## Results are given on the == (not the response) scale.
## Confidence level used: 0.95
```

```
g + geom_smooth(mapping=aes(y=predict(mM, case2001, type="response")+1))
```



```
summary(mI)
## Call:
## glm(formula = Status == "Survived" ~ Sex * Age, family = binomial,
      data = case2001)
## Deviance Residuals:
                10 Median
      Min
                                        Max
## -2.2279 -0.9388 -0.5550
                             0.7794 1.6998
##
## Coefficients:
              Estimate Std. Error z value Pr(>|z|)
## (Intercept) 7.24638
                         3.20517 2.261 0.0238 *
## SexMale -6.92805
                         3.39887 -2.038 0.0415 *
       -0.19407
                         0.08742 -2.220 0.0264 *
## Age
                                 1.714
## SexMale: Age 0.16160
                         0.09426
                                          0.0865 .
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
      Null deviance: 61.827 on 44 degrees of freedom
## Residual deviance: 47.346 on 41 degrees of freedom
## AIC: 55.346
## Number of Fisher Scoring iterations: 5
```

```
em <- emmeans(mI, pairwise ~ Sex | Age, at = list(Age = c(15,28,65)))
cm <- confint(em, type = "unlink"): cm$emmeans
## Age = 15:
## Sex
          response SE df asymp.LCL asymp.UCL
   Female 0.98707 0.0251 Inf 6.19e-01
                                         1.000
   Male
           0.45789 0.1641 Inf 1.88e-01
                                           0.755
##
## Age = 28:
   Sex
          response
                   SE df asymp.LCL asymp.UCL
   Female 0.85964 0.1258 Inf 4.42e-01
                                           0.979
   Male
           0.35640 0.0917 Inf 2.02e-01
                                           0.548
##
## Age = 65:
   Sex
          response
                      SE df asymp.LCL asymp.UCL
   Female 0.00464 0.0125 Inf 2.31e-05
                                           0.484
   Male
           0.14274 0.1582 Inf 1.30e-02
                                           0.677
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
```

cm\$contrasts

```
## Age = 15:
## contrast odds.ratio SE df asymp.LCL asymp.UCL
## Female / Male 90.387 187.410 Inf 1.55e+00 5260.2
##
## Age = 28:
## contrast odds.ratio SE df asymp.LCL asymp.UCL
## Female / Male 11.060 12.352 Inf 1.24e+00 98.7
##
## Age = 65:
## contrast odds.ratio SE df asymp.LCL asymp.UCL
## Female / Male 0.028 0.084 Inf 7.83e-05 10.0
##
## Confidence level used: 0.95
## Thtervals are back-transformed from the log odds ratio scale
```

```
et <- emtrends(mI, pairwise ~ Sex, var = "Age")
ct <- confint(et): ct
## $emtrends
   Sex
         Age.trend SE df asymp.LCL asymp.UCL
   Female -0.1941 0.0874 Inf -0.365 -0.0227
   Male
        -0.0325 0.0353 Inf -0.102
                                       0.0366
##
## Results are given on the == (not the response) scale.
## Confidence level used: 0.95
##
## $contrasts
   contrast estimate SE df asymp.LCL asymp.UCL
   Female - Male -0.162 0.0943 Inf -0.346 0.0232
## Note: contrasts are still on the == scale
## Results are given on the == (not the response) scale.
## Confidence level used: 0.95
```

```
g + geom_smooth(mapping=aes(y=predict(mI, case2001, type="response")+1))
```

